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CHARACTERIZATION OF THE *MLO* GENE FAMILY IN ROSACEAE AND GENE EXPRESSION ANALYSIS IN *MALUS DOMESTICA*

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ABSTRACT

Background

Powdery mildew (PM) is a major fungal disease for thousands of plant species, including many cultivated Rosaceae. Specific homologs of the *MLO* gene family act as PM-susceptibility genes, as their loss-of-function mutations grant durable and broad-spectrum resistance. PM pathogenesis is associated to a pathogen-dependent up-regulation of *MLO* genes during early stages of infection, causing down-regulation of plant defense pathways.

We carried out a genome-wide characterization of the *MLO* gene family in apple, peach and strawberry, and we isolated apricot *MLO* homologs through a PCR-approach. Evolutionary relationships between *MLO* homologs were studied and syntenic blocks constructed. Homologs that are candidates for being PM susceptibility genes were inferred by phylogenetic relationships with functionally characterized *MLO* genes and, in apple, by monitoring their expression following inoculation with the PM causal pathogen *Podosphaera leucotricha*.

Genomic tools available for Rosaceae were exploited in order to characterize the *MLO* gene family. Candidate *MLO* susceptibility genes were identified. In follow-up studies it can be investigated whether silencing or a loss-of-function mutation in one or more of these candidate genes leads to PM resistance.