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ANTIBIOTIC SUSCEPTIBILITY PATTERN AND PHENOTYPIC CHARACTERIZATION OF EXTENDED-SPECTRUM-BETA-LACTAMASE-PRODUCING *Enterobacteriaceae* ISOLATED FROM VARIOUS CLINICAL SAMPLES

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Abstract

The spread of antibiotic resistant organisms and those producing extended spectrum β -lactamases (ESBL) has become a health care problem worldwide in communities and hospitals, as it leads to more complicated infections, longer duration of treatment, and increases in patient mortality. In the present study, we analyzed 226 clinical samples in order to assess the spread of ESBL-producing *Enterobacteriaceae*. 196 *Enterobacteriaceae* were identified and classified as members of the genera *Pantoea*, *Klebsiella*, *Escherichia*, *Enterobacter*, *Serratia*, *Proteus*, *Citrobacter*, and *Raoultella*. The results of susceptibility testing of isolated strains to 19 antibiotics showed that the most part of the isolates were highly resistant ($p < 0.01$) to the tested β -lactams: penicillins and penicillin like antibiotics (amoxicillin, ticarcillin and amoxicillin-clavulanic acid), first-generation cephalosporins (cephalexin), and second generation cephalosporins (cefoxitin). 60.20% of the *Enterobacteriaceae* isolates were multi-drug resistant (MDR) strains. Resistant isolates to third generation cephalosporins were tested for ESBL by three methods, concluding its presence in 29.59% of the isolates by double-disk synergy test, 27.55% by the disk approximation method and by 31.63% double-disk test. High levels of MDR strains and ESBL-producing *Enterobacteriaceae* in our study suggest the need for applying specific infection control measures, and rational antibiotic use to reduce the selection pressure and prevent dissemination of resistant bacteria.

Keywords: antimicrobial susceptibility, clinical samples, *Enterobacteriaceae*, extended-spectrum β -lactamases (ESBL)- producing and multi-drug resistance.

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