

## The complete genome sequence of *Xanthomonas albilineans* provides insights into pathogenicity of this sugarcane pathogen and allows further assessments of the large diversity within this species.

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### Objectives:

*Xanthomonas albilineans* is a xylem-invading pathogen that causes leaf scald, one of the major diseases of sugarcane. Previous studies revealed that i/ two important genomic features differentiate *X. albilineans* from other sequenced species of *Xanthomonas*: genome erosion and the presence of a type III secretion system (T3SS) of the SPI-1 family (1-2), and ii/ large variability exists among strains of *X. albilineans* and all strains involved in outbreaks of sugarcane leaf scald disease since the late 1980s belong to the same genetic group called PFGE-B (3). In the present study, we used the genome sequence of *X. albilineans* strain GPE PC73 to describe all pathogenicity-related features either shared with all species of *Xanthomonas* or specific to *X. albilineans*, and to further investigate the large diversity of this species.

### Results

Among the major virulence factors described so far in *Xanthomonads*, most of them are conserved in *X. albilineans*, except the T3SS of the Hrp family and the *gum* gene clusters, and Hrp T3SS effectors. The genome of *X. albilineans* also encodes specific pathogenicity-related factors including twelve non ribosomal peptide synthetases and five enzymes harboring a specific cellulose binding domain. Several DNA fragments present in PFGE-B strains and absent in other strains of the pathogen were isolated by suppression subtractive hybridization (SSH). Additionally, occurrence of methylation of genomic DNA by a specific Dam methyltransferase in PFGE-B strains, but not in other strains, was experimentally demonstrated. Large inter-strain variability in *X. albilineans* was confirmed using multi locus sequence analysis (MLSA), clustered regularly interspaced short palindromic repeats (CRISPR) and SSH markers.

### Conclusions

This study allowed us to identify several new candidate pathogenicity genes. In-depth functional analyses are now necessary to explore the role of these genes in the successful invasion of the sugarcane xylem vessels by *X. albilineans*.

1. Pieretti et al. 2009. *BMC Genomics*, 10:616.
2. Marguerettaz et al. 2010. *Molecular Plant-Microbe Interactions*, 24:246-259.
3. Davis et al. 1997. *Phytopathology*, 87:316-324.