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Development of markers closely linked to the scab resistant locus ‘*Rvi12*’ (*Vb*) from *Malus baccata* ‘Hansen’s baccata #2’

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Abstract: Apple scab is a disease caused by the fungus *Venturia inaequalis* which causes significant economic losses in apple production especially in temperate regions. Breeding programs are attempting to introgress scab resistance genes from wild apple varieties into commercial cultivars for the control of the disease. Most of the commercially available scab resistance varieties to date rely mostly on the single resistance gene *Rvi6* (*Vf*) from *Malus floribunda* 821. The evolution of new pathotypes of *V. inaequalis*, which have caused the breakdown of *Rvi6* based resistance at least in northern Europe reiterates the need for the identification and use of different scab resistance genes, and the development of closely linked markers for the selection of resistant seedlings and pyramiding of scab resistance genes for durable disease resistance. In this study, a population of 115 plants from the cross ‘Gala’ × ‘Hansen’s baccata #2’ which segregates for the scab resistance gene *Rvi12* was used. Based on previous studies, *Rvi12* was mapped to linkage group 12 between two SSR markers Hi02d05 (28.9 cM) and Hi07f01 (63.6 cM). We have developed five new SSR markers which are closely linked (<5cM) to the *Rvi12* scab resistance gene and one of the five SSR markers co-segregates with the *Rvi12* resistance gene. These closely linked SSR markers can be used in efficiently identifying resistant seedlings, fine-mapping and the eventual cloning of the resistance gene.

Keywords: Apple Scab, Mapping, Marker-Assisted Selection, Molecular markers

Type of presentation: [Poster](#)

Topics:

[Molecular mapping and marker development](#)

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