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Poster Abstract – A.51

ISOLATION OF SSR MARKERS TIGHTLY ASSOCIATED TO THE VM APPLE SCAB RESISTANCE GENE

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The hypersensitive reaction is a resistance mechanism in which after cellular contact between pathogen and the host, a plant reaction can be observed, usually leading to the fast death of the pathogen's underlying cells. Hypersensitivity-based resistance is well studied in many model systems: basically, the defence cascade, which often ends macroscopically with hypersensitivity and biochemically with the synthesis of phytoalexins, is activated through host recognition of the pathogen. In *Malus* this is the case of *Vm* resistance. Historically, Dayton and Williams (1970) used *Vm* to denote the resistance gene conditioning the pit-type HR reaction carried by *M. micromalus* 24538 and *M. atrosanguinea* 804. The interest around this gene derives not only from its evident, typical and fast hypersensitive response, but also from the fact that this is a monogenic resistance, relatively easy to be introgressed in commercial apples.

Two molecular markers—OPB12SCAR (Cheng *et al*., 1998) and SSR Hi07h02— tightly linked to *Vm* gene have already been reported (Patocchi *et al*., 2005). The SSR marker allowed the mapping of *Vm* on linkage group 17 in a region where also scab resistance QTL have been reported (Durel et al., 2004).

Considering all these knowledge, a program to create the conditions for a rapid isolation of the apple scab resistance gene *Vm* was started.

Large *Vm*-segregating populations have been created, phenotyped in greenhouse after pathogen inoculation and genotyped using molecular markers associated with the *Vm* resistance gene. A Florina BAC library from Vinatzer et al. (1998) has been pooled to perform an 'heterologous' chromosome walking aimed at identifying new markers tightly linked to the *Vm* gene. The BAC library screening with the Hi07h02 marker resulted in the identification of three BAC clones carrying the marker alleles of Florina. The BAC-ends of these clones were sequenced and both used to develop new SSRs tightly linked to the *Vm* gene and to perform a second chromosome walking step. Two new microsatellites showing an high level of polymorphism in different populations (Fiesta x Discovery, Golden Delicious x Murray, Galaxy x Murray) were developed and mapped in the distal part of the LG 17. One of these new SSR markers (Vm1SSR) showed no recombinants among 1260 tested seedlings and the other (Vm2SSR) showed only 6 recombinants. Genetic distances from *Vm* were 0 and 0.47 cM, respectively therefore the resistance gene has been located between Vm2SSR and the SSR Hi07h02 (this marker showed 7 recombinants).

A new BAC library from cv. Murray DNA (carrying the *Vm* resistance gene) was constructed and pooled in order to identify clones containing the genomic region containing the *Vm* gene. Two BAC clones amplifying the resistance allele in coupling with the *Vm* gene were isolated and the sequencing is in progress to identify candidate resistance genes.