TITLE: MOLECULAR TYPING AND VIRULENCE TRAITS OF *Pseudomonas aeruginosa* ISOLATES FROM A REFERENCE HOSPITAL IN PARÁ STATE, AMAZON REGION, BRAZIL

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ABSTRACT:

Pseudomonas aeruginosa is one of the major causes of hospital-acquired infections, contributing to an increase in mortality rates and treatment costs, particularly of critically ill patients. Characteristics that favor its pathogenicity and persistence in different environments are related to its high adaptability and wide repertoire of virulence factors. Molecular typing of isolates provides insights into the transmission dynamics and genetic diversity of *P. aeruginosa*. In the present study, we determined the genetic diversity and virulence traits of *P. aeruginosa* isolated from intensive care unit (ICU) patients at a reference hospital. A total of 54 non-duplicate *P. aeruginosa* isolates recovered from patients admitted to the adult, pediatric and neonatal ICUs, were evaluated. Molecular typing was performed by semi-automated rep-PCR (Diversilab®) and multilocus sequence typing (MLST). The presence of 19 virulence-associated genes (*algU, algD, lasA, lasB, aprA, toxA, exoS, exoU, exoT, exoY, phzI, phzII, phzM, phzS, phzH, lasI, lasR, rhIL* and *rhIR*) was investigated by PCR. All isolates were genotyped by rep-PCR, which demonstrated the presence of 36 clones, where 26 were considered unrelated (≤ 97% similarity) and 10 clustering two or more clonally-related isolates (similarity > 97%). One isolate from each pattern was genotyped by MLST, which revealed the presence of 22 different sequence type (ST), including the emergence of seven novel STs (ST 2524, ST 2541, ST 2552, ST 2554, ST 2555, ST 2556 and ST 2603). At least five genes per isolate were detected and 17 of the 19 investigated genes were present in more than 50% of the isolates ($p< 0.01$). Moreover, the detection of virulence-related genes revealed a high prevalence of the *toxA, exoS, lasR, phzI, lasI* and *algD* genes (>90.0% of isolates) and *lasB*, *rhlL* and *rhlR* in the all isolates. The genotype *exoS*$^{+}$/*exoU*$^{-}$ was detected in 23 isolates (42.6%) and *exoS*$^{-}$/*exoU*$^{+}$ in four isolates (7.4%). In conclusion, we observed a wide genetic diversity, with the identification of 7 novel STs, and high virulence potential of the isolates from the study site. Our results may help in establishing control strategies and reduce the risk of potentially lethal outbreaks.

Keywords: *Pseudomonas aeruginosa*, molecular typing, virulence

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