TITLE: CHARACTERIZATION OF ACQUIRED ANTIMICROBIAL RESISTANCE DETERMINANTS IN CLINICAL ISOLATES OF MULTIDRUG RESISTANT *Pseudomonas aeruginosa* FROM SOUTHERN BRAZIL

AUTHORS: [1]PALERMO, R. L., [1]ROMANIN, P., [1]CAVALINI, J. F., [1]PAULA, S. B., [1]VENANCIO, E. J., [2]TOGNIM, M. C., [1]CARRARA-MARRONI, F. E, [1]OGATTA, S. F. Y.

INSTITUTION: [1]UNIVERSIDADE ESTADUAL DE LONDRINA (RODOVIA CELSO GARCIA CID, PR 445 KM 380, CEP 86057-970, LONDRINA-PR, BRAZIL); [2]UNIVERSIDADE ESTADUAL DE MARINGÁ (AVENIDA COLOMBO 5790 CEP 87020-900 MARINGÁ-PR, BRAZIL)

ABSTRACT:

The emergence of Multidrug Resistant *P. aeruginosa* (MDR-PA) strains 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 among isolates recovered from January 2015 to December 2016 at the University Hospital of Londrina (UHL). The identification and antimicrobial susceptibility tests were performed by automated systems 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, Rmt and *qnr* genes. Molecular identification was performed for *P. aeruginosa* and the clonal relation was analyzed by ERIC-PCR. A total of 198 MDR-PA isolates were analysed and with exception of polymyxins (100% susceptible) high resistance rates were obtained for all antimicrobials. Worrisome rates were found for carbapenems: 81,5% (imipenem) and 82,5% (meropenem). Among the 198 MDR-PA, 38 (19,2%) presented β-lactamases codifying genes and 26 (13,1%) borne carbapenemases genes, diverging of the two previous searches where a rate of 33,0% was obtained. Furthermore, the new distribution of β-lactamases codifying genes was verified: 10 harbored the bla_{KPC}, 14 bla_{SPM}, 2 bla_{IMP}, 6 $bla_{CTX\text{-}M\text{-}2}$ and 6 bla_{GES}, indicating a greater rate of KPC-producing isolates and a reduction of SPM-producing isolates in comparison with the previous searches. None of the investigated genes for *mcr-1*, 16S-RMTases and quinolones were detected in the isolates. The 32 MDR-PA codifying β-lactamases genes were typed in 12 clones (A-L) distributed over the period analysed in diverse hospital units. The isolates harboring the bla_{SPM} gene were grouped in one single clone, suggesting a clonal dissemination and that the clone A is the responsible for the maintenance of this resistance determinant in UHL. For the 10 KPC-producing isolates 7 clones were obtained revealing 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 floated in our institution and that the surveillance and detection of them is essential to establish infection control measures in order to safeguard the effectiveness of the drugs in the treatment of *P. aeruginosa* infections.

Keywords: Acquired resistance determinants, multidrug resistant, *Pseudomonas aeruginosa*

Development Agency: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior