

Characterization of bacteriocins in *Xanthomonas citri*

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Abstract

The resistance against antimicrobial components shows up as a growing concern worldwide and makes treating infectious diseases spread in humans, animals, and plants impracticable. In crops, *Xanthomonas citri* is a Gram-negative bacterium that infects plants within the Citrus genus, responsible for developing citrus canker and causing considerable economic losses. However, this microorganism produces some secondary metabolites, such as bacteriocins, that appear as an alternative to elucidate the problem since they can inactivate or kill microorganism targets. Thereby, this study aims to identify and characterize potential bacteriocins produced by *X. citri*. We have evaluated in silico 78 complete genomes in GenBank/NCBI database. The RAST server automatically annotated these genomes. After that, the annotated sequences were submitted to BAGEL4 and antiSMASH to identify genomic regions containing potential bacteriocins. Results obtained from BAGEL4 showed 76 genomes presenting the zoocin A, which was characterized as a bacteriocin-like inhibitory peptide of class III that attaches with the peptidoglycan region of some bacterias causing its lysis. The only ones that haven't shown zoocin A were *Xanthomonas citri* pv. *mangiferaeindicae* XC01 that has revealed a rhodonadin and a microcin and *Xanthomonas citri* pv. *phaseoli fuscans* CFBP7767 that hasn't shown any area of interest. Both of them have a lasso structure, which gives them more stability. Furthermore, the results obtained from antiSMASH revealed 22 bacteriocins and 55 lasso peptides in those genomes, except for three: *Xanthomonas citri* pv. *aurantifolii* str. 1566, *Xanthomonas citri* pv. *aurantifolii* FDC 1561 and *Xanthomonas citri* pv. *vignicola* CFBP7113. Therefore, we suggest that *X. citri* can produce metabolites with antimicrobial activity that could be used for industrial applications and to characterize this bacteriocin repertoire in this species.

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Link to Video: