

Functional analysis of *Xanthomonas axonopodis* pv *citri* genome

De Oliveira J.C.F.¹, Facincani, A.P.², Carvalho F.M.S.²; Laia, M.L.²; Ferro, M.I.T.²
and Ferro J.².

¹Departamento de Ciências Biológicas, UNIFESP, Diadema, SP. e-mail:
juliunifesp@yahoo.com.br. ²Departamento de Tecnologia, UNESP, Jaboticabal,
SP.

The citrus canker, caused by the Gram negative bacterium *Xanthomonas axonopodis* pv. *citri* (Xac) is considered one of the main diseases in the citriculture worldwide due to the susceptibility of the host and the lack of an effective and efficient method of control. We have been undertaking a functional post-genomic analysis in order to characterize genes and encoded proteins involved in pathogenicity and virulence. A transposon mutagenesis library was obtained and have been analyzed by individual inoculation in host citrus plants. Approximately 2,300 mutants were screened and some 100 mutants exhibiting altered pathogenicity or virulence profile were selected. The alteration on pathogenicity phenotype varies from subtle reduction or increase on canker symptoms, remarkable reduction of symptoms, or completes absence of canker lesions on inoculated leaves. The expression of Xac genes and proteins were analyzed during infecting conditions, Xac grown for 12 or 20 hours in XAM1 inducing medium or infecting Xac recovered from orange leaves at 3 or 5 days after inoculation. As control, Xac was grown in NB rich non-inducing liquid medium. Using a macroarray approach for the study of PIP (plant inducible promoter) genes, 67 genes were characterized as differentially expressed during infection (*in vitro* or *in vivo* induction). Proteomic analyses were preceded using 2D electrophoresis and MudPIT (multidimensional protein identification technology) approaches, and some 500 differentially expressed proteins were identified as expressed uniquely during infection. All together, the functional genome results can depict us a temporal pattern for the expression of genes and proteins related to bacterial fitness and pathogenicity/virulence mechanisms.

Palavras chave: *Xanthomonas citri*, cancro cítrico, genômica funcional