Genomic analysis of eight native plasmids of the phytopathogen

_Pseudomonas syringae_

José A. Gutiérrez-Barranquero¹, Francisco M Cazorla¹, Antonio de Vicente¹, George W. Sundin²

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

²Department 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.

This work was supported by grants Proyecto de Excelencia, Junta de Andalucía (P07-AGR-02471; P12-AGR-1473) and by Michigan State University AgBioResearch.