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ABSTRACT SUBMISSION FORM

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[] New Tools in Disease Diagnostics and Pathogen Identification
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[1] Bacterial Pathogens and the Phytobiome
[] Natural and Engineered Plant Disease Resistance

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Characterization of the GacS/GacA system in the virulence regulation of *Pseudomonas savastanoi*.

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The two-component regulatory system GacS/GacA is one of the main mechanisms for global regulation in bacteria. GacS/GacA is a highly conserved system that has been studied in many pathogenic bacteria. However, its characterization has been mainly focused on pathogenic bacteria of herbaceous plants. Despite previous works have reported that GacS/GacA regulates the expression of virulence factors, its role in virulence varies among different species and strains. The aim of this work was the identification of virulence factors regulated by the GacS/GacA system in the model bacterium Pseudomonas savastanoi pv. savastanoi (Psv), causal agent of olive knot disease. To this end, we generated a gacA deletion mutant in the strain Psv NCPPB 3335, whose transcriptomic profile was further analyzed using a massive RNA sequencing (RNA-seq) strategy. The bioinformatic analysis of RNA-seq data showed that the Psv GacS/GacA system regulates a large number of genes, including some virulence factors already described, such as those related to the type III secretion system, the biosynthesis of phytohormones and the catabolism of aromatic compounds, among others. In addition, small Rsm-type RNAs and regulatory proteins (RsmA) were identified in the regulatory cascade of the GacS/GacA system. Finally, the involvement of some of the virulence factors of Psv NCPP 3335 were further studied through different phenotypic assays, such as plant virulence assays, induction of hypersensitive response, leaf adhesion tests and translocation of type III effectors. Results obtained in this work indicate that GacS/GacA system presents a role in regulation of virulence factors of Psv NCPPB 3335.