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

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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_{spg}* major-effect QTL (formerly called *GpaMI*) and the *GpaXII_{spg}* minor-effect QTL (formerly *GpaM3*), originating from *S. spgazzinii*, in a *S. tuberosum* background carrying the *GpaVIII_{tr}* QTL.



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