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Bernard Caromel, Marie-Claire Kerlan, Patricio Castro Quezada, Jawad Aarouf, Helene Berges, Didier Mugniery, Véronique Lefebvre

### ► To cite this version:

Bernard Caromel, Marie-Claire Kerlan, Patricio Castro Quezada, Jawad Aarouf, Helene Berges, et al.. Chromosome landing at a quantitative trait locus involved in resistance to cyst nematode in potato. 4. Annual Meeting; COST 872 workshop, May 2010, Lisbon, Portugal. hal-01462645

**HAL Id: hal-01462645**

**<https://hal.science/hal-01462645>**

Submitted on 3 Jun 2020

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Bernard



## **NEMAGENICS**

Exploiting genomics to understand  
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**Proceedings of the FOURTH Annual  
Meeting**

**Lisbon, Portugal  
24-27 May 2010**

Organised by



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Caromel, Bernard<sup>1</sup>; Kerlan, Marie-Claire<sup>2</sup>; Castro, Patricio<sup>1</sup>; Aarrouf, Jawad<sup>1,3</sup>; Berges, Hélène<sup>4</sup>; Mugniéry, Didier<sup>5</sup> & Lefebvre, Véronique<sup>1</sup>

Bernard.Caromel@avignon.inra.fr

<sup>1</sup>INRA-UR1052, Génétique et d'Amélioration des Fruits et Légumes, BP 94, 84143 Montfavet, France

<sup>2</sup>INRA, Agrocampus Rennes, UMR118, Amélioration des Plantes et Biotechnologies Végétales, 35000 Rennes, France

<sup>3</sup>UAPV, département de Biologie, 33 Louis Pasteur 84000 Avignon cedex 9, France

<sup>4</sup>CNRGV – INRA, Chemin de Borde Rouge, BP 52627, 31326 Castanet Tolosan Cedex, France

<sup>5</sup>Univ Rennes 1, UMR1099 Bio3P (Biology of Organisms and Populations applied to Plant Protection), F-35653 Le Rheu, France

QTL characterization, using a positional cloning approach, is usually done by mendelization of the QTL in a contrasted genetic background. In several outbreed species, QTL mendelization is impossible, due to a high inbreeding depression. The genetic determinism of high level resistances to the cyst nematode *Globodera pallida* is oligogenic in several potato related species. In the past years, we mapped two resistance QTLs originating from *Solanum sparsipilum*. The major effect QTL, *GpaV<sub>spl</sub>*, accounted for 76.6% of the resistance. The minor effect QTL, *GpaXI<sub>spl</sub>*, accounted for 12.7% of the resistance (Caromel *et al.*, 2005, MPMI). Our final goal is to identify the gene underlying the *GpaV<sub>spl</sub>* major effect QTL and the aim of this study was to evaluate whether the molecular characterization of a QTL, using a map-based cloning strategy, was feasible in an outbreed species like potato. We first classified 215 clones of the QTL mapping progeny in four classes, according to their their allelic combination at both QTLs: resistance allele at both QTLs, susceptibility allele at both QTLs, resistance allele at the single major or minor effect QTL. We used the means and the standard deviations to generate 10.000 random cyst numbers for each class and then chose upper and lower thresholds ( $\alpha = 0.001$ ). Thanks to the thresholds and to the knowledge of the allelic form at the low effect *GpaXI<sub>spl</sub>* QTL, we were able to deduce the allelic form at the *GpaV<sub>spl</sub>* major effect QTL, for 10 potato clones with a recombination event in the confidence interval of *GpaV<sub>spl</sub>*. This approach permits us to map *GpaV<sub>spl</sub>* like a major gene and to reduce the *GpaV<sub>spl</sub>* interval to 0.8 cM. Seven markers located in this interval were used for homology search in public databases and for hybridization on the *S. tuberosum* BAC library. Two BACs from *S. demissum* and seven BACs from *S. tuberosum* were identified and physically mapped. The minimum interval of *GpaV<sub>spl</sub>* was estimated to be less than 200 kb. By increasing the progeny size to 1500 to 2000 individuals, we should be able to land to one or two genes.