

## **P82 – Characterization of the black rot resistance loci (*Rgb1* and *Rgb2*) of ‘Börner’ and development of associated markers suitable for marker-assisted selection in grapevine breeding**

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### **Abstract**

Since the beginning of the 21<sup>st</sup> century, an increased incidence of grapevine black rot (*Guignardia bidwellii*, anamorph: *Phyllosticta ampellicida*) disease has been reported from regions all over Europe. The hemibiotrophic ascomycete favours a warm and humid climate. Due to climate change, potential distribution areas for black rot will shift to northwestern winegrowing regions of Europe. With the intended reduction of fungicide use and increase of acreage of new mildew-resistant grapevine cultivars in the European Union, there is concern that diseases previously considered secondary, such as black rot, may emerge and become relevant. Therefore, the identification of resistances to black rot and their introgression in new varieties is an important task. In an initial study on a F1 population of a cross of V3125 (‘Schiava Grossa’ x ‘Riesling’) x ‘Börner’ (*Vitis riparia* x *Vitis cinerea*), two QTL (quantitative trait loci) were described conferring resistance to black rot. They were localized on chromosome 14 (*Rgb1*) and 16 (*Rgb2*) of ‘Börner’. In the course of haplophase-specific analysis to reveal the origin of the black rot resistance, *Vitis riparia* was clearly identified as the resistance donor of both resistance loci. The use of an improved version of the integrated genetic map based on SSR markers led to a further reduction of the size of the *Rgb2* locus. Using SSR markers linked with the *Rgb1* locus, we could demonstrate the stable inheritance of the black rot resistance into the next generation (pseudo-backcross with ‘Pinot blanc’). These SSR markers are highly suitable for marker-assisted selection (MAS) and valuable tools to extend the focus of grapevine breeding towards the introgression of black rot resistance into new varieties. To further reduce the size of the *Rgb* loci and define candidate genes for black rot resistance, a local mapping approach will be followed analyzing recombinant individuals of the enlarged V3125 x ‘Börner’ and derived pseudo-backcross populations.

**Keywords:** black rot, *Guignardia bidwellii*, resistance, QTL mapping, ‘Börner’, MAS, *Vitis riparia*