

**PHENOTYPIC AND GENOMIC ANALYSIS OF *Xanthomonas arboricola* STRAINS ALLOWED TO IDENTIFY FEATURES ASSOCIATED TO PATHOGENESIS IN *X. arboricola* pv. *pruni***

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*Xanthomonas arboricola* is a bacterial species that includes nine pathovars classified according to their phytopathogenic specialization and molecular characteristics. One of these pathovars is *X. arboricola* pv. *pruni*, a quarantine organism in the EU, which is the causal agent of bacterial spot disease on *Prunus* spp. After an initial molecular and phenotypic characterization of pathogenic and non-pathogenic strains of *X. arboricola* isolated from *Prunus* in Spain, seven strains were selected for complete genome sequencing. Comparisons of general characteristics of the genomes, and particularly, the presence of 408 orthologs associated with initial stages of pathogenesis (sensing, adhesion, chemotaxis and motility) and of those involved in mechanisms of interaction after bacterial penetration into the host tissue (xanthan biosynthesis, type II secretion system, secretion of degradative enzymes, type II secretion system, type III effectors and type IV secretion system) were carried out. The analyses included the *Prunus*-isolated strains and other *X. arboricola* of pathovars *corylina*, *juglandis* and *celebensis* isolated from hazelnut, walnut and banana, respectively. The comparative analysis allowed to identify genomic variants among pathogenic and non-pathogenic *Prunus* strains as well as among the three pathovars analysed, which reveals insights associated with pathogenicity features and host specificity in *X. arboricola* pv. *pruni*.

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