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Fine mapping and isolation of Rvi5 (Vm) scab resistance locus in apple (*Malus* x *domestica* Borkh.)

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Abstract: TheRvi5(Vm) apple scab resistance gene has been previously mapped on the distal end of Linkage group 17 by analysing 95 plants of a cross population between 'Golden Delicious' and 'Murray'. For the purpose of fine mapping and isolation of putative Rvi5 locus, two new populations were developed from crosses between 'Golden Delicious' × 'Murray' and 'Galaxy' × 'Murray'. A total of 1243 plants that were obtained from above crosses were screened by using Simple Sequence Repeat (SSR) markers. SSR markers Hi07h02 and CH05d08 previously reported as co-segregating and not co-segregating with Rvi5(Vm) gene were used as starting and end point of 'Murray' BAC library screening. Nine new SSR markers were designed for the region in between SSR Hi07h02 and CH05d08 using the 'Golden Delicious' genome sequence. Among the designed new SSR markers only four were polymorphic for the parents and Polymorphic markers (SSR FMACH_Vm1 to SSR FMACH_Vm4) were used to identify the positive BAC clones. With this strategy five BAC clones were identified, BAC extremities were sequenced using universal M13 forward and reverse primers to check the complete coverage of region and orientations of BAC clones. Using bio-informatics tools it has been confirmed the complete coverage of region of interest by spanning about 545kbps region with respect to 'Golden Delicious' genome sequence, then the BACs were sequenced by developing paired end libraries and assembled.
By analyzing recombinant plants, we were able to recognize the Rvi5 (Vm) locus in between SSR FMACH_Vm2 and FMACH_Vm4 in a region of 228 kbps in size. In addition, our study revealed that Rvi5 locus is more towards the SSR CH05d08 and newly developed marker, SSR FMACH_Vm3 is co-segregating with the locus.

Keywords: Rvi5, Apple Scab, Venturia inaequalis, SSR markers, Vm

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