

Identifying protein-protein interactions of two-component systems of the  
phytopathogen *Xanthomonas axonopodis* pv. *citri*

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Citriculture is an important sector of the State of Sao Paulo economy. Citrus canker, caused by *Xanthomonas axonopodis* pv. *citri* (*Xac*), is a devastating disease responsible significant economic losses annually. In this work, we used the yeast two-hybrid system to identify protein-protein interactions involving the large set of as yet uncharacterized two-component systems coded by the genome of this phytopathogen. These systems make up modular signal transduction pathways whose principal components are histidine kinase (HK) and response regulator (RR) domains, both of which can be phosphorylated and exchange phosphate groups in transphosphorylation reactions. These domains are found in a variety of protein architectures in combination with sensor and effector domains. The *Xac* genome codes for 37 histidine kinases (HK) and 60 response regulators (RR), as well as 21 hybrid proteins containing both domains. The complexity of these systems makes genomic analysis an important tool in their analysis and the elucidation of signalling pathways that allow bacteria to infect the host. Our results revealed specific interactions between several components of these systems, notably the following HKs and their respective RRs: XAC0135 and XAC0136, XAC0620 and XAC0621, XAC0683 and XAC0684, XAC0759 and XAC0760, besides XAC1669 and XAC1670 and XAC1669 and XAC1284, the later possibly involved in bacterial chemotaxis.