

TITLE: IDENTIFICATION AND ANALYSIS OF MULTIDRUG RESISTANT ENTEROBACTERIACEAE ISOLATED FROM FECAL SAMPLES AT AN UNIVERSITY HOSPITAL, RIO DE JANEIRO, BRAZIL.

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ABSTRACT:

The human gut microbiota hosts complex microorganisms, is a reservoir of bacterial species involved in the infection process and, establishment of hospital and community environments. *Enterobacteriaceae*, gram-negative bacterial rods with clinical importance, are part of human's and animal's intestinal tracts and able to colonize skin, urinary and respiratory tracts. Fecal samples were collected from outpatients and ward ones attended at the Pedro Ernesto University Hospital (HUPE/ UERJ) of the State University of Rio de Janeiro (UERJ). Four main groups of antimicrobials were used for the phenotypic analysis: cephalosporins, aminoglycosides, fluoroquinolones and carbapenems. The strains were isolated through selective MacConkey media containing 32µg/mL of cephalexin and 8µg/m of gentamicin. A total of 99 strains from 35 outpatient's fecal samples and 112 strains from 30 hospitalized ones were analyzed by antimicrobial susceptibility test (AST). The most prevalent bacteria were *Pantoea agglomerans* (26.2%), *Klebsiella pneumoniae* (16.1%), *Escherichia coli* (15.1%), *Enterobacter cloacae* (16.1%) and *Citrobacter freundii* (7.0%) for outpatients. Among the hospitalized patients, the highest percentages were *E. coli* (25.0%), *K. pneumoniae* (21.4%), *C. freundii* (16.0%), *P.agglomerans* (10.7%) and *E. cloacae* (8.9%). Regarding resistance to antimicrobial groups of outpatient strains, 68.6% were resistant to first-generation cephalosporins, 9.0% of second-generation, 23.2% of third-generation, 13.1% of fourth-generation, 9.0% resistant to aminoglycosides, 11.1% resistant to fluoroquinolones and 12.1% resistant to carbapenems. In relation to the strains of wards, 71.4% were resistant to first-generation cephalosporins, 22.3% of second-generation, 33.0% of third-generation, 35.7% of fourth-generation, 16.0% resistant to aminoglycosides, 42.8% resistant to fluoroquinolones and 21.4% resistant to carbapenems. The strains considered multidrug resistant were those that had resistance to 3 or more antimicrobial groups, corresponding to 50 outpatient strains (70.4%) and 85 strains of hospitalized patients (85.9%). Considering the transfer of genetic elements of antimicrobial resistance is occurring in the nosocomial and community environment, these results reinforce that barrier to the transmission of microorganisms and the more judicious use of antimicrobials are necessary for the control of the dissemination of microorganisms housing elements of resistance.

Keywords: gut microbiota, enterobacteriaceae, multiresistance, nosocomial infections

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