

Genomic-based development of a real-time PCR protocol for improving the diagnosis of *Xanthomonas arboricola* pv. *pruni*, the causal agent of bacterial spot disease of *Prunus* spp.

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Comparative genomics of *Xanthomonas arboricola* species has unveiled a detailed view of the intraspecific evolutionary history of this plant-pathogen as well as a characterization of its pathogenic arsenal associated with the disease process. In addition to these analyses, phenotypic and pathogenic assays have revealed the presence of non-pathogenic strains which are phylogenetically different to those pathogenic strains of the pathovars *pruni*. Comparative analyses among these two groups showed up a wide range of genomic regions that could be useful to differentiate these two intraspecific groups that cohabit on *Prunus*. Taking advantage of the variation in this genomic feature, a real-time PCR protocol, based on a partial sequences of the *xopE3* gene, has been developed to differentiate *Prunus*-pathogenic and non-pathogenic strains of *X. arboricola* and to refine the diagnosis of this quarantine pathogen in the EU. The use of this new protocol in conjunction with a previous protocol based in the amplification of the gen *ftsX* showed a high specificity to differentiate pathovar *pruni* from the other intraspecific groups of *X. arboricola* as well as a high sensitivity (100 cfu/ml or 100 pg/μl of DNA) and efficiency (1.8-2.0, being 2.0 a 100% of efficiency). This new protocol is a valuable molecular tool for the improvement of the diagnosis of the causal agent of bacterial spot of stone fruits and almond.