

518 COMPARATIVE GENOMIC ANALYSIS OF NATIVE PSEUDOMONAS SYRINGAE PLASMIDS BELONGING TO THE PPT23A FAMILY REVEALS THEIR ROLE IN P. SYRINGAE EPIPHYTIC AND PATHOGENIC LIFESTYLES

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Backgrounds

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.

Objectives

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 of PFPs from three different *P. syringae* pathovars and perform a comprehensive comparative genomic analysis.

Methods

In this work plasmid DNA isolation, purification by CsCl-EtBr gradients, and sequencing using 454 platform, were carried out 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.

Conclusions

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 bases of the role of PFPs in different *P. syringae* lifestyles.

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