Presence of large number of highly expressed transposase and transposase helper genes in the genome of *Pseudomonas syringae* DC3000

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Abstract

An important plant pathogen that infects multitude of plant species across the world, *Pseudomonas syringae* has attracted significant research attention for the past decades. Specifically, the genome sequence of the Gram-negative plant pathogen has been sequenced, and RNA-seq has been employed to probe the differential gene expression programmes that exist in the bacterium, and which may be correlated with plant pathogenesis. Analysis of one such RNA-seq experiment (ArrayExpress accession number: E-MTAB-3779) with a corresponding Genbank genome file (Genbank accession number: NCBI Reference Sequence: NC_004578.1) revealed the presence of large number of highly expressed transposase and transposase helper proteins in phyllosphere inhabitant, *P. syringae* DC3000. Given that high transposase activity meant a corresponding relative instability in the genome of the species, *P. syringae* DC3000 may derive part of its pathogenicity to high mutability of its genes, that enabled the species to effectively evade the immune response of different plant species. Hence, presence of large number of highly expressed transposase and transposase helper genes in *P. syringae* DC3000 highlights one area in which efforts to retard the spread of this plant pathogen could be focused on: i.e., in using CRISPR-Cas9 in inactivating these genes; thereby, partially negating the pathogenicity of this important plant pathogen.

Keywords: *Pseudomonas syringae* DC3000, transposase, transposase helper protein, RNA-seq, gene inactivation,

Subject areas: plant biology, microbiology, molecular biology, biochemistry,

Conflicts of interest

The author declares no conflicts of interest.

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