# ANTIMICROBIAL RESISTANCE ANALYSIS OF CLINICAL ESCHERICHIA COLI

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**Introduction.** Antibiotic resistance (AMR) is a major public health challenge when it comes to tackling infectious diseases. The Pasteur Institute identified AMR as a priority scientific area in its Strategic Plan for. According to the World Health Organization, Geneva, Switzerland, antibiotic resistance is rising to dangerously high levels in all parts of the world, leading to increased morbidity and mortality. Hence, the six leading mortality-causing pathogens - *Escherichia coli, Staphylococcus aureus, Klebsiella pneumonia, Streptococcus pneumoniae, Acinetobacter baumannii*, and *Pseudomonas aeruginosa* - were responsible for 929.000 deaths linked to AMR and 3.57 million deaths associated with AMR in 2019. *E. coli* is the most common gram-negative bacterium responsible for a variety of diseases as a result of community and hospital-acquired clinically significant bloodstream infections, and causes a major number of deaths at all ages, due to these infections.

**The aim** of this study was to analyze antibiotic resistance and detect some antimicrobial resistance genes in *E. coli* strains.

**Material and methods.** This cross-sectional study was conducted between February 2020 and January 2022. The identification of *E. coli* isolates was done by MALDI-TOF MS, VITEK 2 Compact, and AST was performed with the Kirby–Bauer disk diffusion and VITEK 2 Compact. Extended-spectrum β-lactamases (ESBLs) were detected with discs containing cefotaxime, cefotaxime/clavulanate, ceftazidime, and ceftazidime/clavulanate, and carbapenemase was detected with the modified carbapenem inactivation method (mCIM) and EDTA-mCIM (eCIM). Antibiotic resistance genes were identified by polymerase chain reaction.

**Results.** The study aimed to investigate the antibiotic resistance patterns of, *E. coli* strains isolated from blood, cerebrospinal fluid and urine. Phenotypic analysis by the disk diffusion method showed that the *E. coli* isolates were resistant to penicillin (40.3%), fluoroquinolones (38.1%), cephalosporins (42.1%), and aminoglycosides (16.9%). 39.5% of the *E. coli* isolates were multi-drug resistant (i.e., resistant to 3 or more classes of antibiotics), and 31.7% of those were positive for extended spectrum β-lactamase. The carbapenemase-producing strains were further evaluated for the presence of resistance genes. It was observed that blaOXA-48 was detected in 4.9% of carbapenemase- produsing isolates, while blaNDM was detected in 2.9% of the same group.

**Conclusions.** Drug-resistant *E. coli* has become an important and complex problem in clinical treatment. This work reports a high rate of antimicrobial resistance, including ESBL positivity and multidrug resistance. The data reported here are highly relevant for local antimicrobial prescription practice. In the future, this research can be expanded to increase sample size and the type and to enable evaluation of the correlation between clinical manifestations and antibiotic resistance. This newly available information about *E. coli* resistance will help improving clinical evaluation and decision-making.

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