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

Dudenhöffer, J.¹, Zyprian, E.¹, Töpfer, R.¹

¹ Julius Kühn-Institute, Institute for Grapevine Breeding Geilweilerhof, Siebeldingen
Email of corresponding author: jens.dudenhoeffer@ jaki.bund.de

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.

Among several other partners the Julius Kühn-Institute in Siebeldingen is involved in the project which is called “Bacchus” and is funded by the interregional program “Interreg IV Upper Rhine” of the objective “European territorial cooperation”. The grant is provided by the “European Regional Development Fund” (ERDF) allocated by the European Union (EU).