

## SCREENING OF MULTI-DRUG RESISTANT ENTEROBACTERIACEAE IN PATIENTS, HEALTH CARE WORKERS AND HOSPITAL ENVIRONMENT USING PHENOTYPIC AND MOLECULAR TECHNIQUES.

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Healthcare-associated infections (HAI) are considered a serious public health threat, especially when it involves MDR (multi-drug resistant) bacteria. The Enterobacteriaceae is a family of Gram-negative bacteria (GNB) commonly found in HAI. The aim of this study was to identify and characterize the enterobacteria present in a University Hospital (HU-UFSC, Florianópolis/SC, Brazil) using phenotypic and molecular techniques. Samples were collected in Mar/Apr/May-2015 (n=570) from health care workers, patients and high-touch surfaces at 4 different hospital units: Emergency (EMG), Intensive Care (ICU), Surgical Center (SC), Surgical Inpatient (SIU) and Medical Inpatient (MIU). The collect was done using Amies swabs and the samples were cultured on MacConkey agar plate to select GNB. The species and the AST (antimicrobial susceptibility test) were determined by an automated method (Vitek2; bioMérieux). The species were also identified by 16S rDNA sequencing (Neopropecta Microbiome Technologies S/A; MiSeq Sequencing System, Illumina, Inc). The presence of 5  $\beta$ -lactamases genes was tested by PCR (KPC, NDM, CTX-M-1, -2, -9). The results show that 190 GNB were isolated from the 570 samples, among them 65% were enterobacteria with HAI importance. The most common were *Klebsiella pneumoniae* (37%), *Escherichia coli* (22%) and *Enterobacter cloacae* (18%). Analyzing the AST, 53% of the enterobacteria were MDR (resistant to 3 or more antimicrobial classes) and 30% were resistant to 1 or 2 antimicrobial classes. The detection of resistance genes showed that 29% were positive for the KPC gene, 30% for CTX-M-1, 13% for CTX-M-9, 4% for CTX-M-2 and no positives for NDM gene were found. Some interesting results include the presence of MDR *K. pneumoniae* on the portable shower (+KPC/+CTX-M-9) at the ICU and *K. pneumoniae* (+KPC/+CTX-M-1, 2, 9) and *E. cloacae* (+KPC) in the health care workers snack room at MIU. It was interesting to note that 4 isolates of *E. coli* from different patients rectal swabs were sensitive to all antimicrobials tested, but they were positive for the resistance genes KPC and CTX-M-1. This result shows the importance of resistance genes detection in HAI screening and control. These previous results show some critical points that should be taken into account when analyzing the dissemination of resistance genes in the hospital. Studies with similar approaches could be used as powerful tools to control the HAI by MDR bacteria.

**Key words:** healthcare-associated infections (HAI), multidrug-resistant bacteria (MDR), Enterobacteriaceae, resistance genes, new generation sequencing (NGS).

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