

### Functional genomics of *Xylella fastidiosa*

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*Xylella fastidiosa* was the first phytopathogen to have its genome fully sequenced. This became a landmark in the understanding of its biology since the knowledge generated in this work allowed a major development in functional studies. The strategies taken for functional genomics studies include high throughput evaluations of the expressed genome and confirmation of particular genes, obtaining of mutants, and protein analysis. Most of these works are focused on pathogenicity, which results from the formation of biofilms inside the xylem vessels. This colonization leads to the blockage of the vessels and a consequent interruption in the transport of sap from the roots. Our team has investigated the changes that occur in the *X. fastidiosa* biofilm related with its formation, resistance to antimicrobial compounds and interaction with the plant host. These studies involved gene and protein expression analyses. We have observed that *X. fastidiosa* biofilm presents distinguishing characteristics that give it important adaptation advantage including higher resistance to antimicrobial compounds and higher virulence, increasing the success of the pathogen colonization. Analysis of gene expression associated with these characteristics reveals important factors related to the pathogenicity, especially virulence and adaptation factors, like multidrug-resistance efflux pump. Among the virulence factors, the adhesins deserve special attention. Both fimbrial and afimbrial adhesins were up-regulated in biofilm growth condition and in bacterial cells obtained from infected plants. These adhesins show different behavior during the biofilm development *in vitro* and *in planta*, suggesting distinct, but important roles in this process.

Financial support: CNPq and FAPESP

Keywords: biofilm, gene expression, protein expression