Studies on the resistance locus *Rpv12* against downy mildew of grapes (*Plasmopara viticola*)

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Plasmopara viticola is the causative agent of grapevine downy mildew, a widespread severe disease. The heterothallic obligate biotrophic oomycete *P. viticola* was imported to Europe in 1878 from North America, together with grape phylloxera resistant rootstock vines. Since then, the pathogen has caused considerable yield losses. The pathogen hibernates in leaf debris and soil as sexual oospores. In spring, oospores germinate at a temperature above 11°C and form macrosporangia. Under wet conditions, macrosporangia liberate flagellated zoospores. With the rain, zoospores are splashed to the leaves onto the lower surface, where they can reach the stomata to cause infection. After 5-9 days yellow lesions called „oil spots“ appear on the upper site of the leaf surface. Under good weather conditions (high humidity and 20-25°C) *P. viticola* sporulates and a secondary infection starts.

Because *P. viticola* causes a high crop loss annually, research and breeding of resistant grape varieties is essential for a sustainable viticulture. Only with precise knowledge of the resistance mechanisms and the genetic location a targeted breeding is possible to reduce the annual amount of consumed pesticides. 2013 Venuti *et al.* identified the resistance locus *Rpv12* using QTL analysis of *V. amurensis*. *Vitis amurensis* is native to the cool climates of the Far East (China and Russia) and shows a resistance against *P. viticola*.

In the early 20th century the asiatic *Vitis amurensis* ‘Ruprecht‘ was crossed with *Vitis vinifera* ‘*Getsh*‘ (‘Michurinets‘). Other interesting cultivars are ‘Kunbarat‘ and ‘Kunleany‘. They posses resistance characteristics due to *Rpv12.* This locus was detected on Chromosome 14 and is inherited independently of other resistance genes. Within the locus *Rpv12* 13 CC-NB-LRR genes (coiled coil-nucleotide binding site – leucine rich repeats) have been identified within reference genome. An additive effect with *Rpv3* was detected. It confers a foliar resistance to strains that are virulent on *Rpv3* cultivars. For identification of the responsible gene for the resistance, we compare susceptible grapevine with resistant cultivars by leaf disc assay and light microscopy. The aim is to identify physiological responses of the cell. These results should reveal molecular mechanisms and the candidate genes involved, which shall be later evaluated by amplification, comparative sequencing and gene expression analysis.