PHYLOGENOMICS OF THE *PSEUDOMONAS SYRINGAE* SPECIES GROUP

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The genus *Pseudomonas* is taxonomically divided in two phylogenetic lineages (*P. aeruginosa* and *P. fluorescens*) based on multilocus sequence analysis (MLSA) of four housekeeping genes (16S rRNA, *gyrB*, *rpoB* and *rpoD*). *P. fluorescens* lineage is divided into six groups, one of them represented by *Pseudomonas syringae*. Currently, the *P. syringae* species group is subdivided into more than 60 pathovars defined by pathogenic characters, nine genomospecies defined by DDH and 13 phylogenetic groups (phylogroups) defined by MLSA.

With the objective to clarify the taxonomic species delineation in the *P. syringae* group, more than 100 strains of species within the group and whose genomes have been sequenced and are available in databases were analysed by a phylogenomic approach. MLSA, Average nucleotide identity based on BLAST (ANIb) and Mummer (ANIm), Genome-to-Genome Distance Calculator (GGDC) as well as core and pangenome analyses were performed to delineate genomic species. Genes encoding virulence factors, secretion systems and effectors, were studied in detail to clarify the pathogenicity potential of strains in the *P. syringae* group. Genome comparison of close-related pathogenic and non-pathogenic strains were also performed.

All methods tested were concordant and allowed to infer the taxonomic affiliation of all genomes analysed, some of them not correctly assigned to species. The pathovars did not follow the genomic clusters already defined. New genomic groups can be distinguished belonging to putative novel species. Genomic and phylogenetic approaches will provide the basis for a more reliable demarcation of *Pseudomonas* phytopathogenic species.