

Induction of resistance mechanisms in *Solanum lycopersicum* in response to *Ralstonia pseudosolanacearum*: a proteomic perspective

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Tomato (*Solanum lycopersicum* L.) stands out as one of the most economically important vegetables in the world. *Ralstonia pseudosolanacearum* (Rp), a phytopathogenic bacterium that infects the xylem of tomato plants, triggering bacterial wilt (BM). This disease is a limiting factor for tomato cultivation in tropical regions, making production unviable in parts of the northern and northeastern regions, and an impediment to the expansion of cultivated areas and greenhouses. The use of resistant cultivars is the most effective control method from an economic and ecological point of view, due to the wide range of hosts and the potential variability of the pathogen. This study aimed to clarify, at the proteomic level, the resistance mechanisms in two Rp-resistant cultivars: Hawaii 7996 and Yoshimatsu, after inoculation with the Rp strain CCRMRs202 (Biovar 3, Phylotype 1, Sequevar I-18), originating from the city of Gravatá-PE (Rosa Mariano Culture Collection/UFRPE). The experiment was carried out in a randomized block design, conducted in a greenhouse. The plant material was inoculated with Rp, collected four days after inoculation, and total soluble proteins were obtained from phenolic extraction. After quantification and trypsinization of the protein extract, the samples were injected into a nano-LC-MS/MS mass spectrometer, analysis of the spectra obtained using Maxquant software, statistical analysis and selection of differentially accumulated proteins (DAPs) using Perseus software, in addition to categorization by gene ontology using UniProt and Blast2GO/OmicsBox software, and protein-protein interaction networks were generated using String software. Mass spectrometry analysis identified 1385 proteins in total. The presence of several pathogenesis-related proteins (PR-proteins) with antimicrobial action was observed, such as PR5 and PR14 in the Hawaii 7996 cultivar and PR10 in both cultivars. The Hawaii 7996 cultivar showed greater accumulation of proteins related to the antioxidant system, such as annexins, while Yoshimatsu stood out for accumulating proteins associated with the cell wall. Protein-protein interaction networks and GO term enrichment analysis revealed key biological processes involved in the defense response against pathogens. The study provided a comprehensive view on the proteomic mechanisms of Rp resistance in tomato cultivars, highlighting the importance of PR proteins and antioxidants in the defense against bacterial wilt. The results may assist in the development of breeding programs for the selection of resistant genotypes, contributing to the sustainability of tomato production against phytopathogenic challenges.

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