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Identification of a genetic factor determining the durability of a plant major resistance gene and quantitative resistance to virus accumulation

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Genetic resistance provides efficient control of crop diseases but is limited by pathogen counteradaptation. The durability of the *pvr2³* allele, conferring resistance to *Potato virus Y* (PVY), was demonstrated to depend on the plant genetic background. In order to identify genetic factors affecting the durability of the *pvr2³* resistance, QTL mapping was performed using doubled-haploid (DH) lines issued from the F1 between two *Capsicum annuum* lines: ‘Perennial’ carrying *pvr2³* in a partially resistant background and ‘Yolo Wonder’ carrying the susceptible *pvr2⁺* allele in a susceptible background. 350 DH lines were genotyped with 234 markers and the linkage map was established. The 156 DH lines carrying the *pvr2³* allele but segregating for the genetic background were evaluated for two traits: the breakdown frequency of *pvr2³* (following inoculation with a PVY clone nonpathogenic (avirulent) towards *pvr2³*) and the PVY accumulation (following inoculation with a mutant of the previous PVY clone carrying a single mutation conferring pathogenicity towards *pvr2³*). Genotypic variance was highly significant for the two traits with heritabilities of 0.76 and 0.47. One major QTL, explaining 29% of the variance of *pvr2³* breakdown frequency was identified on chromosome 3 and two QTLs, explaining 25% and 9% of PVY accumulation variation, were identified on chromosomes 3 and 6, respectively. Interestingly, the major QTL for the 2 traits mapped to the same region of chromosome 3. A putative pleiotropic effect affecting simultaneously the two traits, the underlying mechanism and the perspective in breeding for resistance durability will be discussed.

Keywords:

Quantitative trait locus, resistance durability, quantitative resistance, pepper, *Potato virus Y*, eukaryotic translation initiation factor 4E.

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