Investigating the population structure of *Xanthomonas citri* pv. *citri*. Which molecular markers to use to distinguish between low polymorphic bacterial populations?

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Comprehensive knowledge of pathogen population structures is crucial to understand the epidemiology and history of infectious diseases, but such data is largely unavailable for plant pathogenic bacteria. This constitutes a challenge for genetically monomorphic bacteria. *Xanthomonas citri* pv. *citri*, which causes asiatic citrus canker, a major disease and potential threat of citrus worldwide, is listed as a quarantine organism in many countries. Analysis of the molecular epidemiology of this bacterium is hindered by a lack of molecular typing techniques suitable for surveillance and outbreak investigation. We report a comparative evaluation of two typing techniques, insertion sequence ligation-mediated PCR (IS-LM-PCR) typing and multilocus variable-number tandem-repeat analysis (MLVA), in terms of the information derived from the techniques and their effectiveness for analysis of genetic and population structure of 557 strains of *X. citri* pv. *citri* originating from Vietnam. The results were as follows: (1) a higher level of polymorphism was observed for MLVA as shown by the greater number of haplotypes and the higher value of Simpson's index of diversity for MLVA data; (2) Pairwise correlations between genetic distances among individual strains or pairwise population genetic differentiation were highly significant for two typing methods; (3) The two molecular markers yielded similar phylogenetic trees and population structure of *X. citri* pv. *citri* in Vietnam. These results provide guidance for the effective use of these molecular methods in the genetic analysis and epidemiology of *Xanthomonas citri* pv. *citri* at different temporal or spatial scales.