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High-density linkage mapping and QTL identification of black rot resistance towards marker-assisted breeding in grapevine

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Today sustainability is a pivotal objective for viticulture, but it also presents us with new challenges. The decrease in treatments has in fact changed grapevine-pathogen interactions and dynamics causing the reaffirmation of diseases previously considered secondary. This is the case of black rot (BR, caused by Phyllosticta ampelicida), which is spreading with increasing pressure in warm-humid regions causing the loss of entire crops. The interinstitutional DAMAGE project between Edmund Mach Foundation (FEM) and the Institute for Grapevine Breeding (JKI-Geilweilerhof) aims to characterize BR resistance and to develop a toolkit of molecular markers (MM) to be routinely used in marker-assisted breeding for the introgression of this trait into mildew resistant backgrounds. The first fungal strain was isolated from infected leaves collected in Trentino-Italy and mixed with a second strain isolated in southwestern Germany. This inoculum has been used to screen a segregating population derived from 'Merzling' (V. rupestris × V. lincecumii, mid-resistant) × 'Teroldego' (V. vinifera, susceptible). BR resistance phenotyping consisted of a newly developed inoculation protocol on potted plants. The F1 individuals were genotyped with the Vitis18KSNP chip and a high-density genetic map has been constructed, following the integration of 190 informative SSRs. Moreover, explorative QTL analyzes have been conducted on phenotypic data of 2020 and 2021 seasons. Finally, upon the genomic interval characterization, new MM will be designed, tested and validated on various segregating populations with different genetic backgrounds.

Keywords: Vitis spp., Guignardia bidwellii, marker-assisted selection, disease resistance, plant phenotyping