Exploration of late blight quantitative resistance in potato diversity: QTL meta-analysis including the novel resistance sources Solanum sparsiplum and Solanum spegazzinii

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#154: Exploration of late blight quantitative resistance in potato diversity: QTL meta-analysis including the novel resistance sources Solanum sparsipilum and Solanum 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 durable partial 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. Here, we report the identification of QTLs in two novel wild species and integrate the mapping results in a meta-analysis for late blight resistance in potato together with the data of 19 other published studies.

Two mapping diploid progenies were assessed with a stem assay in controlled conditions and a foliage assay in outdoor conditions. QTL analysis was performed with 16 traits describing late blight resistance on the 4 parental maps sharing common genetic markers. Considering both progenies, a total of 75 detected QTLs were mapped on 11 of the 12 potato chromosomes. High-effect QTLs were detected on chromosomes I, V, VIII and X with QTL colinearities across parental maps. Anchor literature markers highlighted colinearities with reported R-genes and QTLs.

Thanks to the QTL meta-analysis, a consensus map of potato with the projection of late blight resistance meta-QTLs was constructed. Also, markers with a high frequency occurrence among experiments were selected to constitute an advisable potato set for new genetic map construction.

Results showed (i) the resistance potential of S. sparsipilum and S. spegazzinii for breeding programs, (ii) the efficiency of the stem test as a complement to the foliage test to assess quantitative resistance, (iii) close relationships between quantitative and qualitative resistance factors, and (iv) highlight the allelic diversity of late blight resistance QTLs.