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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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Véronique Lefebvre, Céline Vandecasteele, Melissa Cantet, Stéphane Mallard, Sonia S. Vautrin, et al.. Identifying a candidate gene for the broad-spectrum resistance qtl to *Phytophthora* root rot and blight in pepper. 9. Solanaceae Conference (SOL2012), Aug 2012, Neuchâtel, Switzerland. hal-02746226

HAL Id: hal-02746226

<https://hal.inrae.fr/hal-02746226>

Submitted on 3 Jun 2020

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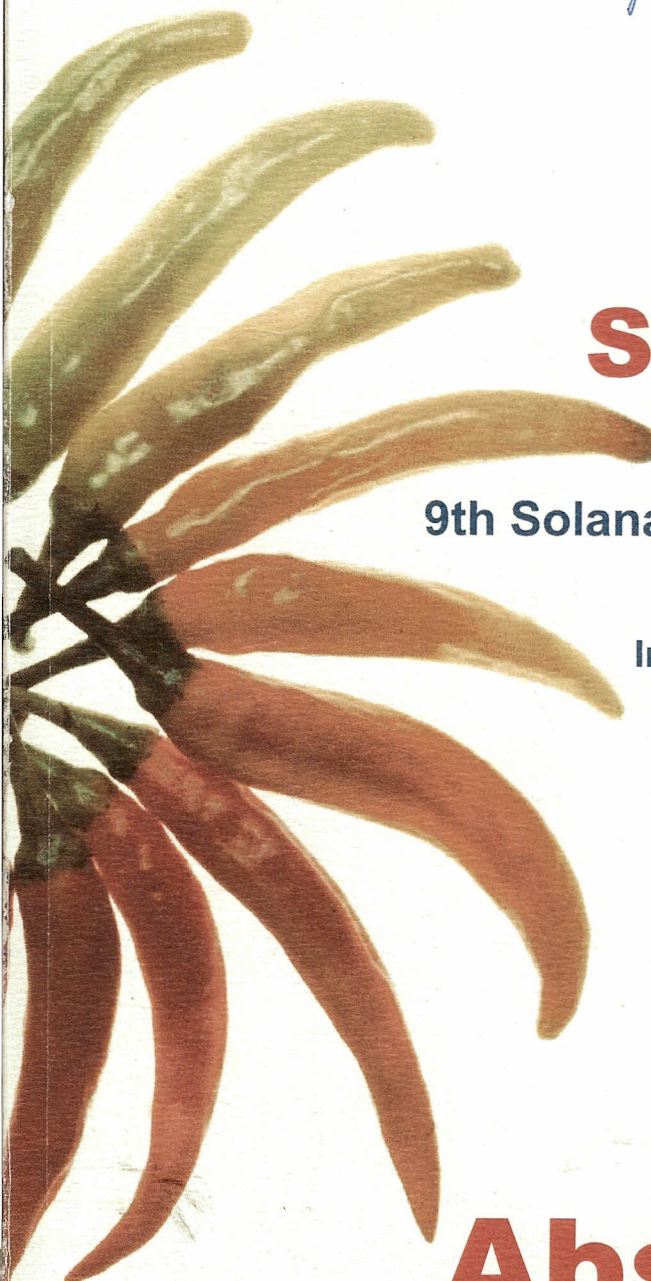
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Veronique Lefebvre



SOL2012

9th Solanaceae Conference
August 26-30, 2012
From the Bench to
Innovative Applications



Abstract
Book

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

Véronique Lefebvre, Céline Vandecasteele, Mélissa Cantet, Stéphanie Mallard, Sonia Vautrin, Abdelhafid Bendahmane and Hélène Bergès

INRA, Montfavet – Avignon, France

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.

Thanks to A. Bachellez, J.P. Bouchet, A. Massire, and C. Troadec. Supports from INRA, Génoplante, ANR, the French Ministry of Agriculture and Fishing (MAAPRAT), and the competitiveness cluster PEIFL.

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