



Prevalence of *bla*_{CTX-M}, *bla*_{SHV}, and *bla*_{TEM} Genes in *Escherichia coli* Strains Isolated From Urinary Tract Infection Samples of Patients in the Intensive Care Unit in Qom, Iran

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Abstract

Background: *Escherichia coli* is considered as one of the causes of opportunistic infections. Nowadays, due to the increase in drug resistance, the treatment of these infections has become very difficult and they are recognized as the main causes of death in hospitalized patients.

Objectives: The aim of this study was to determine the prevalence of *bla*_{TEM}, *bla*_{SHV}, and *bla*_{CTX-M} genes in *E. coli* strains isolated from the urinary tract infection in patients in Intensive Care Units of three different hospitals in Qom, Iran.

Methods: This study was conducted in three months from October to December 2014. A total of 200 *E. coli* samples were taken from the patients with urinary tract infections in Intensive Care units of Qom hospital. The disc diffusion method was used to determine the susceptibility pattern of antibiotic and phenotypic confirmatory tests for screening of the expanded spectrum beta-lactamase (ESBL) isolates. The presence of *bla*_{TEM}, *bla*_{SHV}, and *bla*_{CTX-M} genes was evaluated by the polymerase chain reaction (PCR) assay.

Results: Of 200 samples, ampicillin (96%) and nitrofurantoin (19.5%) showed the highest and lowest drug resistance, respectively. A total of 156 isolates (78%) were identified as ESBLs using the phenotypic method. Moreover, 76 (38%), 90 (45%), and 123 (61.5%) isolates consisted of *bla*_{CTX-M}, *bla*_{SHV}, and *bla*_{TEM}, respectively.

Conclusions: Overall, the findings of this study showed that *bla*_{TEM} was the most common gene with a frequency of 61.5% in ESBL *E. coli*.

Keywords: *Escherichia Coli*, Cephalosporins, Beta-Lactamase, Intensive Care Units (ICU)

1. Background

Escherichia coli (*E. coli*) is recognized as one of the causes of nosocomial infections (1). Nowadays, due to the high prevalence of antibiotic resistance, *E. coli* is recognized as one of the most resistant bacteria to broad-spectrum antibiotics (2). Also, beta-lactam antibiotics are the most important drugs that are commonly used worldwide to treat bacterial infections (3). Resistance to beta-lactam antibiotics is created by different mechanisms, such as beta-lactamase enzymes, such as expanded spectrum beta-lactamase (ESBL), efflux pumps, and porins (4). ESBL-producing bacteria are associated with several crucial health problems in the world (5). Currently, more than 300 ESBLs have been identified, forming after mutation of beta-lactamase enzymes (6). The main encoding genes of the ESBLs are CTX-M, TEM, and SHV groups of Amber molecular class (7).

ESBL-producing bacteria are mainly found in Intensive Care Units (ICUs) of the hospitals (8). Also, they are resistant to other antibiotic groups (3). Therefore, suitable drugs to treat the bacteria will be very limited, which is the main concern regarding the spread of ESBL strains (9). Identification of this bacteria and increasing knowledge about its presence in a geographical location are effective in the proper and effective use of suitable antibiotics in the region (10). Accordingly, it is the responsibility of health and microbiological officials of each region to monitor and track the growth rate of bacteria resistant constantly, especially ESBLs strains, to control and prevent drug-resistant outbreaks (11). Also, the information on the growth and spread rate of these enzymes helps in the treatment and prevention of infections caused by Gram-positive and Gram-negative bacteria (12).

2. Objectives

The purpose of this study was to determine the prevalence of antibiotic resistance and ESBL in *E. coli* isolates of the urine samples taken from the patients in Qom hospitals using the phenotypic and genotypic methods.

3. Methods

3.1. Separation of the Isolates

As stated earlier, during three months (October to December 2014), 200 samples suspected of *E. coli* were taken from the urinary tract infection (UTI) of the hospitalized patients in ICUs of three different hospitals in Qom, Iran, and then evaluated. Microbiological standard tests, such as gram stain, IMViC, oxidase, catalase, and fermentation/oxidation tests were used to identify the isolates (13) (all strains were Gram-negative bacilli, indol positive, citrate negative, Voges-Proskauer (VP) negative, and methyl red (MR) positive).

3.2. Antibiotic Susceptibility Pattern

To identify the antibiotic susceptibility pattern, the disk diffusion agar test (Kirby Bauer method) (14) was performed using 17 different antibiotic types (Mast, UK). These antibiotic disks included ampicillin (30 µg), Piperacillin (30 µg), cefuroxime (30 µg), imipenem (30 µg), nitrofurantoin (30 µg), amikacin (30 µg), aztreonam (30 µg), carbocillin (30 µg), Cefepime (30 µg), Ceftriaxone (30 µg), Ciprofloxacin (30 µg), Trimethoprim-sulfamethoxazole (30 µg), Gentamicin (30 µg), Ofloxacin (30 µg), Nalidixic acid (30 µg), Cefotaxime (30 µg), and Ceftazidime (30 µg) in terms of the Clinical and Laboratory Standards Institute (CLSI) procedures (14).

3.3. ESBLs-Producing Isolates by Combination Disc Method

Combined carbohydrate-deficient transferrin (CDT) testing was applied to screen the ESBL-producing *E. coli*. The CDT phenotypic test was performed by the disks of ceftazidime (30 µg) and cefotaxime (30 µg) alone and in combination with clavulanic acid (10 µg) in Muller Hinton Agar. After 24 h of incubation at 37°C, an increase in zone size of ≥ 5 mm was considered as a positive ESBL isolate. In the present study, *K. pneumoniae* ATCC 700603 (prepared by the Pasteur Institute, Tehran, Iran) was used as positive control (15).

3.4. DNA Extraction and PCR Amplification for TEM, SHV, and CTX-M Genes

DNA extraction was performed using the boiling method. Then, the quality and quantity of all the extracted DNAs were evaluated by the spectrophotometer and gel electrophoresis. The presence of TEM, CTX-M, and SHV were studied using the polymerase chain reaction (PCR) assay (16). The ingredients of the PCR mixture were as follows for 25 mL PCR reaction: 50 mM of Tris-HCL, 50 mM of (pH = 8) KCL, 15 mM of MgCl₂, 0.2 mM dNTP mix, 20 pM of each primer (Table 1), and 5 mg of the extracted DNA. PCR was performed at the temperature conditions shown in Table 2. The PCR products were exposed to electrophoresis in 1.5% agarose gel.

3.5. Statistical Analysis

The results of antibiotic susceptibility pattern, a confirmatory test for ESBL production, and the existence of *bla*_{TEM}, *bla*_{SHV}, and *bla*_{CTX-M} genes were analyzed using SPSS software (version 16) and Fisher's exact test.

4. Results

The experiment was performed on 200 *E. coli* isolates taken from the urine samples of cases in the ICU in Qom hospitals, of whom 152 (76%), 25 (12.5%), and 23 (11.5%) patients were women, men, and infants, respectively. The result of the antibiotic sensitivity test is shown in Table 3. According to the results, most of the isolates (192, 96%) were resistant to ampicillin and the least resistance was found to Nitrofurantoin (39, 19.5%). Based on the results of the combined disk tests, 156 samples (78%) were producers of ESBLs, and 44 strains (22%) were non-ESBLs producers.

According to the result of PCR assay, 123 (61.5%), 76 (38%), and 90 (45%) *Escherichia coli* strains posed *bla*_{TEM}, *bla*_{CTX-M}, and *bla*_{SHV} genes, respectively (Figure 1).

5. Discussion

Over one million people hospitalized for different medical conditions and during a hospital stay have been infected with nosocomial infections. Nosocomial infection is the most common cause of complications and problems for medical personnel, patients, and all hospitals in Iran (17).

The risk of nosocomial infections has been reported to be from at least 0.27 (0%) to more than 6/27 (22.2%) between 2010 and 2015, respectively (18). These infections can easily be transmitted among patients and their visitors, hospital personnel, and those with direct contact with the hospital

Table 1. Primers Used for Amplification of *bla*_{TEM}, *bla*_{SHV}, and *bla*_{CTX-M} Genes in the Present Study

Genes	Primer Sequences (5' → 3')	Temperature, °C	Length, bp	References
<i>bla</i> _{SHV}	Forward: -GCTTCCCATGATGAGCACC	60	292	Primers were designed by the authors
	Reverse: -AGGCGGGTGACGTTGTCGC	61		
<i>bla</i> _{TEM}	Forward: -GGTGAAAGTAAAAGATGCTGAAG	59	559	
	Reverse: -AACTTATCCGCTCCATC	60		
<i>bla</i> _{CTX-M}	Forward: -GCGAAAAGCACGTAAT GGG	62	427	
	Reverse: -GCCAGATCACCGGATATC	61		

Table 2. Polymerase Chain Reaction Conditions for Amplification of *bla*_{TEM}, *bla*_{SHV}, and *bla*_{CTX-M} Genes in the Present Study

Steps	Temperature, °C			Time, min		
	SHV	CTX-M	TEM	SHV	CTX-M	TEM
Initial denaturation	95	95	95	3	3	3
Denaturation	95	95	95	0.5	0.5	0.5
Annealing	57	60	55	0.5	0.5	0.5
Extension	72	72	72	1	1	1
Final extension	72	72	72	5	5	5
Cycle number	35 Cycle					

Table 3. Antibiotics Sensitivity Pattern of the *Escherichia coli* Strains^a

Antibiotic	Resistant	Intermediate	Sensitive
Carbenicillin	90 (45)	11 (5.5)	99 (49.5)
Piperacillin	175 (87.5)	21 (10.5)	4 (2)
Ofloxacin	69 (34.5)	19 (9.5)	112 (56)
Nitrofurantoin	39 (19.5)	110 (55)	51 (25.5)
Amikacin	57 (28.5)	71 (35.5)	72 (36)
Ceftriaxone	90 (45)	62 (31)	48 (24)
Ampicillin	192 (96)	8 (4)	-
Imipenem	77 (38.5)	43 (21.5)	80 (40)
Ciprofloxacin	72 (36)	27 (13.5)	101 (50.5)
Aztreonam	182 (91)	16 (8)	2 (1)
Cefepime	83 (41.5)	52 (26)	65 (32.5)
Gentamicin	55 (27.5)	41 (20.5)	104 (52)
Nalidixic acid	133 (66.5)	23 (11.5)	44 (22)
Co-trimoxazole	137 (38.5)	4 (2)	59 (29.5)
Cefuroxime	180 (90.5)	19 (9.5)	59 (29.5)
Cefotaxime	160 (80)	31 (15.5)	9 (4.5)
Ceftazidime	94 (47)	60 (30)	46 (23)

^aValues are expressed as No. (%).

environment (1). The highest number of nosocomial infections occurs in the ICU, therefore, it is known as one of the most important responsibilities of lab technicians to iden-

tify and control these infections (9). Additionally, *E. coli* is the most evident and frequent organism, which is also a critical pathogen for UTI (19).

In our investigation, the highest and lowest resistances were found to ampicillin and nitrofurantoin, respectively. However, various resistant rates have been reported from different parts of the world, mostly due to the different patterns of antibiotic use. Rajabnia et al. (19) in Iran indicated that cefotaxime and meropenem had the highest and lowest resistance rates, whereas Jena in India (2017) reported ceftazidime and colistin with the highest and lowest resistance rates (19, 20).

Previous studies conducted in India, Poland, Africa, Iraq, Iran, and other countries showed different rates of antibiotic resistance in *E. coli* strains (20-24).

We also found a high rate of *bla*_{TEM} (61.5%), *bla*_{CTX-M} (45%), and *bla*_{SHV} (38%) genes in clinical strains isolated from the patients with UTI admitted to the ICU. However, *bla*_{SHV} was less than the other two types of genes. Moreover, another study conducted in India reported that 93.47%, 82.60%, and 4.34% of *bla*_{TEM}, *bla*_{CTX-M}, and *bla*_{SHV} genes in *E. coli* were isolated from adult patients with UTI, respectively (20). Polse et al. (23) in a study performed in Iraq indicated that *E. coli* strains isolated from UTI included 87.2%, 54.5%, and 21.8% of *bla*_{CTX-M}, *bla*_{TEM}, and *bla*_{SHV} genes, respectively. In contrast, a recent study by Nojoomi and Ghasemian (25) in 2016 in Iran the prevalence of *bla*_{CTX-M-1}, *bla*_{SHV} and *bla*_{TEM} was 77.4% (n = 86), 47.4% (n = 53) and 2.4% (n = 2), respec-

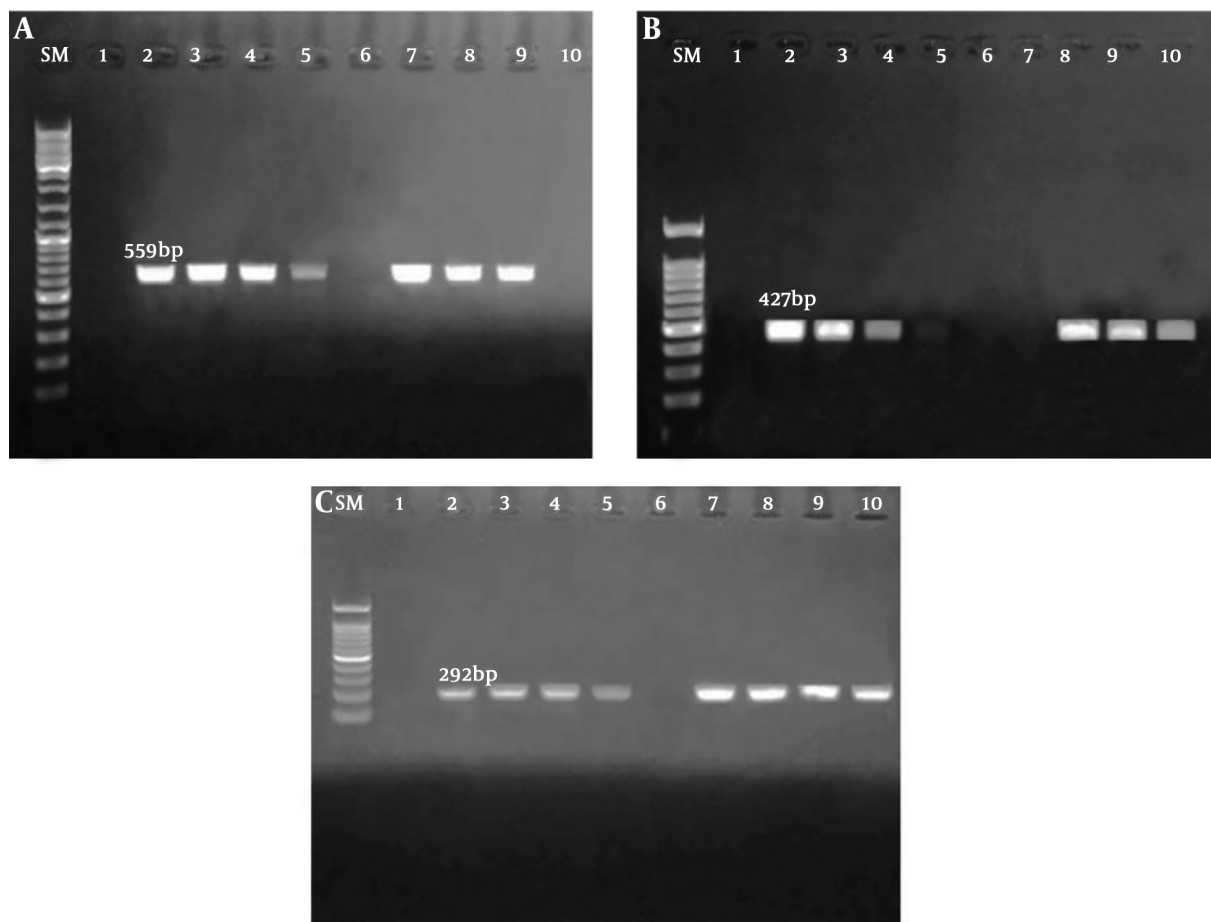


Figure 1. A, SM: Marker size (100 bp), lane 1: negative control, lane 2: positive control, lanes 3, 4, and 7-9: *Escherichia coli* strains *bla*_{TEM} positive, and lane 6 and 10: negative *E. coli* strains for *bla*_{TEM}; B, SM: marker size (100 bp), lane 1: negative control, lane 2: positive control, lanes 3, 4, 5, and 7-10: positive *E. coli* strains for *bla*_{SHV}, and lane 6: negative *E. coli* strain for *bla*_{SHV}; C, SM: marker size (100 bp), lane 1: negative control, lane 2: positive control, lanes 3, 4, and 7-9: positive *E. coli* strains for *bla*_{CTX-M}, and lane 6: negative *E. coli* strains for *bla*_{CTX-M}.

tively.

Interestingly, these findings are consistent with a previous study reflected a high rate of ESBL genes in clinical isolates, which clearly indicates the current challenges for the centers for infection control at hospitals and health centers in ICU Qom, Iran. Financial problems and the lack of facilities for molecular typing methods for epidemiology studies, such as pulsed-field gel electrophoresis (PFGE), multilocus sequence typing (MLST) that are effective in finding the relationship between strains, and ultimately finding their origin are some of the limitations of our study. The patients admitted to the ICU in our hospitals were not evaluated for the extent of beta-lactamase genes in the urine samples, which can be considered as the strength of the present study.

It is also hoped that in future studies, we will be able to take some effective steps to help in controlling nosocomial

infections through molecular typing methods.

5.1. Conclusions

In conclusion, our results showed that among the examined genes, the most common gene was *bla*_{TEM}, with a frequency of 61.5% in ESBL-producing *E. coli* taken from the patients with UTI admitted to the ICU in Qom, Iran.

Due to the high level of drug resistance of the studied isolates, it was very difficult to treat the infections. Accordingly, considering the high rate of drug resistance in our study, further studies are needed to find effective drugs, including nanoparticles, for eliminating these bacteria that are resistant to antibiotics.

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Footnotes

Authors' Contribution: Study concept and design: Mohammad Reza Zolfaghari. Acquisition of data: Shima Sadat Lesani. Analysis and interpretation of data: Mohammad Soleimani. Drafting of the manuscript: Pegah Shakib. Critical revision of the manuscript for important intellectual content: Mohammad Reza Zolfaghari. Statistical analysis: Mohammad Soleimani. Study supervision: Mohammad Reza Zolfaghari.

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References

- Abreu AG, Marques SG, Monteiro-Neto V, Carvalho RM, Goncalves AG. Nosocomial infection and characterization of extended-spectrum beta-lactamases-producing Enterobacteriaceae in Northeast Brazil. *Rev Soc Bras Med Trop.* 2011;**44**(4):441-6. doi: [10.1590/s0037-86822011000400008](https://doi.org/10.1590/s0037-86822011000400008). [PubMed: [21860889](https://pubmed.ncbi.nlm.nih.gov/21860889/)].
- Hashemizadeh Z, Kalantar-Neyestanaki D, Mansouri S. Clonal relationships, antimicrobial susceptibilities, and molecular characterization of extended-spectrum beta-lactamase-producing Escherichia coli isolates from urinary tract infections and fecal samples in Southeast Iran. *Rev Soc Bras Med Trop.* 2018;**51**(1):44-51. doi: [10.1590/0037-8682-0080-2017](https://doi.org/10.1590/0037-8682-0080-2017). [PubMed: [29513841](https://pubmed.ncbi.nlm.nih.gov/29513841/)].
- Shahcheraghi F, Nasiri S, Noveiri H. The survey of genes encoding beta-lactamases, in Escherichia coli resistant to beta-lactam and non-beta-lactam antibiotics. *Iran J Basic Med Sci.* 2010;**13**(1):230-7.
- Forward KR. Extended-spectrum beta-lactamases. *Can J Infect Dis Med Microbiol.* 2006;**17**(suppl 6):6B-8B. doi: [10.1155/2006/726808](https://doi.org/10.1155/2006/726808).
- Carlet J, Pittet D. Access to antibiotics: A safety and equity challenge for the next decade. *Antimicrob Resist Infect Control.* 2013;**2**(1):1. doi: [10.1186/2047-2994-2-1](https://doi.org/10.1186/2047-2994-2-1). [PubMed: [23305311](https://pubmed.ncbi.nlm.nih.gov/23305311/)]. [PubMed Central: [PMC3599140](https://pubmed.ncbi.nlm.nih.gov/PMC3599140/)].
- Bali EB, Accedil L, Sultan N. Phenotypic and molecular characterization of SHV, TEM, CTX-M and extended-spectrum-lactamase produced by Escherichia coli, Acinobacter baumannii and Klebsiella isolates in a Turkish hospital. *Afr J Microbiol Res.* 2010;**4**(8):650-4.
- Ambler RP. The structure of beta-lactamases. *Philos Trans R Soc Lond B Biol Sci.* 1980;**289**(1036):321-31. doi: [10.1098/rstb.1980.0049](https://doi.org/10.1098/rstb.1980.0049). [PubMed: [6109327](https://pubmed.ncbi.nlm.nih.gov/6109327/)].
- Ehlers MM, Veldsman C, Makgotlho EP, Dove MG, Hoosen AA, Kock MM. Detection of blaSHV, blaTEM and blaCTX-M antibiotic resistance genes in randomly selected bacterial pathogens from the Steve Biko Academic Hospital. *FEMS Immunol Med Microbiol.* 2009;**56**(3):191-6. doi: [10.1111/j.1574-695X.2009.00564.x](https://doi.org/10.1111/j.1574-695X.2009.00564.x). [PubMed: [19453751](https://pubmed.ncbi.nlm.nih.gov/19453751/)].
- Vincent JL, Bihari DJ, Suter PM, Bruining HA, White J, Nicolas-Chanoine MH, et al. The prevalence of nosocomial infection in intensive care units in Europe. Results of the European Prevalence of Infection in Intensive Care (EPIC) Study. EPIC International Advisory Committee. *JAMA.* 1995;**274**(8):639-44. [PubMed: [7637145](https://pubmed.ncbi.nlm.nih.gov/7637145/)].
- Paterson DL, Hujer KM, Hujer AM, Yeiser B, Bonomo MD, Rice LB, et al. Extended-spectrum beta-lactamases in Klebsiella pneumoniae bloodstream isolates from seven countries: dominance and widespread prevalence of SHV- and CTX-M-type beta-lactamases. *Antimicrob Agents Chemother.* 2003;**47**(11):3554-60. doi: [10.1128/aac.47.11.3554-3560.2003](https://doi.org/10.1128/aac.47.11.3554-3560.2003). [PubMed: [14576117](https://pubmed.ncbi.nlm.nih.gov/14576117/)]. [PubMed Central: [PMC253771](https://pubmed.ncbi.nlm.nih.gov/PMC253771/)].
- Adenipekun EO, Jackson CR, Ramadan H, Iwalokun BA, Oyedeji KS, Frye JG, et al. Prevalence and multidrug resistance of Escherichia coli from community-acquired infections in Lagos, Nigeria. *J Infect Dev Ctries.* 2016;**10**(9):920-31. doi: [10.3855/jidc.7997](https://doi.org/10.3855/jidc.7997). [PubMed: [27694724](https://pubmed.ncbi.nlm.nih.gov/27694724/)].
- Datta P, Gupta V, Sidhu S. Extended spectrum beta lactamase positive uropathogenic E. coli epidemiological factors and resistance. *BJMP.* 2014;**7**(2):7.
- Bailey P, Scott S. *Diagnostic microbiology*. 13rd ed. USA: Elsevier Health Sciences; 2013.
- Clinical and Laboratory Standards Institute. *Performance standards for antimicrobial susceptibility testing; 21th informational supplement*. Wayne PM-S; 2019.
- National Committee for Clinical Laboratory Standards. *Performance standards for antimicrobial susceptibility testing, 15th informational supplement*. Wayne: Pa; 2005.
- Mirzaee M, Owlia P, Mansouri S. Distribution of CTX-M β -lactamase genes among Escherichia coli strains isolated from patients in Iran. *Lab Med.* 2009;**40**(12):724-7. doi: [10.1309/lmuuwbhmzedytbw5](https://doi.org/10.1309/lmuuwbhmzedytbw5).
- Wollheim C, Guerra IM, Conte VD, Hoffman SP, Schreiner FJ, Delamare AP, et al. Nosocomial and community infections due to class A extended-spectrum beta-lactamase (ESBLA)-producing Escherichia coli and Klebsiella spp. in southern Brazil. *Braz J Infect Dis.* 2011;**15**(2):138-43. [PubMed: [21503400](https://pubmed.ncbi.nlm.nih.gov/21503400/)].
- Kim YH, Yang EM, Kim CJ. Urinary tract infection caused by community-acquired extended-spectrum beta-lactamase-producing bacteria in infants. *J Pediatr (Rio J).* 2017;**93**(3):260-6. doi: [10.1016/j.jpeds.2016.06.009](https://doi.org/10.1016/j.jpeds.2016.06.009). [PubMed: [27842212](https://pubmed.ncbi.nlm.nih.gov/27842212/)].
- Rajabnia M, Forghani MS, Hasani S, Bahadoram M, Mohammadi M, Barahman M. Prevalence and antibiotic resistance pattern of extended spectrum beta lactamase producing Escherichia coli isolated from urinary tract infection. *J Renal Inj Prev.* 2018;**8**(2):78-81. doi: [10.15171/jrip.2019.15](https://doi.org/10.15171/jrip.2019.15).
- Jena J, Sahoo RK, Debata NK, Subudhi E. Prevalence of TEM, SHV, and CTX-M genes of extended-spectrum beta-lactamase-producing Escherichia coli strains isolated from urinary tract infections in adults. *3 Biotech.* 2017;**7**(4):244. doi: [10.1007/s13205-017-0879-2](https://doi.org/10.1007/s13205-017-0879-2). [PubMed: [28710743](https://pubmed.ncbi.nlm.nih.gov/28710743/)]. [PubMed Central: [PMC551117](https://pubmed.ncbi.nlm.nih.gov/PMC551117/)].
- Ojdana D, Sacha P, Wieczorek P, Czaban S, Michalska A, Jaworowska J, et al. The occurrence of blaCTX-M, blaSHV, and blaTEM genes in extended-spectrum β -lactamase-positive strains of Klebsiella pneumoniae, Escherichia coli, and Proteus mirabilis in Poland. *Int J Antibiot.* 2014;**2014**:1-7. doi: [10.1155/2014/935842](https://doi.org/10.1155/2014/935842).
- El Bouamri MC, Arsalane L, El Kamouni Y, Zouhair S. Antimicrobial susceptibility of urinary Klebsiella pneumoniae and the emergence of carbapenem-resistant strains: A retrospective study from a university hospital in Morocco, North Africa. *Afr J Urol.* 2015;**21**(1):36-40. doi: [10.1016/j.afju.2014.10.004](https://doi.org/10.1016/j.afju.2014.10.004).
- Polse RF, Yousif Y, Assafi MS. Prevalence and molecular characterization of extended spectrum beta-Lactamases-producing uropathogenic Escherichia coli isolated in Zakho, Iraq. *J Microbiol Infect Dis.* 2016;**6**(4):163-7. doi: [10.5799/jmid.328863](https://doi.org/10.5799/jmid.328863).
- Seyedjavadi SS, Goudarzi M, Sabzehali F. Relation between blaTEM, blaSHV and blaCTX-M genes and acute urinary tract infections. *J Acute Dis.* 2016;**5**(1):71-6. doi: [10.1016/j.joad.2015.07.007](https://doi.org/10.1016/j.joad.2015.07.007).
- Nojoomi F, Ghasemian A. Prevalence of ESBL phenotype, blaCTX-M-1, blaSHV and blaTEM genes among uropathogenic Escherichia coli isolates from 3 military hospitals of Tehran, Iran. *J Coastal Life Med.* 2016;**4**(8):616-8. doi: [10.12980/jclm.4.2016j6-38](https://doi.org/10.12980/jclm.4.2016j6-38).