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A broad and operational classification framework to address the ecology of *Pseudomonas syringae* populations

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Summary

Understanding ecology of pathogens like *Pseudomonas syringae* is central to addressing the complexity of disease emergence and pathogen evolution and to develop effective and sustainable methods of control. An indispensable prerequisite is a classification tool that represents as much of the diversity as possible and delimits accurately the boundaries. By adopting an intensive sampling strategy from several continents and multiple substrates within and beyond agricultural zones we made reliable phylogroup delimitation through multi-locus sequence typing (MLST). We identified 23 clades of *P. syringae* within 13 phylogroups among which the seven previously described were included. The robustness of MLST-phylogroups was confirmed by the phylogeny of the core genome of representative strains. We demonstrated that the citrate synthase (*cts*) housekeeping gene can accurately predict phylogenetic affiliation for more than 97 % of more than 700 strains and we proposed a list of *cts* sequences to be used as a simple tool for quickly and precisely classifying new strains. We therefore proposed an expandable framework mainly based on a broad database and *cts* genetic analysis into which more diversity can be integrated. Phenotypic traits rarely provided means for classification even if some combinations were highly probable in some phylogroups. However, by clarifying the classification of strains from a wide range of habitats and describing the genotypic and phenotypic profiles of the different phylogroups, we revealed a fascinating diversity of life histories and adaptive strategies deployed within the *P. syringae* complex. This has led us to also develop specific genetic markers, one allowing the assignment of strains to the *P. syringae* complex at large and others to the individual phylogroups. Using these markers in simple, rapid, reliable and cheap multiplex PCR will allow a medium throughput screen of *P. syringae* strains leading to easy assessment of population structure in a wide range of samples.

Key Words: Phylogeny, data base, classification tool, citrate synthase, specific PCR.

Thematic Area: b) Evolution, taxonomy and systematics