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Bernard Caromel, Marie-Claire Kerlan, Sarah Danan, Didier Mugniery,  
Véronique Lefebvre

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**Re-evaluation of the *Globodera pallida* resistance QTLs originating from the wild potato species *Solanum spgazzinii*.**

B. Caromel<sup>1</sup>, M.C. Kerlan<sup>2</sup>, S. Danan<sup>1</sup>, D. Mugniéry<sup>3</sup> & V. Lefebvre<sup>1</sup>

1. INRA-UR1052, Génétique et Amélioration des Fruits et Légumes, BP 94, 84143 Montfavet, FRANCE.
2. INRA - Agrocampus Ouest - Univ Rennes 1, UMR118, Amélioration des Plantes et Biotechnologies Végétales, 29260 Ploudaniel, FRANCE.
3. INRA, Agrocampus Rennes, Univ Rennes 1, UMR1099 BiO3P (Biologie des Organismes et des Populations appliquée à la Protection des Plantes), 35653 Le Rheu, FRANCE

Most of the resistances to the cyst nematode *Globodera pallida*, uncovered in the potato gene pool, originate from wild species related to *Solanum tuberosum*. Using the Interval Mapping (IM) method, we mapped, in a previous study, three QTLs (Quantitative Trait Loci) affecting the number of *G. pallida* newly formed cysts, on the *S. spgazzinii* genome (Caromel *et al.* 2003). Using the Composite Interval Mapping (CIM) method and taking into account the root system size, we re-analysed our data and found that i) one of the previously detected minor-effect QTLs was in fact due to its effect on the variation of root size, ii) it exists minor-effect QTLs originating from the cultivated susceptible parent, which had remained undetected with the IM method, and iii) the individual effects of the previously detected QTLs were overestimated. Evaluation of *G. pallida* development in roots of plants carrying different allelic combinations at resistance QTLs allowed us to confirm or infirm the effect of these QTLs on resistance to *G. pallida*. We conclude that a high level of resistance to *G. pallida* could be obtained by introgressing the *GpaV<sub>spg</sub>* major-effect QTL (formerly called *GpaMI*) and the *GpaXII<sub>spg</sub>* minor-effect QTL (formerly *GpaM3*), originating from *S. spgazzinii*, in a *S. tuberosum* background carrying the *GpaVIII<sub>tr</sub>* QTL.



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