INVESTIGATING THE SIGNAL TRANSDUCTION AND GENE EXPRESSION NETWORKS RESPONSIBLE FOR THE EXPRESSION OF THE TYPE III SECRETION SYSTEM IN XANTHOMONAS AXONOPODIS PV CITRI.

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Type III secretion systems (TTSS) are key virulence determinants used by bacteria to deliver effector proteins directly into the host cell cytoplasm. The ability of several plant pathogens to multiply inside their hosts and produce disease is dependent on their *hrp* genes (TTSS genes) whose transcription is controlled by multicomponent regulatory networks that integrate diverse sets of environmental signals. In *Ralstonia solancearum* the transduction of the plant signal to activate the *hrp* genes involves an outer membrane protein PrhA, an inner membrane protein PrhR, an ECF sigma factor PrhI, and the transcription factors PrhJ, HrpG and HrpB. PrhI induces transcription of *prhJ*, leading to expression of *hrpG* which activates *hrpB*, which in turn actives the remaining *hrp* genes. In the genome of *Xanthomonas axonopodis* pv. citri (*Xac*), gene homologs to the above-mentioned *R. solancearum* regulators have been identified, but the functions of several of them remain unknown. Using two-hybrid assays we have analyzed protein-protein interactions involving PrhI homologs (XAC2191 and XAC4129) and PrhR homologs (XAC2192 and XAC4130). These interactions are now being analyzed by *in vitro* assays. We are also attempting to identify which of the nine *Xac prhJ* homolog promotors can be bound or activated by PrhI using DNA mobility shift and GUS reporter activation assays.

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