

**TITLE:** INTER-HOSPITAL DISSEMINATION OF OXA-23 AND ArmA CO-PRODUCING-*Acinetobacter baumannii* DURING THE PERIOD OF THE COVID-19 PANDEMIC

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## ABSTRACT

With the advent of the Covid-19 pandemic, a significant increase in resistant gram-negative isolates causing nosocomial infections was observed. *Acinetobacter baumannii* is a non-fermenting gram-negative coccobacillus, with a multidrug resistance profile, leaving few therapeutic options. The production of carbapenemase enzymes, which degrade carbapenems, and RMTases, which methylate the aminoglycoside binding site of 16S rRNA in the subunit 30S, has caused concern. The aim of this study was to characterize outbreaks caused by *A. baumannii* isolates in hospitals in the cities of Araçatuba and Marília, both located in the west region of the state of Sao Paulo. The isolates were sent to the Regional Laboratory Centers (CLR) of the Adolfo Lutz Institute (IAL), and redirected to the Marília CLR between April and August 2021; after bacterial confirmation by biochemical and molecular techniques, antimicrobial susceptibility tests (AST) were performed by disk diffusion (amikacin, gentamicin, tobramycin, imipenem, meropenem, ciprofloxacin, levofloxacin, sulfamethoxazole-trimethoprim) and broth microdilution for polymyxin B. The AST results were read and interpreted by BrCAST. The presence of resistance genes for carbapenemases *bla*<sub>OXA5</sub>, and *armA* and *rmt* (aminoglycoside resistance) was confirmed by PCR and epidemiological molecular typing by REP-PCR. Thirty isolates, 9 (30%) from a hospital in Marília and 21 (70%) from a hospital in Araçatuba, were referred to the IAL/Marília, 26 (87%) were obtained from tracheal secretion and 4 (13%) from anal swab. Of the isolates tested, all (100%) showed resistance to aminoglycosides (no growth-inhibitory zone), carbapenems and sulfamethoxazole-trimethoprim; ciprofloxacin and levofloxacin were tested in 27 (90%) and 29 (97%) isolates, respectively, and all showed resistance. Twenty-nine isolates were susceptible (97%) to polymyxin B and 1 was resistant (3%). All isolates (100%) had the *bla*<sub>OXA-23</sub> and *bla*<sub>OXA-51</sub> genes (confirming *A. baumannii*) and the *armA* gene. The epidemiological profile showed a single clone, classified as "A". In conclusion, a single clone of *A. baumannii* co-producing OXA-23 and ArmA was responsible for the inter-hospital spread of the two cities during the increase in hospitalizations due to the COVID-19 pandemic, which leads to great concern about the dissemination of these microorganisms.

**Keywords:** *Acinetobacter baumannii*, OXA-23, ArmA, RMTases, COVID-19

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