Genomic analysis of eight native plasmids of the phytopathogen *Pseudomonas syringae*

José A. Gutiérrez-Barranquero[1], Francisco M Cazorla[1], Antonio de Vicente[1], George W. Sundin[2]

[1]Instituto de Hortofruticultura Subtropical y Mediterránea La Mayora (IHSM-UMA-CSIC), Departamento de Microbiología, Facultad de Ciencias, Universidad de Málaga, Málaga, Spain

[2]Department of Plant, Soil, and Microbial Sciences, Michigan State University, East Lansing, Michigan 48824, USA

The pPT23A family of plasmids (PFPs) appears to be indigenous to the plant pathogen *Pseudomonas syringae* and these plasmids are widely distributed and widely transferred among pathovars of *P. syringae* and related species. PFPs are sources of accessory genes for their hosts that can include genes important for virulence and epiphytic colonization of plant leaf surfaces. Further understanding of the evolution of the pPT23A plasmid family and the role of these plasmids in *P. syringae* biology and pathogenesis, requires the determination and analysis of additional complete, closed plasmid genome sequences. Therefore, our main objective was to obtain complete genome sequences from PFPs from three different *P. syringae* pathovars and perform a comparative genomic analysis. In this work plasmid DNA isolation, purification by CsCl-EtBr gradients, and sequencing using 454 platform, were used to obtain the complete sequence of *P. syringae* plasmids. Different bioinformatic tools were used to analyze the plasmid synteny, to identify virulence genes (*i.e.* type 3 effectors) and to unravel the evolutionary history of PFPs. Our sequence analysis revealed that PFPs from *P. syringae* encode suites of accessory genes that are selected at different levels (universal, interpathovar and intrapathovar). The conservation of type IVSS encoding conjugation functions also contributes to the distribution of these plasmids within *P. syringae* populations. Thus, this study contributes to unravel the genetic basis of the role of PFPs in different *P. syringae* lifestyles.

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