

Title: INVESTIGATION OF SUSCEPTIBILITY PROFILE, AMINOGLYCOSIDES RESISTANCE GENES AND GENETIC SIMILARITY OF *Acinetobacter baumannii* ISOLATES IN A TERTIARY HOSPITAL

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Abstract:

A. baumannii is often found in nosocomial infections, causing ventilator-associated pneumonia, bacteremia, urinary tract infections and secondary meningitis. In recent years, the extensive use of antibiotics in hospitals has contributed to the rise and emergence of strains resistant to antimicrobials, including carbapenems, the main antibiotics recommended for treatment. Thus, aminoglycosides gain importance as therapeutic options. Resistance to aminoglycosides is mainly due to the Aminoglycoside Modifying Enzymes (AMEs) and 16S rRNA Methylases production. To the present, three classes of AMEs and several methylases were described. These enzymes are codified by genes located in mobile genetic elements with high dissemination capacity. In Brazil, high rates of infection by carbapenem-resistant *A. baumannii* are observed, however information about the aminoglycoside susceptibility profile and diversity of codifying genes are scarce. Therefore, this study was designed to evaluate the antimicrobial susceptibility profile, the presence of genes for AMEs and 16S rRNA Methylases and the genetic similarity among *A. baumannii* isolates with clinical importance in a Tertiary Hospital in São José do Rio Preto, SP. A total of 32 isolates collected between December 2013 and May 2014 were evaluated. Species identification was performed using automated methodology and confirmed by Duplex-PCR. The susceptibility profile was determined by automated and disc-diffusion tests (for aminoglycosides AK, CN, TOB and K), according to CLSI, 2014 and FDA, 2013. Multiplex-PCR was used for the detection of AMEs' and 16S rRNA Methylases' genes and the molecular typing was performed by REP-PCR. All isolates were confirmed as *A. baumannii*. Sixteen resistance profiles were observed. The highest percentual of non-susceptibility was observed for CRO, CAZ, FEP, IPM, MEM, TZP and CIP (detected in 93,7% of the isolates). In 28 isolates at least one AME gene was detected, and among them, the most frequent was *aph(3')-VI* (53,1%), followed by *aph(3')-Ia* (34,4%), *aac(3)-Ia* (31,2%), *aac(6')-Ib* (28,1%) and *aac(3)-IIa* (6,25%). Molecular typing showed 8 clusters widely disseminated in the Intensive Care Units. These data suggest the occurrence of high aminoglycoside resistance rates and dissemination of AMEs' genes among *A. baumannii* isolated in the studied hospital.

Keywords: *Acinetobacter baumannii*, AMEs, Molecular Typing.

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