

Evolutionary History of the Plant Pathogenic Bacterium *Xanthomonas axonopodis*

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R sum  en anglais

Deciphering mechanisms shaping bacterial diversity should help to build tools to predict the emergence of infectious diseases. *Xanthomonads* are plant pathogenic bacteria found worldwide. *Xanthomonas axonopodis* is a genetically heterogeneous species clustering, into six groups, strains that are collectively pathogenic on a large number of plants. However, each strain displays a narrow host range. We address the question of the nature of the evolutionary processes - geographical and ecological speciation - that shaped this diversity. We assembled a large collection of *X. axonopodis* strains that were isolated over a long period, over continents, and from various hosts. Based on the sequence analysis of seven housekeeping genes, we found that recombination occurred as frequently as point mutation in the evolutionary history of *X. axonopodis*. However, the impact of recombination was about three times greater than the impact of mutation on the diversity observed in the whole dataset. We then reconstructed the clonal genealogy of the strains using coalescent and genealogy approaches and we studied the diversification of the pathogen using a model of divergence with migration. The suggested scenario involves a first step of generalist diversification that spanned over the last 25 000 years. A second step of ecology-driven specialization occurred during the past two centuries. Eventually, secondary contacts between host-specialized strains probably occurred as a result of agricultural development and intensification, allowing genetic exchanges of virulence-associated genes. These transfers may have favored the emergence of novel pathotypes. Finally, we argue that the largest ecological entity within *X. axonopodis* is the pathovar.

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