TITLE: MOLECULAR EPIDEMIOLOGY OF KPC-PRODUCING *Pseudomonas aeruginosa* OVER A 10-YEARS IN A TEACHING HOSPITAL OF SOUTHERN BRAZIL.

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ABSTRACT:
The emergence of Multidrug Resistant *P. aeruginosa* (MDR-PA) isolates is a major public health concern, since antimicrobial resistance determinants are acquired through lateral gene transfer. This study aimed to detect genes of acquired antimicrobial resistance in MDR-PA and to establish a clonal relation and genetic context among isolates of KPC-2-producing *P. aeruginosa* recovered from January 2008 to December 2017 at the Hospital Universitário de Londrina (HU). The identification and antimicrobial susceptibility tests were performed by Vitek-2 (BioMéuriex®) automated system and conventional biochemical tests. The following antimicrobial resistance codifying genes were screened by multiplex PCR to: carbapenemases A, B and D of Ambler classes, *mcr*-1, 16S rRna methyltransferases (16S-RMTases) *qnr* and genes encoding virulence factors. Molecular identification was performed for *P. aeruginosa* and the clonal relation was analyzed by ERIC-PCR and the genetic context of bla_{KPC} gene was determined by PCR-*mapping*. A total of 19 MDR-PA isolates KPC-2-producing were analysed and with exception of polymyxins (100% susceptible) high resistance rates were obtained for all tested antimicrobials. Considerable increase of KPC-producing isolates was detected in comparison with previous searches in the same hospital, where the prevalent antimicrobial resistant determinant in *P. aeruginosa* was the bla_{SPM} gene. None of the investigated genes for *mcr-1*, 16S-RMTases and quinolones were detected in the isolates; however, multiple genes associated with virulence were found in all isolates. The 19 MDR-PA isolates codifying bla_{KPC} gene were typed in 8 clones (A-H) distributed over the period analysed in diverse hospital units. The 8 clones obtained reveal the adaptation of this resistance determinant in our hospital, probably moved by the selective pressure of the carbapenem usage. These results show that the rates and the distribution of acquired antimicrobial resistance genes can floating in an institution over the years and that the surveillance and detection of them is essential to establish the infection control measures in order to safeguard the effectiveness of the drugs in the treatment of *P. aeruginosa* infections.

Keywords: *Pseudomonas aeruginosa,* carbapenemase, genetic diversity

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