Population structure and molecular epidemiology of *Xanthomonas citri* pv. *citri* refine citrus canker epidemiology

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The genetic characterization of isolates and structure analysis of pathogenic bacterial populations are useful to investigate their epidemiology. Short-term epidemiological questions such as the identification of inoculum sources or the interconnection of different outbreaks could be approached by molecular tracing. *Xanthomonas citri* pv. *citri* (*Xcc*), the causal agent of Asiatic citrus canker, is a bacterium displaying little genetic diversity, based on genotyping tools such as MLST or rep-PCR. It presents low levels of recombination, which result in clonal populations. For pathogens such as *Xcc*, common genotyping tools are often not discriminant enough to address questions at a rather small time or spatial scale. Variable Number of Tandem Repeats targeting 14 loci were developed to detect variations and to discriminate between isolates within a strain collection from Vietnam, where Asiatic citrus canker is endemic with no current control, and from Brazil, where the pathogen is currently under containment in Saõ Paulo state.

Four hundred and sixty four haplotypes out of 557 Vietnamese *Xcc* isolates from twelve provinces were identified. The Structure model-based clustering algorithm allows inference on genetic ancestry and identified two populations, V1 and V2, that have distinctive allelic frequencies and a Nei diversity index of 0.77 and 0.21, respectively. V1 was distributed in all provinces whereas V2 was limited in three northern provinces. A clonal complex analysis by eBurst produced 35 complexes, where all haplotypes are a single locus variant (SLV) of at least one other haplotype in the group, and 313 singletons. Nine complexes were distributed among different provinces. The largest clonal complex included 108 *Xcc*-V2 strains from three provinces with the founder located in a national citrus propagation center.

Two hundred and twenty seven haplotypes were identified out of the 308 isolates in our Brazilian collection. Two ancestral populations were most significantly inferred by the Structure Bayesian approach. Population B1 was only found in the two southern states of Rio Grande do Sul (RS) and Santa Catarina (SC). Population B2 was inferred in the states of Parana (PR), Saõ Paulo (SP) and RS. Twenty-six clonal complexes, all within SP state, and 147 singletons were identified. Most clonal complexes were composed of strains from a single location and year of isolation, indicative of epidemic clonality. Allelic richness calculated by the rarefaction method and diversity index were a little higher for the group of strains from SC, RS and PR than for SP strains which are under eradication, with values of 6.22 / 0.67 and 5.25 / 0.54, respectively. At a larger level, allelic richness and diversity index were greater in Vietnam than in Brazil with values of 12.9 / 0.74 and 8.4 / 0.60, respectively.

Molecular epidemiology and population's genetics may contribute to improve and refine our knowledge in the epidemiology of plant pathogenic bacteria even in the case of genetically monomorphic pathogens.