

Abstract of Poster Presentation

The complete genome sequence of *Xanthomonas albilineans* provides new insights into the reductive genome evolution of the xylem-limited Xanthomonadaceae

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The Xanthomonadaceae includes two xylem-limited plant pathogenic bacteria, *Xanthomonas albilineans* and *Xylella fastidiosa*. The complete genome of *X. albilineans* was sequenced, providing not only strong clues to identify new pathogenicity factors in this pathogen causing sugarcane leaf scald disease, but also new insights into the evolution of Xanthomonadaceae. Previous phylogenetic analysis suggested that the *Xanthomonas* and *Stenotrophomonas* genera of Xanthomonadaceae form a coherent group excluding *X. fastidiosa*. Surprisingly, phylogenetic analysis using *X. albilineans* genomic sequences resulted in a different tree in which *X. fastidiosa* belongs to the *Xanthomonas* group. Based on this latter tree, *X. albilineans* and *X. fastidiosa* are derived from the progenitor of the *Xanthomonas* genus which itself is derived from the progenitor of *Stenotrophomonas*. Comparative genomic analysis identified 551 ancestral genes which are present in both *Xanthomonas axonopodis* pv. *vesicatoria* and *Stenotrophomonas* but absent in both *X. fastidiosa* and *X. albilineans*, revealing that these two latter species experienced a similar reductive genome evolution during their descent from the progenitor of the *Xanthomonas* genus. This degenerative evolution is probably driven by adaptation to the nutrient-poor xylem elements and to the cloistered environmental niche of xylem vessels. Comparable genomic erosion is observed among intracellular animal bacteria and is associated with a mutualistic life style. Adaptation of *X. albilineans* and *X. fastidiosa* to a xylem-limited life style is also illustrated by the unique characteristics of the enzymes involved in cellulose degradation, and the absence of a type III secretion system of the Hrp1 and Hrp2 injectisome families.