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Research Paper

# Detection of *bla*$_{CTX-M}$, *bla*$_{TEM}$ and *bla*$_{SHV}$ Genes in *Enterobacter cloacae* Isolates

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## Extended Abstract

### Introduction

*Enterobacter cloacae* is a Gram-negative, facultatively anaerobic bacterium commonly found in the human gut but is also associated with a wide range of nosocomial infections, including urinary tract infections (UTIs), pneumonia, and sepsis. The increasing antibiotic resistance among *Enterobacter* species, particularly due to the production of extended-spectrum beta-lactamases (ESBLs), poses a significant public health challenge. ESBL-producing strains hydrolyze a broad range of beta-lactam antibiotics, making treatment difficult. Among the most common ESBL genes are *blaCTX-M*, *blaTEM*, and *blaSHV*, which contribute to multidrug resistance (MDR) in Enterobacter species. This study aimed to determine the prevalence of these genes in *Enterobacter cloacae* isolates from patients with UTIs in Shahrekord, Iran, and assess their antibiotic resistance profiles.

### Methods

This cross-sectional study was conducted over one year, from June 2019 to June 2020, on 1000 urine samples collected from patients suspected of UTIs in Shahrekord, Iran. The bacterial isolates were identified using standard biochemical and microbiological methods. Antibiotic susceptibility testing was performed using the disk diffusion method following Clinical and Laboratory Standards Institute (CLSI) guidelines. The

presence of *blaCTX-M*, *blaTEM*, and *blaSHV* genes was detected using polymerase chain reaction (PCR) with specific primers.

## Results and Discussion

Of the 1000 urine samples, 300 were culture-positive for UTI pathogens, among which 65 isolates (21.66%) were identified as Enterobacter cloacae. The prevalence of infections was significantly higher in female patients (76.92%) compared to males (23.08%). The highest infection rates were observed in patients aged above 60 years and those aged between 15-30 years. Antibiotic susceptibility testing revealed high resistance rates among the isolates, with the highest resistance observed against trimethoprim-sulfamethoxazole (84.62%) and the lowest resistance against nitrofurantoin (23.08%). Multidrug resistance (MDR) was detected in over 50% of the isolates. The phenotypic confirmatory test for ESBL production showed that 25 (38.26%) isolates were ESBL producers. PCR analysis detected *blaCTX-M* in 28% of isolates, *blaTEM* in 32%, and *blaSHV* in 10%. Some isolates harbored multiple resistance genes, with co-occurrence of *blaTEM* and *blaSHV* in 4%, *blaSHV* and *blaCTX-M* in 8%, and *blaCTX*-M and *blaTEM* in 16% of isolates. The presence of ESBL-producing Enterobacter cloacae in urinary tract infections (UTIs) represents a significant clinical concern, primarily due to its strong association with antimicrobial treatment failures, prolonged infection duration, and increased patient morbidity. Such infections often require extended hospital stays, more complex therapeutic regimens, and may result in higher healthcare costs. The high prevalence of ESBL resistance genes detected in the isolates underscores the urgent need to re-evaluate current empirical antibiotic treatment protocols, as conventional regimens may no longer provide adequate coverage against multidrug-resistant (MDR) strains. Furthermore, the findings reinforce the importance of integrating continuous microbiological surveillance into clinical practice to detect emerging resistance trends in real time. Routine monitoring would enable healthcare providers to adapt antibiotic policies proactively, minimizing the risk of ineffective therapy. Such programs should encompass evidence-based prescription guidelines, and public awareness campaigns to limit the selection pressure driving resistance. Ultimately, a coordinated strategy involving early detection, targeted therapy, and robust infection control measures is essential to mitigate the spread of ESBL-producing bacteria and to preserve the efficacy of existing antimicrobial agents.

## Conclusion

This study provides evidence of a high prevalence of ESBL-producing *Enterobacter cloacae* strains, with a significant presence of *blaCTX-M*, *blaTEM*, and *blaSHV* genes. The increasing resistance to commonly used antibiotics underscores the urgent need for infection control measures and judicious use of antimicrobials. Implementing molecular surveillance and incorporating novel therapeutic strategies will be crucial in controlling the dissemination of resistant strains.

**Keywords:** *Enterobacter cloacae*, ESBLs, Antibiotic resistance.

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