

P6 – *Rpv32* – A new downy mildew resistance locus from the unexploited wild species *Vitis coignetiae*

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Abstract

Downy mildew, caused by the obligate biotrophic oomycete *Plasmopara viticola*, is one of the most damaging threats to grapevines growing in a warm and humid climate. Extensive application of fungicides is necessary to avoid serious yield losses, but this leads to a severe environmental impact and decreasing acceptance in society. In contrast to the conventional downy mildew management strategies, cultivars showing durable resistance are in high demand due to their contribution towards a sustainable and environmentally friendly viticulture. Therefore, genetic resistances with different defense mechanisms are necessary to prevent pathogen adaptation and to breed durable resistant varieties. This study aims to identify and genetically map a resistance for downy mildew from the unexploited East Asian wild species *V. coignetiae*. The individuals of a bi-parental F1 population (N=496) derived from the cross of 'Morio Muskat' x COxGT2 (*V. coignetiae* x 'Gewürztraminer') were phenotyped for resistance to *P. viticola* in an artificial leaf disc infection assay in the laboratory. A first framework map was generated based on 109 SSR markers. Using 647 transferable rhAmpSeq haplotype markers, a high-resolution map was obtained with a total map length of 1147.36 cM on 19 linkage groups, accounting for 96% of the physical coverage and an average distance between loci of 3.2 cM. Quantitative trait locus (QTL) analysis with each genetic map detected a single and highly significant stable QTL on chromosome 14 in four independent experiments that explains up to 36.4% of the phenotypic variation. This QTL maps to a different position as *Rpv8* and *Rpv12* from *V. amurensis* and shares no SSR marker alleles with them. It was therefore named *Rpv32* (Resistance Plasmopara viticola 32). A rhAmpSeq haplotype allele and a SSR marker were identified to be strongly associated with the novel resistance locus and have the potential to be exploited as selection markers for introgression of *Rpv32* into breeding lines.

Keywords: Downy mildew, QTL, mapping, resistance locus, *Rpv32*, *Vitis coignetiae*