

ISOLATION AND MOLECULAR MAPPING IN *CAPSICUM ANNUUM* OF THE TOMATO *VE2* GENE CONFERRING RESISTANCE TO *VERTICILLIUM* SPP.

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Verticillium wilt is a widespread fungal disease caused by two soil-borne pathogens: *Verticillium dahliae* and *Verticillium albo-athrum*. They are responsible of important yield and quality losses in a wide range of crops. Few strategies are at present available for the control of these pathogens.

To date tolerance to Verticillium wilt has been found in *Capsicum chinense*, *C. frutescens* and *C. baccatum* genotypes, while no tolerant lines have been identified in *C. annuum*, the most commercially important species.

In tomato the genetic resistance is conferred by two inverted independent genes: *Ve1* and *Ve2*, which have been mapped on the short arm of chromosome T9.

Our aim was to isolate sequences homologues to *Ve1* and *Ve2* in pepper and identify their location in three previously developed maps, based on the following intra-specific *C. annuum* progenies: (i) 297 F6 RILs from the cross ‘Yolo Wonder’ x ‘Criollo de Morelos 334’ (YC); (ii) 114 doubled haploids from the cross ‘Perennial’ x ‘Yolo Wonder’ (PY); (iii) 101 doubled haploids from the cross ‘H3’ x ‘Vania’ (HV).

C. annuum leaves were used for mRNA extraction and cDNAs generated by reverse transcription. Primers were designed on the tomato *Ve1* (AF272367) and *Ve2* (AF365929) gene sequences and applied for amplifications of pepper homologous cDNAs. PCR products (860 bp) were obtained only with *Ve2* primers. After sequencing, a nucleotide database search (blastn) revealed high similarity (87% identity) with the tomato *Ve2* gene.

Specific pepper primers were designed for analysing the allelic forms of the pepper homologous *Ve2* gene (*CaVe2*) in the five parents of the mapping populations. A SNP between ‘Yolo Wonder’ and ‘Criollo de Morelos 334’ was identified, and a specific co-dominant marker developed by means of the software dCAPS Finder 2.0 (<http://helix.wustl.edu/dcaps/dcaps.html>). Segregation analyses made possible to localize *CaVe2* locus on chromosome P9, in a position analogous to the one of the tomato *Ve* loci.

After successful full length *CaVe2* isolation, new primer pairs were designed for the development of specific co-dominant markers useful for mapping the gene in PY and HV progenies; segregation analyses are at present underway.

Further studies are in progress to evaluate the role played by this gene in the pepper tolerance to *Verticillium*.