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-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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