

TITLE: FREQUENT CONCOMITANCE OF ANTIMICROBIAL RESISTANCE MOLECULAR MARKERS IN GRAM-NEGATIVE BACILLI RESISTANT TO CARBAPENEMS

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ABSTRACT:

Gram-negative bacilli (GNB) producers of carbapenemases are the main cause of Healthcare-Associated Infections in Brazil nowadays, partially because limited effective antibiotic therapy. The co-existence of genes encoding antimicrobial resistance in these microorganisms has been reported in several regions of the world, further reducing the therapeutic options. Our aim was to investigate the co-existence of molecular determinants of antibiotic resistance in GNB resistant to carbapenems. There were evaluated 157 clinical isolates collected during 9 consecutive years in a private general hospital in southern Brazil. Identification of the species was performed by automated method and the evaluation of antibiotic susceptibility by disc-diffusion in agar. The occurrence of genes *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like}, *bla*_{OXA-58-like}, *bla*_{OXA-143-like}, *bla*_{OXA-48-like}, *bla*_{VIM}, *bla*_{IMP}, *bla*_{SPM-1}, *bla*_{NDM-1}, and *bla*_{KPC} was investigated by polymerase chain reaction. The isolates analyzed were derived from bronchoalveolar lavage (31%, n = 48), rectal swab (20%, n = 32), wound secretion (15%, n = 24), urine (14%, n = 22), blood (6%, n = 9) and other less frequent sample types (14%, n = 22). Most of isolates were collected at the Intensive Care Unit and at the hospitalization units (37%, n = 58; 41%, n = 65, respectively). *Acinetobacter calcoaceticus* - *Acinetobacter baumannii* complex (ABC) strains comprised the majority of isolates (46%, n=72), followed by *Pseudomonas aeruginosa* (27%, n = 43), *Klebsiella pneumoniae* (20%, n = 31), *Enterobacter cloacae* (4%, n = 7) and 4 (3%) isolates distributed in species with less frequency. Genes co-existence was observed in 85 (54%) isolates, most of them belonging to ABC (82%, n = 70), followed by *K. pneumoniae* (13%, n = 11). The concomitants found were *bla*_{OXA-51-like} + *bla*_{OXA-23-like} (62%, 53/85), in *K. pneumoniae*; *bla*_{KPC} + *bla*_{OXA-51-like} + *bla*_{OXA-23-like} (8%, 7/85) and *bla*_{VIM} + *bla*_{OXA-51-like} + *bla*_{OXA-23-like} (7%, 6/85), both among ABC; *bla*_{NDM-1} + *bla*_{VIM} in strains identified as *E. cloacae* complex (n = 2), *K. pneumoniae* (n = 1) and *P. aeruginosa* (n = 2). Of note, among isolates of ABC, 97% (70/72) showed co-existence of the investigated genes, an expressive rate when compared with corresponding frequencies in *K. pneumoniae* and *P. aeruginosa* (35% and 9%, respectively). In conclusion, it was observed a high frequency of resistance markers concomitance, especially in the most recent years of the historical series analyzed.

Keywords: antimicrobial resistance, carbapenem resistance, gram-negative bacilli, multiple antibiotic resistance, resistance markers

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