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Receptor-like proteins (RLPs) in the transcriptome of *Vitis* spp. under inoculation of *Xanthomonas citri*

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ABSTRACT
Receptor-like Proteins (RLPs) are membrane-anchored glycoproteins with leucine-rich repeat – LRRs and a transmembrane domain. Together with other classes of resistance genes and pattern recognition receptors, these proteins have been important targets for developing cultivars aimed at resistance to various plant diseases. Thus, the objective was to identify and characterize transcripts encoding RLPs proteins in two accessions of *Vitis* inoculated with *Xanthomonas citri*. Accessions with contrasting resistance to *Xanthomonas citri* pv. *Viticola* (*Xcv*) RNA-Seq libraries were generated from mRNAs of leaf tissues of the cultivar Red Globe (susceptible to *Xcv*) and the hybrid IAC-572 (moderately resistant to *Xcv*) collected after 90 minutes after inoculation with the pathogen. The identification of RLP transcripts was performed using BLASTp (cutoff ≤ e-^{05}) and HMMER v.3.1b1 using Pfam domains (PF01462, PF08263, PF00560, PF07723, PF13516, and PF13855). Redundant RLP sequences were removed and analyzed in CD-Search and Pfam to confirm the presence of the LRR catalytic domain. The prediction of the isoelectric point (pI), molecular weight (MW) and the subcellular location were performed using JVirGel 2.0 and LocTree3. The identified transcripts were mapped in the genome of *V. vinifera* through the Phytozome database. Finally, the RLP proteins were submitted to gene ontology analysis using the AgriGO v.2 program (FDR<0.05). 204 candidate sequences were identified that displayed the conserved and complete LRR catalytic domain. The proteins presented ORFs ranging from 134 to 1686 amino acids, with MW between 14.81-187.86 kDa and p.I. from 3.51 to 10.14, with the majority (85%) of the RLP proteins directed to the plasma membrane. The others were distributed among the cytoplasm (7.6%), chloroplast (0.4%), extracellular region (4%), and core (3%), with an average accuracy of 83.81%. The Chr09 and Chr16 pseudochromosomes had the highest abundance of RLP transcripts, with 31 and 30 transcripts mapped, respectively, while the others mapped to at least in one of the *V. vinifera* chromosomes, except for pseudochromosome five (Chr5), which did not present any mapped transcripts. Furthermore, 11 transcripts did not anchor in any of the 19 pseudochromosomes, being grouped in ChrUn. Gene ontology indicated that all transcripts were mapped only to molecular function, with 93.6% of RLPs related to protein binding (GO:0005515 and GO:0005488). In contrast, other transcripts mapped to transmembrane signaling receptor activity (GO:0004888), molecular transducer (GO:0060089), transmembrane receptor (GO:0099600, GO:0004872), and receptor signaling (GO:0038023). The results obtained allowed the selection of RLPs responsive to *X. citri* for validation by real-time PCR and subsequent application in crop breeding programs.

KEYWORDS: Bacterial canker; Grape; Resistance genes

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