PROTEOMIC PROFILE OF RESISTANT AND SUSCEPTIBLE VARIETIES OF Solanum lycopersicum L. IN RESPONSE TO Ralstonia PSEUDOSOLANACEARUM, CAUSING BACTERIAL WILT DISEASE

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Tomato (Solanum lycopersicum L.), a solanaceous plant native to South America, is the second most widely used vegetable in the world. Northeastern Brazil accounts for 13.3% of tomato production in Brazil, and the state of Pernambuco ranks 11th in national production. Diseases caused by phytopathogens are one of the main limiting factors for the expansion of tomato cultivation, specially on Bacterial Wilt, a disease caused by a complex of bacterial species of the genus Ralstonia. In the state of Pernambuco, there is a prevalence of R. solanacearum in the backland region, and R. pseudosolanacearum (Rp) in the agreste region and the metropolitan region of Recife. The Yoshimatsu cultivar is resistant to wilt, but its productivity and fruit quality are poorly accepted by producers and consumers. The cultivar Caline IPA-7, developed by the Agronomic Institute of Pernambuco (IPA), presents good agronomic performance and fruit characteristics, but is susceptible to bacterial wilt. Aiming to indicate functional markers useful in the selection of genotypes resistant to bacterial wilt, this study investigated the leaf proteome of the cultivars Yoshimatsu (resistant) and Caline IPA-7 (susceptible), in response to inoculation with the Rp strain CCRMRs202, four days after inoculation. The isolate CCRMRs202O of Rp, Biovar 3, Phylotype 1, Sequevar I-18, obtained in the city of Gravatá-PE (Rosa Mariano Culture Collection/UFRPE), was used. The experiment was conducted in a randomized block design in a greenhouse. Seedlings aged 11 days after germination were used and inoculated by the root cut method using a bacterial cell concentration of approximately 1x108 CFU mL-1. Leaf tissue was collected 4 days after inoculation, and total soluble proteins were extracted using the phenolic method. The samples were quantified, trypsinized, and injected into a nano-LC-MS/MS system. Bioinformatics analyses were performed using the Maxquant and Perseus for DAPs (Differentially accumulated proteins) identification, Uniprot, Blast2GO, ShynyGO, and String/Cytoscape platforms. A total of 1385 DAPs were obtained, of which those directly linked to the defense response of the Yoshimatsu and Caline IPA-7 cultivars were selected. Several classes of pathogenesis-related proteins (PRs) with antimicrobial action were identified, with PR10 standing out, observed exclusively in the Yoshimatsu cultivar. The universal stress protein (PHOs/USP) was up-accumulated in Yoshmatsu, and this DAP is known for promoting resistance to multiple stresses, regulating ROS homeostasis and regulating plant growth/development. Downregulation was observed in the Caline IPA-7 cultivar in several metabolic processes (“stress” and “redox”, “cell development”, “signaling”, “hormone metabolism” and “nucleotide metabolism”), indicating inefficiency in using these pathways in response to the applied stress. The identification and characterization of DAPs in tomato plants in response to Rp constitutes an important strategy for identifying functional markers, contributing significantly to the assisted selection of tomato genotypes resistant to bacterial wilt. This is the first report of a shotgun proteomic study using cultivars from Northern/Northeastern Brazil in response to Rp aiming at the identification of functional biomarkers for the recent precision breeding approach.

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