HIGH-RESOLUTION GENETIC MAP OF THE \textit{Rvi1} (\textit{Vg}) APPLE SCAB RESISTANCE LOCUS

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Apple scab, caused by the fungal pathogen \textit{Venturia inaequalis}, is one of the most prejudicial apple diseases for apple (\textit{Malus x domestica}) commercial orchards, especially in temperate countries. Apple scab strongly decreases fruits quality and yield, whereas fresh market sales require high-quality fruits standards. In order to control this disease, traditional methods use 15 to 20 fungicide treatments per year, which causes health and ecological problems. Since genetic resistance is an alternative to the chemical control of this disease, it has been largely studied and many apple scab resistance genes have been identified in wild or domestic apple species (Gessler et al., 2006, Soufflet-Freslon et al., 2008). One of them is the major gene \textit{Vg} from the cultivar Golden Delicious, firstly identified by Bénaouf and Parisi (1997) and then confirmed and mapped on linkage group 12 by Durel et al (2000). This gene confers resistance towards \textit{Venturia inaequalis} strains of race 7 and this race is virulent to varieties carrying the \textit{Vf} major gene (confers resistance to races 1 to 5). Thus \textit{Vg} and \textit{Vf} genes are complementary to confer a large spectrum of resistance in breeding programs. The apple genome of the cultivar ‘Golden Delicious’ has been recently sequenced by the Research and Innovation Center of IASMA (Velasco \textit{et al}, submitted). By this way, the fine mapping and cloning of the major gene \textit{Vg} becomes strategic. This work will have practical issues supplying accurate molecular markers to screen the gene in Marker-Assisted Selection.