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**Towards identification of genes involved in pathogenicity of *Xanthomonas albilineans*, the pathogen causing sugarcane leaf scald**

Champoiseau P.<sup>1,2</sup>, Daugrois J.-H.<sup>1</sup>, Cociancich S.<sup>2</sup>, Pieretti I.<sup>2</sup>, Royer M.<sup>2</sup>, Rott P.<sup>2</sup>

<sup>1</sup>CIRAD, UPR Multiplication Végétative, Station de Roujol, 97170 Petit-Bourg, Guadeloupe, French West Indies ; <sup>2</sup>UMR 385 AGRO.M-CIRAD-INRA Biologie et Génétique des Interactions Plante-Parasite, TA 41/K. Campus International de Baillarguet. 34398. Montpellier Cedex 5. France.

Monique.royer@cirad.fr

The *hrp* or *avr* genes found in most plant pathogenic bacteria were not found in *Xanthomonas albilineans*, the causal agent of sugarcane leaf scald. This pathogen produces, however, a pathotoxin called albicidin that is involved in disease symptom development. Recently, all genes involved in albicidin biosynthesis were cloned and sequenced. Variation in these genes was, however, not correlated with variation in pathogenicity of *X. albilineans*. In this study, we attempted to identify new pathogenicity genes of *X. albilineans* using several approaches and 19 strains of the pathogen differing in disease severity and stalk colonization in Guadeloupe. The *in vitro* production of albicidin varied among strains of *X. albilineans*, but all strains showed the same RFLP (restriction fragment length polymorphism) pattern with albicidin biosynthetic genes and the same *SpeI* PFGE (pulsed-field gel electrophoresis) pattern. In contrast, variation among strains was found by AFLP (amplified fragment length polymorphism) with 16 selective primer combinations, after enzymatic digestion of total genomic DNA with *SacI* and *MspI*. No relationship between this genetic variation and variation in pathogenicity was, however, identified. A phylogenetic study with housekeeping genes *ihfA* and *efp* suggested that *X. albilineans* is on an evolutionary road between the *Xanthomonas campestris* group and *Xylella fastidiosa*, another vascular plant pathogen that does not possess *hrp* or *avr* genes. Sequencing of the whole genome of *X. albilineans*, in progress at Genoscope/France, will be the next step in unravelling pathogenicity of this sugarcane pathogen.