

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 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) and *Rpv10* (Asian origin) have been identified.

In this study on the one hand we try to compare *Rpv3* and *Rpv10* carriers for example by performing leaf disc assays

of *Plasmopara viticola* infections and comparative RNA sequence analysis to identify differentially expressed genes. On the other hand we will analyze the genomic DNA sequence of 'Solaris' (*Rpv10*) to find possible candidate genes which are responsible for the expression of resistance against *Plasmopara viticola*. Furthermore the project is aimed at developing new markers closely linked to *Rpv10* to improve the marker-assisted breeding of new resistant grapevine cultivars.

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