

Genetic characterization of the phylloxera resistance QTL *Rdv1* in both haplotypes of the grapevine rootstock variety 'Börner'

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Abstract

In the 19th century, phylloxera (*Daktulosphaira vitifoliae*) caused a crisis of unprecedented dimension for viticulture and questioned the survival of viticulture in general, as *Vitis vinifera* proved to be susceptible at the rootsystem. Only grafting of susceptible *V. vinifera* cultivars onto phylloxera-tolerant rootstocks derived from American wild *Vitis* species or their interspecific hybrids rescued viticulture. The phylloxera plague remains a serious burden even if it is controlled at the moment. One newly developed rootstock variety is the cultivar 'Börner', an interspecific hybrid derived from a cross of the American *Vitis* genotypes *V. riparia* GM183 and *V. cinerea* Arnold. 'Börner' inherited resistance to phylloxera from *V. cinerea* and plants afflicted by phylloxera do not develop nodosities or tuberosities. At the genetic level, the quantitative trait locus (QTL) *Rdv1* for resistance to phylloxera was identified on chromosome 13 in the 'Börner' genome.

We generated a fully haplotype-separated, high-quality 'Börner' genome sequence assembly in two phases using PacBio long reads. A comprehensive gene annotation was performed, genes were functionally annotated and resistance gene analogs were predicted. True haplotype phasing was verified and the *Rdv1* locus was selected for detailed characterization. This genetically mapped resistance locus was previously described with a size of approximately 1.5 – 3 Mbp, but could be reduced to about 300 kbp using a local mapping approach in which selected recombinant F1 individuals were analyzed with additional markers. Comparing the *Rdv1*-carrying haplotype BoeCin with other haplotypes from *Vitis* varieties conferring susceptibility or only tolerance, *Rdv1* was further delimited based on striking deviation of the sequence synteny. This region of the highly size-reduced *Rdv1* locus was characterized regarding its unique gene content. A set of putative disease resistance gene analogs was identified that represent likely candidates for conferring resistance to phylloxera.

Keywords: Assembly, PacBio sequencing, phylloxera, 'Börner', *Rdv1*, rootstock, genome, annotation, resistance, resistance gene analogs