

THE IRON STIMULON OF *XYLELLA FASTIDIOSA* INCLUDES GENES FOR TYPE-IV PILUS AND COLICIN V-LIKE BACTERIOCINS

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ABSTRACT

Xylella fastidiosa (*Xf*) is the etiologic agent of a wide range of plant diseases including citrus variegated chlorosis (CVC), a major threat to citrus industry in Brazil. The genomes of several strains of this phytopathogen were completely sequenced, enabling largescale functional studies. DNA microarrays representing 2608 (91.6%) coding sequences (CDS) of *Xf* CVC strain 9a5c were used to investigate transcript levels under growth in different iron availabilities. When treated with the iron chelator 2,2'-dipyridyl, 193 CDS were considered as up-regulated and 216 as down-regulated. Upon incubation with 100 μ M of ferric pyrophosphate, 218 and 256 CDS were considered as up- and down-regulated, respectively. Differential expression for a subset of 44 CDS was further evaluated by RT-qPCR. Several CDS involved with regulatory functions, pathogenicity and cell structure, were modulated in both conditions assayed suggesting that major changes in cell architecture and metabolism occur when *Xf* cells are exposed to extreme variations in iron concentration. Interestingly, the modulated CDS include those related to colicin V-like bacteriocin synthesis and secretion and to pili/fimbriae functions. We also investigated the contribution of the ferric uptake regulator Fur to the iron stimulon of *Xf*. The promoter regions of strain 9a5c genome were screened for putative Fur boxes and candidates were analyzed by electrophoretic mobility shift assays. Taken together, our data support the hypothesis that Fur is not solely responsible for the modulation of the iron stimulon of *Xf* and present novel evidence for iron regulation of pathogenicity determinants.

FUNDING AGENCIES

Funding for this project was provided by the São Paulo State Foundation for Research Support (FAPESP), and the National Council of Research and Development (CNPq).

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