# Polyphasic study of plant- and clinic-associated Pantoea agglomerans strains reveals indistinguishable virulence potential.

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**Abstract**

Pantoea species are ubiquitous in nature and occasionally associated with infections caused by contaminated clinical material. Hence, Pantoea agglomerans is considered as an opportunistic pathogen of humans. Since species of the genus Pantoea and closely related species of other Enterobacteriaceae genera are phenotypically very similar, many clinical isolates are misassigned into P. agglomerans based on the use of quick commercial-offered biochemical tests. Our objective was to find markers enabling discrimination between clinical and plant isolates and to assess their virulence potential. We characterized 27 Pantoea strains, including 8 P. agglomerans isolates of clinical, and 11 of plant origin by biochemical tests and genotyping, including analysis of 16S rDNA and gapA gene sequences, and pattern polymorphisms of ITS- and ERIC/REP-DNA. All data showed that no discrete evolution occurred between plant-associated and clinical P. agglomerans isolates. Based on the typing results, five clinical- and five plant-associated P. agglomerans strains representing the majority of clades were tested on a model plant and in

embryonated eggs. On soybean plants P. agglomerans strains independent of their origin could develop stable epiphytic populations. Surprisingly, in the embryonated egg model there was no difference of virulence between clinical and vegetable P. agglomerans isolates. However, these strains were significantly less virulent than a phytopathogenic P. ananatis isolate. We suggest that, independent of their origin, all P. agglomerans strains might possess indistinguishable virulence potential.

## Involved units

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