TITLE: Molecular characterization of antimicrobial resistance genes in *Escherichia coli* isolated from hospital and community environment.

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ABSTRACT:

Urinary tract infection is one of the most common diseases in the world. Escherichia coli is involved in about 70% to 85% of cases. Treatment of E. coli infections encompasses a wide variety of antimicrobials, however, inadequate use of antibiotics may result in the selection of drug-resistant strains. Within the various mechanisms of resistance, we highlight the production of extended spectrum beta-lactamase (ESBL), enzymes classified into several genetic groups according to their amino acid sequence, which are encoded by genes and easily transferred from the bacteria. The objective of this study was to detect the genes *blatem*, *blactx-m*, *blashv*, and *blaoxa* responsible for ESBL coding and to perform the genetic classification of these isolates. A total of 200 E. coli isolates obtained from urine samples from the hospital and community environment were analyzed. The bacterial DNA was extracted by the phenol-chloroform technique and subjected to multiplex PCR amplification in which the result was visualized by gel electrophoresis 1% agarose. About 90.5% of the samples presented resistance genes, with prevalence of the *bla_{TEM}* gene. The *bla_{SHV}* and *bla_{OXA}* genes were present in isolates from the hospital and community environment respectively. The data obtained will be relevant to the in-depth knowledge of the epidemiological profile of urinary tract infection, allowing the planning and implementation of prevention and control measures.

Key-words: Microorganisms. Hospitalar. Disease. Collect. Analyze. Antimicrobial. Detection. Genetic.

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