Evaluation of the Prevalence of bla_{SHV}, bla_{TEM}, and bla_{CTX} Genes in *Escherichia coli* Isolated From Urinary Tract Infections

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**Background:** Beta-lactamases are the most important factors in the resistance to beta-lactam antibiotics among gram-negative bacteria, especially *Escherichia coli*. Today, the prevalence of infections caused by extended-spectrum beta-lactamases (ESBLs)-producing *E. coli* is increasing, as one of the emerging health problems worldwide. This study aimed to investigate the prevalence of bla_{SHV} (sulfhydryl variable beta-lactamase), bla_{TEM} (temoneira beta-lactamase), and bla_{CTX} (cefotaximase beta-lactamase) genes in *E. coli* isolated from urinary tract infections (UTIs).

**Methods:** In this study, 3192 midstream urine samples collected from Babol and Qaemshahr counties, Mazandaran province (Iran) were cultured on eosin methylene blue and blood agars. An antibiotic susceptibility test was performed to determine ESBL-producing *E. coli* isolates using the combined disk method. Finally, the ESBLs were evaluated for the presence of bla_{SHV}, bla_{TEM}, and bla_{CTX} genes by the polymerase chain reaction (PCR) technique.

**Results:** Of the 3192 cultured urine samples, 192 isolates were identified as *E. coli* by the IMViC and biochemical tests. In addition, the ESBL producers were detected in 45 (28.12%) out of 192 *E. coli* isolates by the double-blind synergism test. The PCR of the 45 ESBL-producing *E. coli* isolates demonstrated that the bla_{TEM} was the most abundant gene (89%), followed by bla_{CTX} (27%) and bla_{SHV} (20%). Eventually, the co-existence of bla_{SHV}, bla_{CTX}, and bla_{TEM} was detected in 3 (7%) isolates.

**Conclusions:** Due to the high prevalence of ESBL-producing uropathogenic *E. coli* (UPEC) in the studied region, future studies are recommended to perform phenotypic or genotypic tests to detect ESBL-producing isolates in laboratories to select appropriate antibiotics for treating UTIs.

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beta-lactamase genes (i.e., TEM-1, TEM-2, or SHV-1) by mutations that change the amino acid sequence at their active site (12). The genes encoding ESBLs are located on the bacterial chromosome or plasmid (13). The blaSHV, blaTEM, and blaCTXM types are regarded as the most common ESBLs (14). The UPEC strains contain blaSHV, and blaTEM genes which cause resistance to beta-lactam antibiotics and the bacterium also possesses a blaCTXM gene that hydrolyzes cepotaxime and ceftazidime (15). Given the importance of resistance to penicillins, cephalosporins, and carbapenems, mediated by extended-spectrum beta-lactamases and carbapenemases, this study was performed to investigate the prevalence of ESBL enzymes in the UPEC strains isolated from patients with UTIs.

Materials and Methods
Isolation and Detection of Escherichia coli
This study was conducted on 3192 patients who referred to the therapeutic centers of Babol and Qaemshahr, Mazandaran Province, Iran between March and December 2017. The urine samples were streaked on eosin methylene blue and blood agars (Merk Company, Germany) and placed at 37°C for 24 hours. UPEC strains were identified using the gram-stain, the IMViC test, beta-hemolytic activity, and the other conventional biochemical tests. These strains were then stored in Luria-Bertani (LB) broth (Merk Company, Germany) and placed at 37°C C for future studies (34).

Combined Disc Test for the Phenotypic Detection of Extended-Spectrum beta-Lactamases
One hundred and ninety-two E. coli isolates were studied to detect the presence of ESBLs by the combined disc method. A 0.5 McFarland suspension of E. coli was spread on the Mueller-Hinton agar. In this study, ceftazidime (30 μg) disks (MAST, UK) alone and in the combination of ceftazidime and clavulanic acid (30/10 μg) disks (MAST, UK) were placed on the Mueller-Hinton agar at a distance of 20 mm from each other and were placed at 3°C for 24 hours. The isolates that displayed an increase of ≥5 mm in the inhibition halo of the combined disk (ceftazidime plus clavulanic acid) were considered as an ESBL producer compared to the ceftazidim disc alone (16,17). The polymerase chain reaction (PCR) detection was carried out on all positive ESBLs. The isolates were confirmed by the PCR and the Basic Local Alignment Search Tool (BLAST) sequence analysis was used as a positive control.

Extraction of DNA by Boiling Lysis Method
A single colony was used for inoculating 5 mL of LB broth and then was incubated at 37°C for 24 hours. Next, 1 mL of bacterial suspension was transferred to a 1.5 mL microcentrifuge tube and was centrifuged at 6000 rounds per minute (rpm) for 5 minutes. The supernatant fluid was discarded as well. The pellet was resuspended in 200 μL nuclease-free distilled water and boiled for 10 minutes and chilled immediately on the ice for 5 minutes. After the ice incubation, the tubes were centrifuged at 10000 rpm for 5 minutes at 4°C and the supernatant was transferred into a new tube. An aliquot of 3 μL of the supernatant was used in the PCR mixes (18). This method of DNA purification was selected to harvest both plasmid and chromosomal DNA.

Genotypic Detection of ESBL Genes
All the ESBL-producing E. coli strains confirmed by the phenotypic assay were screened using the uniplex PCR for the detection of blaTEM, blaSHV, and blaCTXM genes. The PCRs were carried out in a final volume of 25 μL. The oligonucleotide primers used in the investigation are listed in Table 1.

The PCRs were performed with a 25 μL reaction mixture containing 3 μL of the solution containing DNA, 12.5 μL of super PCR master mix 2X (Yekta Tajhiz Azma), 1 μL of each primer (20 pmol), and 7.5 μL of distilled water. In addition, the PCR was performed for 5 minutes. The BLAST analysis revealed that the PCR product sequences all 3 genes show high similarity with the corresponding genes in the GenBank database thus confirming the genes. A clinical isolate containing blaTEM, blaSHV, and blaCTX genes confirmed by the PCR and sequencing techniques were used as positive control and sterile distilled water was utilized as a negative control. The PCR products were identified on 2% agarose gel electrophoresis and the

![Table 1. The Primers Used in This Investigation](image)

\[
\begin{array}{|c|c|c|c|}
\hline
\text{Gene} & \text{Primer Sequence} & \text{Ampli} & \text{Annealing} & \text{Reference} \\
& 5'→3' & \text{Size (bp)} & \text{Temperature} & \\
\hline
\text{TEM-F} & \text{TTGGGTGCACGAGTGCGT} & 500 & 52 & (19) \\
\text{TEM-R} & \text{TATCCGCGCGAAGCTA} & & & \\
\hline
\text{SHV-F} & \text{AGATGTAGCTGCTTTTG} & 392 & 54 & (20) \\
\text{SHV-R} & \text{ATTTGCTGATTTCGCTCG} & & & \\
\hline
\text{CTX-M-F} & \text{ACCGCAGATTTCCGAGAT} & 585 & 58 & (21) \\
\text{CTX-M-R} & \text{GATACTGTTGGTGTCGACATA} & & & \\
\hline
\end{array}
\]
The Prevalence of *bla*<sub>SHV</sub>, *bla*<sub>TEM</sub>, and *bla*<sub>CTX</sub> Genes in *E. coli*

Gels were stained with ethidium bromide and then were visualized by the UV trans-illuminator (19,20, 21).

Data Analysis
The data were analyzed by SPSS software, version 16. The prevalence of resistance genes was calculated using $\chi^2$ and fisher extract tests for each gene. Statistical significance was considered at the $P<0.05$.

Results
The urine samples were collected from hospitalized patients (inpatients) and outpatients. Of the 3192 urine samples cultured on the eosin methylene blue and blood agars, 192 isolates were identified as *E. coli* by IMViC and biochemical tests. Among these 192 *E. coli* strains, the ESBL producers were detected in 45 cases (28.12%) by the combined disc test. Figures 1, 2, and 3 illustrate the PCR product bands of *bla*<sub>TEM</sub>, *bla*<sub>SHV</sub>, and *bla*<sub>CTX-M</sub> genes. The amplified PCR products for *bla*<sub>TEM</sub>, *bla*<sub>SHV</sub>, and *bla*<sub>CTX-M</sub> genes were 500, 392, and 585 base pairs (bp), respectively. All the 45 *E. coli* isolates confirmed by the phenotypic methods were also positive for at least one ESBL gene by the molecular technique ($P<0.001$), the details of which are provided in Table 2.

The uniplex PCR of the 45 ESBL-producing *E. coli* strains indicated that the *bla*<sub>TEM</sub> was the most abundant gene (89%), followed by *CTX-M* (27%) and *SHV* (20%). The co-existence of the *bla*<sub>CTX-M</sub> and *bla*<sub>TEM</sub> as well as *bla*<sub>SHV</sub> and *bla*<sub>TEM</sub> genes was detected in 9 (20%) and 5 (12%) isolates, respectively. The co-existence of all 3 genes (i.e., *bla*<sub>SHV</sub>, *bla*<sub>CTX-M</sub>, and *bla*<sub>TEM</sub>) were observed in 3 isolates (7%).

Discussion
Cephalexin or amoxicillin/clavulanate is considered as one of the first options in the treatment of acute uncomplicated cystitis and can be prescribed in the treatment of cystitis caused by gram-positive cocci because it is effective against enterococci and staphylococci (22). The ESBL-producing bacteria, particularly *E. coli* and *K. pneumoniae* has emerged as a significant problem in the treatment of bacterial infections worldwide (23). The value of the current study was 0.001 thus the results demonstrated that there is a significant relationship between phenotypic and genotypic methods for the detection of the ESBLs. In our study, the prevalence of ESBL-producing *E. coli* strains was 28.12%. Further, Yılmaz et al. found that the prevalence of ESBL-producing *E. coli* strains was 24% (24). In another study, Jena et al reported that the prevalence of ESBL-producing *E. coli* strains isolated from patients with UTIs was 59.74% (25). Although mutations can cause antibiotic-resistant, the overuse of antibiotics increases the selection and emergence of resistant bacteria strains. Therefore, the prevalence of ESBL-producing UPEC varies in different regions. In the present study, 40 (89%) isolates were positive for the *bla*<sub>TEM</sub> gene, which is consistent with the results of several studies. For example, Liu et al reported a prevalence of

| ESBL Genes | Number | Percent |
|------------|--------|---------|
| *bla*<sub>TEM</sub> | 40 | 89 |
| *bla*<sub>CTX-M</sub> | 12 | 27 |
| *bla*<sub>SHV</sub> | 9 | 20 |
| *bla*<sub>CTX-M</sub> and *bla*<sub>TEM</sub> | 9 | 20 |
| *bla*<sub>SHV</sub> and *bla*<sub>TEM</sub> | 5 | 12 |
| *bla*<sub>SHV</sub>, *bla*<sub>CTX-M</sub>, and *bla*<sub>TEM</sub> | 3 | 7 |

Note: ESBL: Extended-spectrum β-lactamases.
72.1% for the bla\textsubscript{TEM} genotype (26). Furthermore, Jena et al (25) showed that among ESBL-producing E. coli isolated from patients with UTI, the prevalence of bla\textsubscript{TEM} gene was the predominant (93.47%). In the current study, the detection rate for the bla\textsubscript{CTX-M} gene was 12 (27%). In studies conducted by Ruppé et al and Majeed et al, the detection rate of the bla\textsubscript{CTX-M} gene in patients with UTI was 26 (76.4 %) and 26%, respectively (27,28).

The result of our research is nearly similar to the report of Majeed et al, but it differs from that of Ruppé et al. These contradictory results indicate that the prevalence of the bla\textsubscript{CTX-M} gene varies in different regions. Moreover, the results of our study revealed that the prevalence of bla\textsubscript{SHV} was 9 (20%). According to Seyedjavadi et al and Reid et al, the rate of isolation of the bla\textsubscript{SHV} gene in UPEC was 45% and 2.4%, respectively (29,30). The reason for the different rates of the bla\textsubscript{SHV} is that the prevalence varies in various areas. Additionally, our finding showed that 39% of the UPEC isolates contained 2 or more ESBL genes. Similarly, Seyedjavadi et al (29) and Manoharan et al (31) reported the co-existence of different ESBL genes within the same isolate. Based on previous evidence, the co-existence of ESBL genes (i.e., bla\textsubscript{SHV}, bla\textsubscript{CTX-M}, and bla\textsubscript{TEM}) is because they are frequently located on the plasmid and can be transferred to other bacteria (32).

**Conclusions**

Due to the high prevalence of the ESBL uropathogenic E. coli, especially bla\textsubscript{TEM} (89%), it is thought that ESBLS should be detected by phenotypic or genotypic methods for selecting the appropriate antibiotics regarding treating the patients with UTIs. Thus, future studies are suggested to determine the prevalence of the metallo-\(\beta\)-lactamases of the Verona Integron-encoded metallo-\(\beta\)-lactamase, imipenemases, and New Delhi metallo-\(\beta\)-lactamase (33,34).

**Ethical Approval**

There are no ethical issues for this article.

**Conflict of Interests**

Authors declare no conflict of interests associated with this study.

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