Candidate Gene Identification for *Rvi5* Apple Scab Resistance in Apple Cultivar 'Murray'

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Abstract

Apple scab, caused by fungal pathogen *Venturia inaequalis,* is a severe disease of cultivated apple (*Malus × domestica* Borkh.). It is the most studied plant–pathogen interaction of woody plant species using genetic, genomic, proteomic and bioinformatics approaches in both species. Until now 17 monogenic resistances against the disease have been identified in different *Malus* species and some of them are currently used in scab resistance breeding programs. However, the evolution of virulent pathogen strains that has ability to overcome the monogenic resistance raised the need to define new strategies to obtain a durable resistance in apple breeding. Gene pyramiding becomes a successful method to obtain plants with durable resistance. Recently, the *Rvi5* (Vm) apple scab resistance from the cultivar 'Murray' was fine mapped and the region carrying the resistance was restricted into a region of 1cM flanked by two SSR markers (FMACH_Vm4 and FMACH_Vm2). In this study, three bacterial artificial chromosome (BAC) clones spanning the resistance locus were identified, completely sequenced and assembled, which allowed identifying the putative *Rvi5* locus in a region of 154kb in size. The open reading frame prediction and functional annotation of the identified region revealed the presence of one putative gene homologous to TMV resistance protein N-like [Malus x domestica] characterized by a Toll and mammalian interleukin-1 receptor protein nucleotide-binding site leucine-rich (TNL) repeat structure.

Keywords: Apple scab, Candidate gene, *Rvi5*, TNL genes*, Venturia inaequalis*

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