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**XIVTH INTERNATIONAL
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BREEDING AND GENETICS**

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ORAL

Mapping of five loci for black rot resistance in four breeding populations and identification of candidate genes associated with Rgb1

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ABSTRACT

Black rot, caused by *Phyllosticta ampellicida* (*Guignardia bidwellii*), is a serious fungal disease in viticulture. Incidences increased in recent years due to reduced pesticide treatments, neglected phytosanitary measurements, and effects of climate change. Until recently, grapevine cross breeding focused primarily on the development of new varieties with resistances to powdery and downy mildew. More than forty resistance loci were described for the mildew diseases, several of these loci were frequently used in breeding through marker-assisted selection (MAS), and a few resistance genes were identified and characterized. However, only three loci have been described conferring resistance to black rot. Therefore, we used four biparental populations based on the resistance donors 'Börner', 'Merzling', 'Calardis Musqué', 'Villard Blanc' and 'Calardis Blanc' for quantitative trait locus (QTL) analysis to identify new resistance loci. In addition to Rgb1 and Rgb2, three previously unknown QTL were mapped on chromosome 6 (Rgb5), 13 (Rgb6) and 17 (Rgb7), indicating several independent sources of black rot

resistance. Because Rgb1 on chromosome 14 appears to be a very frequently occurring black rot resistance in current breeding material and some disease-resistant varieties, we focused on the refinement of this locus. The genetic maps of the four populations were aligned, comprising the phenotypic and genetic results of more than 750 F1 individuals. With this approach, the Rgb1 locus could be validated and a genomic region around the simple sequence repeat marker UDV-095 was defined as the putative core of the resistance locus. The haplotype-resolved and annotated genomes of the cultivars 'Calardis Musqué' and 'Börner' were compared with PN40024 and analyzed at the Rgb1 locus. Structural variations and possible candidate genes will be discussed, like a gene cluster of pattern recognition receptors. The results obtained enable the development of tightly linked molecular markers for MAS and finally the introgression of Rgb1 into elite breeding lines. The additional resistance loci can be used for pyramiding to strengthen overall resistance to black rot and to prevent a possible resistance breakdown.

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