

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.

Beteiligte Forschungseinheiten

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