Improvement of the identification of the *Pseudomonas syringae* group:  
a molecular approach  

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The genus *Pseudomonas* accommodates a number of pathogenic species. The type species of the genus for instance, *Pseudomonas aeruginosa*, is frequently associated with infections of the urinary and respiratory tracts in humans. Certain species of *Pseudomonas* are well-known plant pathogens; *P. syringae* is frequently isolated from leaves showing yellowing lesions, and *P. marginalis* is a typical ‘soft-rot’ pathogen, infecting stems and shoots but rarely leaves. Because of the impact of these pathogenic species on human economy and health, an accurate identification is of utmost importance.

Unfortunately, taxonomy of the genus *Pseudomonas* is obscure with a lot of strains being misnamed, misclassified and/or poorly described. This is mainly due to the taxonomic history of *Pseudomonas* and inadequate identification tools. For a long time, all Gram-negative, rod-shaped, polar flagellated bacteria were classified in the genus *Pseudomonas*. 16S rRNA gene sequencing revealed the heterogeneity of the genus, resulting in a major reorganisation that started some fifteen years ago and is still ongoing. Yet, clarification of the *Pseudomonas* taxonomy is hampered by the use of identification techniques with insufficient discriminatory power (e.g. API), leading to false nomenclature.

The applicability of other conservative genes (e.g. *rpoB* gene) for taxonomic purposes is currently under investigation. This study reports on the simultaneous use of several conservative genes (among which *rpoB*, *atpA* and *glnA*) to reveal the taxonomic mix-up within the *Pseudomonas syringae* group. Use of the *rpoB* gene has already been described by Ait Tayeb et al. (2005) for identification purposes of pseudomonads and the *atpA* gene has already been used for phylogenetic analysis of vibrios and related species (Thompson et al., 2007), indicating the applicability of these genes in revealing the phylogeny of the *Pseudomonas syringae* group.
