



Molecular tools allow the description of new taxons at species and infra-specific levels among plant pathogenic bacteria

María M. López¹, Pablo López-Soriano¹, Silvia Barbé¹, Javier Peñalver¹, Pablo Llop¹, Ester Marco-Noales¹, Jerson Garita-Cambroner², Aitana Ares-Yebra³, Adela Abelleira³, Olga Aguín³, Jaime Cubero², Ana Palacio-Bielsa⁴

¹ Instituto Valenciano de Investigaciones Agrarias, Moncada, Valencia, Spain

² Laboratorio de Bacteriología, Departamento de Protección Vegetal, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain

³ Estación Fitopatológica do Areeiro, Diputación de Pontevedra, Pontevedra, Spain

⁴ Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain

Diagnostic of plant diseases is evolving and improving day by day. Molecular-based tools such as real-time PCR, LAMP, microarrays, barcoding and Next Generation Sequencing are enhancing the accuracy of the detection and identification of plant pathogenic bacteria. These technologies are currently based on the use of available nucleic acid sequences and information about the molecular interactions bacterial pathogen-plant host. The target DNA sequences selected for these techniques must be distinctive and based on conserved regions, in order to identify only one species, subspecies, pathovar or a particular set of genes. However, the currently available databases contain only a small portion of the sequences of the microbes present in complex environments. The use of integrated approaches for detection and identification of plant pathogenic bacteria has allowed the discovery of differences among strains classified to date in the same species but showing distinct characteristics in molecular identification tests. Three examples are presented: 1) *Erwinia piriflorinigrans*, a new pathogenic species described in Spain as causal agent of necrosis of pear blossoms that is closely related to *E. amylovora*, 2) a new *Xanthomonas* sp., also isolated in Spain and responsible of symptoms similar to those of *Xanthomonas arboricola* pv. *pruni*, but classified as different to this species according to multi-locus sequencing analysis as well as to serological and PCR identification, 3) the new group of *Pseudomonas syringae* pv. *actinidiae* strains described from New Zealand, France and Spain, that show low virulence and different molecular characteristics. The description of new species or infra-specific groups leads to a more comprehensive knowledge of the complex pathosystems in agricultural industry and nature. Moreover, the partial or complete genomes of new taxons that are being determined will offer new omics-based tools for improving the detection, identification and taxonomy of bacterial plant pathogens.