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Mgaloblishvili *Rpv29* and *Rpv31* loci reveal new insights on downy mildew resistance sources in *Vitis vinifera*

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Abstract (250 words)

Downy mildew, a disease caused by *Plasmopara viticola* (Berk. et Curt.) Berl. and De Toni, is one of the strongest threats to grapevine (*Vitis vinifera* L.) production. Recently, sources of resistance to downy mildew were identified among Caucasian germplasm. Among them, the Georgian variety Mgaloblishvili revealed a unique resistance mechanism. A genome wide association study (GWAS) allowed the identification of the genetic bases of Mgaloblishvili resistance, the loci *Rpv29*, *Rpv30* and *Rpv31*. To dissect the three resistance loci, Mgaloblishvili genome was sequenced using PacBio HiFi reads and assembled. A chromosome-scale diploid genome assembly consisting of ~ 986 Mb and a contig N50 length of 25.8 Mb was obtained. A total of 58,912 protein-coding genes were predicted on the two sets of phased chromosomes. A whole genome comparison with the genome of the susceptible reference accession PN40024 was performed. Mgaloblishvili resistance loci were in-depth analyzed in terms of structure, gene content, gene expression and impact of structural variants (SVs) and SNPs (Single Nucleotide Polymorphisms). Furthermore, using DNA sequencing data of Mgaloblishvili self-cross progeny, resistance haplotypes were identified for *Rpv30* and *Rpv31*. The obtained data highlighted Mgaloblishvili resistant phenotype as a consequence of multiple small SVs and SNPs, that eventually results into differential transcriptional regulation. Altogether, these genetic resources will increase the knowledge about downy mildew-grapevine pathosystem. Moreover, they will be available for breeding programs aiming to develop grapevine resistant varieties.

Keywords: Grapevine, biotic stress, QTL, genome, Caucasus.