

New powerful tools for epidemiological analyses of *Xanthomonas citri* pv. *citri* with a strong evolutionary aftertaste

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The aggravation of epidemic situations for bacterial diseases is often correlated with the emergence of new groups of strains, either because changes in the environment have favored such groups or because the strains themselves have evolved to become more fit to their environment (including the host). To understand the parameters of these emergences plant bacteriologists must improve their knowledge of the populations dynamics (ie epidemiology) as well as adaptation mechanisms (ie evolution). They also need to be able to efficiently monitor changes while they happen. For pathogens such as *Xanthomonas citri* pv. *citri* (Xcc), the causal agent of Asiatic citrus canker, common genotyping tools are often not discriminant enough to address questions at rather small time or spatial scales. The sequence of the complete genome of Xcc proved a goldmine of new appropriate markers. In order to delve further into the structure of the populations of Xcc at a large (Asia) or smaller (Vietnam) scale, genotyping schemes involving insertion sequences (IS-LM-PCR) and variable number of tandem repeats (MLVA) were developed and used in addition to a reference technique, AFLP. The data were analyzed by classical population genetics methods, as well as by Bayesian and phylogeographical approaches. The three types of markers were highly congruent in describing the genetic diversity and population structure. Besides a clear identification of the Xcc pathotypes, these genotyping techniques allowed to make assumptions on the relationships between them, to describe the distribution of Xcc in Asia and to understand the population dynamics and genetics of Xcc at a smaller regional scale. The higher genetic diversity of pathotype A\* suggests that it may have a longer evolutionary history than pathotype A. In Vietnam, two differentiated pathotype A populations were identified with characteristics suggesting a recent and massive dissemination of a new population, likely through propagative material.

Conference

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<http://www.plantpath.iastate.edu/xgc2009/sites/default/files/XGC2009BookUpdated.pdf>