

Comparative phenotypic and genotypic properties of pseudomonas aeruginosa isolates from clinical and environmental sources

ABSTRACT

Objective: To provide a better understanding on the potential threat of *P. aeruginosa* as a whole, this study was conducted to compare the phenotypic and genotypic characteristics between isolates from the two different sources. **Method:** Twenty isolates were successfully harvested from soil while 30 clinical isolates were viably available in collection for comparison. Several biochemical tests and 16S rRNA DNA sequence homology were conducted for species identification. Pigmentation, antimicrobial susceptibility pattern and virulence genes distribution were determined and correlated in 2x2 contingency tables. BOX- and ERIC-PCR were done to identify the genetic relationship among the 50 isolates. **Result:** All soil isolates showed only pyoverdine pigment production while clinical isolates produced either pyocyanin or pyoverdine, or both pigments. Soil isolates were largely susceptible to the tested antibiotics while antimicrobial resistance as well as multidrug resistance was observed among clinical isolates. Virulence genes were differentially detected in both clinical and soil isolates with *exoS* being the most dominant in both groups of isolates. Composite analysis of BOX-ERIC-PCR indicated all isolates to have no close genetic relationship. **Conclusion:** Soil isolates are largely susceptible to antibiotics but do carry important virulence genes and pyoverdine. The later was reported to be associated with biofilm capacity which may facilitate survival of isolates in environment as well as during human infection. Therefore, both groups of isolates may pose infection threat at various degrees.

Keyword: *Pseudomonas aeruginosa*; Pigmentation; Virulence genes; Antibiotic susceptibility; Composite BOX-ERIC-PCR