

## **BLACK ROT RESISTANCE OF GRAPEVINE: FROM ORGAN-SPECIFIC QTL MAPPING TO THE SEQUENCING OF THE DONOR TOWARDS CANDIDATE GENE IDENTIFICATION**

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Black rot is considered one of the most problematic emerging fungal diseases in Europe due to the increasing pressure favored by climate change, its destructiveness – which can lead up to 80% of fruit loss – and the susceptibility of a large part of the mildew resistant varieties, so-called PIWI. Therefore, in the perspective of the genomic designing of the cultivars of the future, modern breeding has to focus on the combination of multiple beneficial alleles both for disease resistance and abiotic stress resilience. Doubtless, the genetic dissection of the traits of interest is a necessary starting point.

To this objective, the segregation of black rot resistance has been studied in a population (N=147) derived from the cross between the resistant *Vitis* hybrid 'Merzling' and the susceptible *V. vinifera* 'Teroldego'. The progeny was genotyped with the GrapeReSeq Illumina 20K SNPchip, and 7,175 SNPs were combined with 194 SSRs to generate a high-density linkage map of 1,677 cM. The outcomes uncovered two organ-specific QTLs on chromosome 14. One was associated with the resistance of shoot and co-segregated with the previously mapped *Rgb1* locus. A second newly discovered QTL explained almost 70% of the phenotypic variance of bunch resistance and was designated *Rgb3*. The genes underlying the QTLs have been firstly studied based on the reference *vinifera* genome, PN40024.v4, revealing the absence

of resistance (*R*)-genes and the enrichment of two clusters of 15 pathogenesis-related Germin-like protein 3, and five phloem Sieve occlusion element type B genes associated with bunch and shoot resistance, respectively. A molecular toolkit has been therefore designed for marker-assisted breeding applications. Finally, to propose reliable candidate genes for biotechnological approaches, the genome of the resistance donor 'Merzling' has been sequenced through PacBio HiFi technology. This data has been assembled into a haplotype-resolved and phased genome sequence. Preliminary results will be discussed regarding significant differences with the reference *vinifera* genome, which confirms the high value of exploring the genomes of hybrids.

These findings corroborate the need for the scientific community to engage in building a pangenome to unveil and exploit the genetic variability and informativeness of the highly heterozygous *Vitis* genus.