

Analysis of *Plasmopara viticola* resistance locus *Rpv10* and comparison to *Rpv3*

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The oomycete *Plasmopara viticola* is one of the most important pathogens of grapevine (*Vitis vinifera* L.). Especially all traditional European cultivars used for wine production are highly susceptible. As a result a great quantity of fungicides is necessary to enable a rewarding cultivation of grapes. For that reason newly bred resistant varieties are a major contribution to reduce the fungicidal applications in sustainable viticulture.

Many North American *Vitis* species possess resistance genes due to co-evolution with *Plasmopara viticola*. Beyond that Asian *Vitis* species also exhibit such resistances although their evolutionary origin is not understood yet. Among others, the two loci *Rpv3* (American origin e. g. cv. 'Regent') and *Rpv10* (Asian origin e. g. cv. 'Solaris') have been identified.

In the present study we compare *Rpv3* and *Rpv10* carriers by performing leaf disc assays of *Plasmopara viticola* infections and comparative RNA

sequence analysis to identify differentially expressed genes.

After analyzing the genomic DNA sequence of 'Solaris' at the *Rpv10* locus several candidate genes were found which might be responsible for the expression of resistance against *Plasmopara viticola*. Among these candidates there are five genes with protein domains similar to resistance genes from other plant species. First gene expression studies demonstrated that one major candidate gene was upregulated after infection with the pathogen.

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