Periplasmic Proteins Potentially Related with *In Vitro* Pathogenicity Induction in *Xanthomonas axonopodis*

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Citrus canker is an economically important disease that affects many citrus growing areas around the world. The causative agent is *Xanthomonas axonopodis* (*Xa*), a Gram-negative bacterium. *X. axonopodis* pv. *citri* (*Xac*-A) (reclassified as *X. citri*), *X. axonopodis* pv. *aurantifolii* B (*Xaa*-B) and *X. axonopodis* pv. *aurantifolii* C (*Xaa*-C) (both reclassified as *X. fuscans* subsp *aurantifolii*) are *Xanthomonas* strains that differ in virulence and citrus host. Their genome sequences were determined or are being completed. In this work we compared the protein profiles of the periplasmic fractions of *Xa* strains A, B and C after their growth in pathogenicity inducing medium (XAM1) or non-inducing medium (Nutrient Broth). SDS-PAGE profiles showed differences on protein expression in each strain in the two growth conditions (induction/ non-induction) and among the strains A, B and C. Some differential proteins of *Xac*-A had their amino-terminal sequenced and were identified using the BlastP tool against the *Xac*-A genome database. The proteins TonB-dependent receptor (60% identity), peptidoglycan hydrolase (55% identity) and signal transducer (71% identity) were down-regulated in inducing medium whereas the truncated cellulase S (66% identity) was up-regulated in this medium. Preliminary 2D-PAGE analysis of the *Xac*-A periplasmic fraction also revealed a distinct protein profile between pathogenicity induction and non-induction conditions. The differences in the periplasmic protein profiles of the *Xa* strains may be involved with the distinct virulence and host specificity of these strains. Proteomic analysis is underway.

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