Prediction of bacteriocin-encoding genes in *Xylella fastidiosa* and analysis of their transcript levels

Duarte, R.R.R.; Zaini, P.A.; da Silva, A.M.

Departamento de Bioquímica, Instituto de Química, USP, SP, Brazil

*Xylella fastidiosa* is the etiologic agent of several diseases that occur in economically important plants such as citrus, grapevines and coffee. Attempts to elucidate the virulence and pathogenicity mechanisms of this phytopathogen have pointed out the biofilm formation as a fundamental step for the establishment of the infection and the consequent development of the disease. Additional factors such as the production of toxins might take part in these processes. In this study we performed an *in silico* screening for bacteriocin-encoding genes in *X. fastidiosa* citrus strain 9a5c with a bacteriocin genome mining tool, BAGEL (http://bagel2.molgenrug.nl) plus additional manual inspection. Our analysis revealed 13 CDS (coding sequences) for putative microcins (bacteriocins with molecular mass lower than 10 kDa), including 3 CDS that were not previously annotated in the public version of 9a5c genome. All these predicted proteins contain a double-glycine-type leader sequence, which is typical of some bacterial peptide antibiotics that can also act as *quorum sensing* molecules. Comparative genomic analysis revealed that strains J1a12 (avirulent) and 9a5c (virulent for citrus) share 9 putative microcins while others are exclusive to either one or another. The relative expression of these microcins were evaluated by RT-qPCR in 9a5c and J1a12 cells exposed to heat shock, low and high iron concentration. Our results demonstrated that these CDS are expressed in all conditions tested but no significant differences in expression levels were observed. These observations support further experimentation to investigate if the encoded peptides are indeed produced and secreted by *X. fastidiosa*.

Keywords: Citrus Variegated Chlorosis, genome mining, microcins

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