

TITLE: MONITORING OF MULTIRESTANT GRAM-NEGATIVE BACTERIA FROM AN URBAN RIVER IN JOÃO PESSOA / PB: CLINICAL AND ENVIRONMENTAL IMPACT

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ABSTRACT:

In urbanized areas, rivers can act as reservoirs of multidrug-resistant (MDR) bacteria, facilitating their transmission to humans and animals exposed through drinking or recreational water. In the last years, reports of the occurrence of clinically relevant bacteria in polluted rivers have been increasingly frequent in Brazil and worldwide. From January 2017 to June 2017 was conducted a surveillance study/project monitoring the occurrence of multidrug-resistant (MDR) Gram-negative bacteria isolated from an urban river crossing the metropolitan area of João Pessoa, Paraiba in the northeastern of Brazil. Water samples were collected at from different locations along the Jaguaribe River, and enriched/filtered using a sterile filter membrane (0.45µm pore size). The membranes were placed in tubes with 20ml of BHI broth and vortexed. Aliquots from were streaked onto McConkey agar without aditives and also supplemented with antimicrobials: ceftriaxone (16µg/ml) and meropenem (1µg/ml) plus 70µg/ml of ZnSO₄ and incubated at 37°C/18-24h, in order to detect MDR (ESBL and/or carbapenemases producing) strains. The samples were also streaked in Chomagar/ESBL and Chomagar/KPC (Probac). Isolates growing the selective plates with ceftriaxone were screened for ESBL by the disk approximation test, and strains growing on selective plates with meropenem screened for carbapenemase-producing using the Carba-NP test (Biomerieux). Bacterial identification were determined by standards methods and confirmed using MALDI-TOF (Bruker). Analysis and the antimicrobial resistance patterns were determined by disc diffusion method using antimicrobials belonging to four different classes: quinolones; aminoglycosides; beta-lactams (carbapenems and cephalosporins); fosfomicyn and sulfamethoxazole-trimethoprim, according EUCAST. The carbapenemase-encoding genes were screened by PCR and selected strains were analysed by Whole Genome Sequence (**WGS**) using a MiSeq platform (Illumina Inc., San Diego, CA). As a main result we have a first time isolation of an *Enterobacter cloacae* strain ST 1 was shown to harbor both *bla_{KPC-2}* and *fosA* genes, as well as several other resistance encoding genes. In summary, these results highlight the importance of environmental monitoring of pathogenic bacteria serving as a source of resistance genes of antimicrobial agents, emphasizing the need to adopt measures of control and surveillance the presence of MDR Gram negative bacteria. In this context new strategies should be adopted to inhibit the spread of clinically important high-risk bacterial strains.

Key words: Urban river, bacterial resistance, environmental microbiology.