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Véronique Lefebvre, Sarah Danan, Patrick Signoret, Jean-Baptiste Veyrieras

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Véronique Lefebvre, Sarah Danan, Patrick Signoret, Jean-Baptiste Veyrieras. QTL meta-analysis for late blight resistance in potato including the two novel resistance sources *Solanum sparsipilum* and *S. spegazzinii*. 6. Solanaceae Genome Workshop, Nov 2009, New Delhi, India. hal-02751899

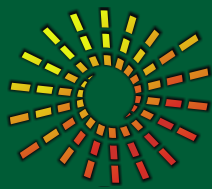
HAL Id: hal-02751899

<https://hal.inrae.fr/hal-02751899v1>

Submitted on 3 Jun 2020

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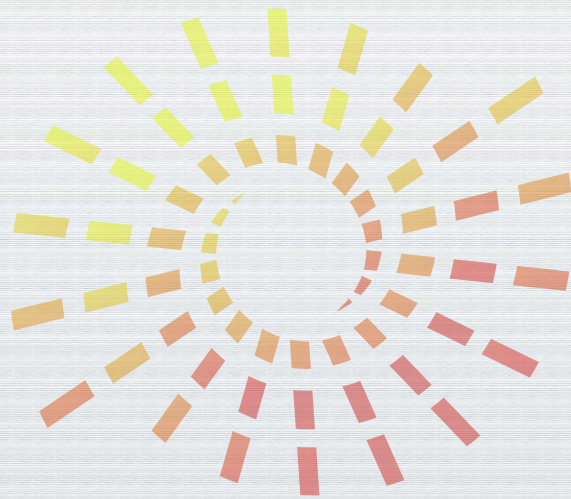
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SOL 2009

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

www.sol2009.org



QTL META-ANALYSIS FOR LATE BLIGHT RESISTANCE IN POTATO INCLUDING THE TWO NOVEL RESISTANCE SOURCES *SOLANUM SPARSIPILUM* AND *S. SPEGAZZINII*

Véronique Lefebvre¹, Sarah Danan¹, Patrick Signoret¹, Jean-Baptiste Veyrieras²

¹INRA, UR 1052 GAFL Génétique et Amélioration des Fruits et Légumes, BP94, 84140 Montfavet, France; ²INRA, UMR UMR 320 Génétique Végétale, Ferme du Moulon, 91190 Gif-sur-Yvette, France.

The resurgence of late blight epidemics in potato (*Solanum tuberosum*) is due to the apparition of new *Phytophthora infestans* strains, resistant to chemicals and overcoming deployed R-genes. The alternative exploitation of polygenic resistance controlled by QTLs requires to inventory resistance sources and to get a better insight of the genetic architecture and diversity of quantitative resistance to late blight in potato. To find out novel resistance sources to late blight in the wild germplasm for potato breeding, we examined the polygenic resistance of *Solanum sparsipilum* and *Solanum spegazzinii* by a QTL analysis (Danan et al., 2009, TAG). The assessment of stem and foliage resistances made possible to identify 30 QTLs including a large-effect QTL region on chromosome X detected in both potato wild species. The mapping of literature-derived anchor markers suggested colinearities with published late blight QTLs or R-genes. We integrated the QTL results in a meta-analysis for late blight resistance in potato together with the data of 19 other published studies. It consisted in constructing a consensus map of potato, on which we projected late blight resistance meta-QTLs. Results highlighted some well-conserved QTLs in the potato related species. The relationships of late blight resistance meta-QTLs with R-genes and maturity QTLs were examined.

[This work was supported by grants from the European BIOEXPLOIT project FOOD CT2005-513959.]

