TITLE: ANTIMICROBIAL RESISTANCE IN *P. AERUGINOSA* ISOLATES FROM PRIVATE AND PUBLIC HOSPITALS OF MARANHÃO

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ABSTRACT:

P. aeruginosa is an opportunistic microorganism frequently isolated of clinical specimens with simultaneous resistance to several antimicrobial agents. The knowledge about its epidemiology is essential to develop measures that prevent the spread of multidrug resistant strains. The goal of this study was to perform a phenotypic and molecular characterization of the antimicrobial resistance in P. aeruginosa strains from public and private hospitals. In general, the strains showed a higher resistance to carbapenems in both hospitals (66.6%). In an attempt to investigate the presence of DNA sequences related to resistance mechanisms, specifically ß-lactamases and efflux pump systems, it was found that the mexT (90.9%), oprJ (89.1%), oprD (87.3%), oprN (83.6%), mexC (68.2%), nfxB (79.1%), and mexA (77.3%) were detected in high frequency, whereas the genes mexE (14.6%), mexX (38.2%), and mexR (40%) were comparatively less prevalent. Among the efflux pump genes analyzed, only the mexXwas associated to resistance to many antibiotics tested (p<0.05). The probability of finding a P. aeruginosa isolate with mexR gene in public hospital was almost threefold (2.91) higher than in the private ones. However, comparing the relationship between the amount of resistance genes and antibiotic resistance classification groups, about 60.4% of the strains showed more than seven resistance genes, confirming the versatility of this microorganism. Therefore, it is necessary to control the P. aeruginosa resistance profile, because the characterized and identified data of strains carrying resistance can help the clinic in choosing of the best therapeutic option.

Keywords: *Pseudomonas*; resistance; efflux pump; β-lactamase.

Development Agencies: FAPEMA