SILENT SPREADERS: COLONIZATION BY MULTIDRUG-RESISTANT Enterobacterales IN A BRAZILIAN HOSPITAL

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Introduction: The prevalence of antibiotic-resistant bacteria has challenged the effective treatment of infectious diseases. Multidrug-resistant (MDR) bacteria play a key role in patient colonization and infection, particularly in healthcare settings. Colonized patients act as reservoirs of resistant strains, contributing to the persistence and dissemination of these pathogens within hospitals and into the environment.

Objective: To characterize the diversity and antimicrobial resistance profiles of Enterobacterales associated with colonization in hospitalized patients.

Methods: Rectal swabs were collected from hospitalized patients in a university hospital. Bacterial identification was performed using MALDI-TOF MS. Antimicrobial susceptibility was assessed by disk diffusion following Clinical and Laboratory Standards Institute (CLSI) guidelines, including cephalosporins (ceftazidime, cefotaxime and cefepime), carbapenems (ertapenem, meropenem and imipenem), aminoglycosides (gentamicin and amikacin), tetracycline, and fluoroquinolone (ciprofloxacin). Minimum inhibitory concentrations (MICs) for polymyxin B were also determined by broth microdilution according to CLSI guidelines. Carbapenemase production was evaluated using modified Carbapenem Inactivation Method (mCIM) and EDTA-modified CIM (eCIM). Polymerase Chain Reaction (PCR) was performed on polymyxin B-resistant isolates to detect mobile colistin resistance genes (*mcr-1* to *mcr-9*).

Results: A total of 66 Enterobacterales isolates were recovered, all classified as MDR. Resistance to polymyxin B was observed in 14 isolates, however, no *mcr* genes were detected. Carbapenemase production was identified in 45 isolates, including 38 producing serine-β-lactamases and 7 producing metallo-β-lactamases.

Discussion: The high frequency of MDR Enterobacterales among colonized patients reinforces the role of the intestinal microbiota as an important reservoir of resistant bacteria in hospital settings. The absence

of *mcr* genes in polymyxin-resistant isolates suggests alternative resistance mechanisms, likely driven by chromosomal mutations. Additionally, the predominance of β-lactamase-producing isolates highlights the selective pressure exerted by antimicrobial use in healthcare settings, favoring the persistence and dissemination of resistant strains.

Conclusion: Colonization by MDR Enterobacterales represents a critical and often overlooked reservoir of antimicrobial resistance. These findings highlight the urgent need for active surveillance and robust antimicrobial stewardship strategies to curb the dissemination of high-risk resistant pathogens.

Agradecimentos: The authors would like to thank the microbiology team of Hospital Universitário Antônio Pedro (HUAP/EBSERH) for their technical support. We also acknowledge the institutional support provided by Universidade Federal Fluminense (UFF) and the Programa de Pós-Graduação em Microbiologia e Parasitologia Aplicadas (PPGMPA/UFF). This study was supported by CAPES.