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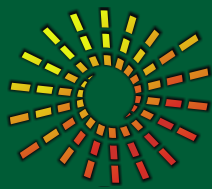
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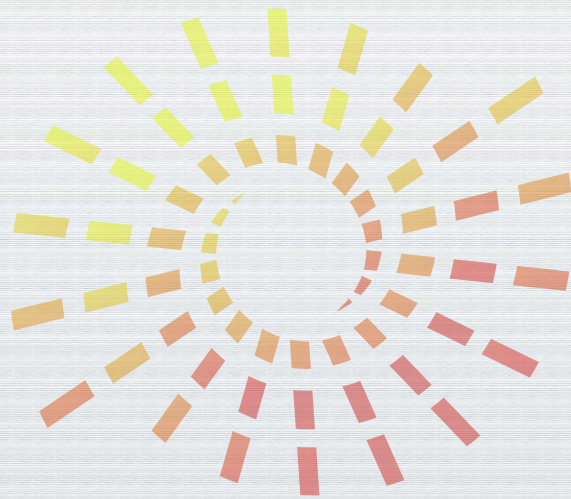
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QTL META-ANALYSIS FOR LATE BLIGHT RESISTANCE IN POTATO INCLUDING THE TWO NOVEL RESISTANCE SOURCES *SOLANUM SPARSIPILUM* AND *S. SPEGAZZINII*

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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.

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