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HIGHLY DENSE LINKAGE MAPPING AND IDENTIFICATION OF A MAJOR QTL ASSOCIATED WITH BLACK ROT RESISTANCE IN THE GRAPEVINE CULTIVAR ‘MERZLING’

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When the urgency of a sustainable transition comes to agriculture, one of the key areas of improvement involves the decrease of chemicals. Although vineyards cover less than 5% of agricultural land in Europe, viticulture is responsible for the use of more than 60% of all fungicides. The exploitation of grapevine varieties resistant to mildews is an efficient strategy already implemented in integrated/organic farming to reduce treatments. However, from the beginning of this century, European viticulture has been threatened by severe outbreaks of black rot (BR), an emergent and destructive disease caused by the ascomycete *Phyllosticta ampelicida* (sexual morph *Guignardia bidwellii*). These events introduced the urgent need for the introgression of BR resistance in mildew-tolerant genotypes. For this purpose, a set of parental lines and breeding selections of the Fondazione Edmund Mach has been screened for BR resistance in a growing chamber with *in vivo* produced spores using an optimized artificial infection protocol. Given the good performance of ‘Merzling’ (a complex genotype derived from *V. vinifera* and *V. rupestris* × *V. aestivalis* var. *lincecumii*), this cultivar was used for a cross with the susceptible variety ‘Teroldego’ (*V. vinifera*) and the segregating offspring was genetically characterized by means of the GrapeReSeq 18K Vitis SNP chip. Five phenotypic experiments were carried out under controlled

conditions on leaves of potted plants, and three on bunches in the field. A dense genetic map was constructed combining 7,175 SNP with 194 SSR markers of a previous map. All QTL analyses revealed the presence of a strong major BR resistance locus on chromosome 14. It explains up to 45% of the trait variability (LOD 10.5) and spans a genomic region of 1.36 Mb. A specific SNP marker was found robustly associated with the resistance trait. No minor QTLs were detected. The genes underlying this region are currently under investigation via bioinformatic analysis, and microscopic inspections of disease progression are in place to understand the biological causes of the resistance trait. Finally, new molecular markers will be developed and validated on segregating populations with different genetic backgrounds, to be implemented in marker-assisted selection for BR resistance in grapevine.