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Stephanie Mallard, Sophie Ewert, Anne Blattes, Véronique Lefebvre. PHY-P5, a major broad-spectrum resistance qtl conferring resistance to Phytophthora in pepper. 6. Solanaceae Genome Workshop, Nov 2009, New Delhi, India. hal-02755733

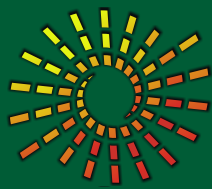
HAL Id: hal-02755733

<https://hal.inrae.fr/hal-02755733>

Submitted on 3 Jun 2020

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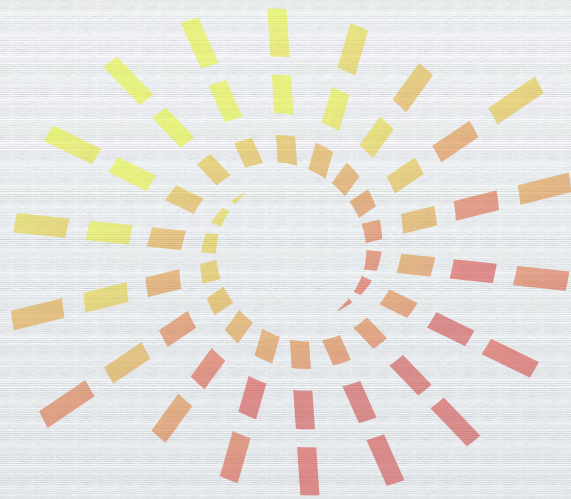
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SOL 2009

The 6th Solanaceae Genome Workshop
8th-13th November, 2009
Le Meridien, New Delhi, India

www.sol2009.org



PHY-P5, A MAJOR BROAD-SPECTRUM RESISTANCE QTL CONFERRING RESISTANCE TO *PHYTOPHTHORA* IN PEPPER

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Blight caused by the pathogen *Phytophthora* spp. (Oomycete) is one of the most damaging diseases of Solanaceae crops. Contrary to monogenic resistances that are easily overcome by virulent strains, polygenic resistances generally confer a durable control of disease severity. Despite the potential importance of polygenic disease resistances, little is known about their molecular bases in plants and the mechanisms of action of the genes controlling them. A major-effect QTL region that confers resistance towards *P. capsici* was detected on pepper chromosome P5 from 5 partially resistant parents and with 11 different isolates. We were not able to determine whether this QTL region, that we called Phy-P5, corresponds to the same QTL in all populations because of the lack of common markers between maps. Moreover, comparative mapping suggested colinearities between Phy-P5 and resistance QTLs to *P. infestans* on potato chromosome IV and on tomato chromosome T4. To determine whether Phy-P5 is a broad-spectrum resistance QTL to *Phytophthora* and to identify candidate genes, we anchored the pepper genomic region harbouring Phy-P5 (i) within the published pepper maps, (ii) with the other members of the Solanaceae family and (iii) with the model plants by developing bridge markers. Up to now, our results showed that Phy-P5 was conserved across 5 genetic backgrounds in pepper and controlled 4 *P. capsici* isolates. We also determined the colinear region of Phy-P5 in tomato, potato and *Arabidopsis* making a step forward the research of functional orthologs of Phy-P5 in those species