The Phylogenetic Relatedness of $bla_{NDM-1}$
Harboring Extended-Spectrum β-Lactamase Producing Uropathogenic Escherichia coli and Klebsiella pneumoniae in the North of Iran

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Background: Escherichia coli and Klebsiella pneumoniae as an important part of Enterobacterales family are important causes of both community- and hospital-acquired infections. The present study aimed to investigate the prevalence of antibiotics resistance and molecular characteristics of uropathogenic isolates of E. coli and K. pneumoniae in Iranian patients.

Methods: This cross-sectional study performed on 223 Escherichia coli and 68 Klebsiella pneumoniae isolates obtained from hospitalized patients in the north of Iran. The isolates were identified by standard microbiologic tests and confirmed by API 20E strip. Disk diffusion method was applied to determine antibiotic susceptibility pattern. The presence of β-lactamases encoding genes was evaluated by PCR method. Analysis of the mutations and homology among sequences was done by the CLC sequence viewer (Qiagen, Denmark), and phylogenetic trees were constructed by the neighbor-joining method (Bootstrap: 1000 times).

Results: The overall rates of extended-spectrum β-lactamases (ESBLs)-producing E. coli and K. pneumoniae isolates were 37.7% and 32.4%, respectively. The overall presence of $bla_{SHV}$, $bla_{NDM-1}$, and $bla_{OXA-1}$ genes was detected in 16 (5.5%), 12 (4.1%), and 48 (16.4%) of isolates, respectively. The neighbor-joining analysis for E. coli KU985246.1 strain showed that the most related $bla_{NDM-1}$ sequences were from China, Singapore, UK, Thailand, and Bangladesh. While K. pneumoniae KU985245.1 strains were mostly related to $bla_{NDM-1}$ sequences form Myanmar, and China.

Conclusion: In summary, the remarkable rate of ESBL-producing uropathogenic Enterobacterales along with the first prevalence of NDM-1 β-lactamases can be a serious concern in our region.

Keywords: uropathogenic, Escherichia coli, Klebsiella pneumoniae, antibiotic resistance, ESBL, NDM-1 β-lactamases

Introduction
Escherichia coli and Klebsiella pneumoniae are Gram negative, facultative anaerobic rods belonging to the family of Enterobacterales which are part of the gastrointestinal tract microbiota. These opportunistic pathogens lead to both community- and hospital-acquired infections with a wide range of complications, such as blood stream, respiratory tract, surgical wounds, gastrointestinal, and urinary tract infections.

Beta-lactam (β-lactam) antibiotics are amongst the widely prescribed agents for managing E. coli and K. pneumoniae related infections. However, recently extended-
spectrum beta-lactamases (ESBLs) producing strains have emerged as a critical health issue. The hydrolyzing activity of ESBLs which results in the inactivation of penicillins, broad-spectrum cephalosporins, and monobactams. These enzymes are divided into several main groups, including SHV, TEM, and CTX-M, which are able to inactivate the beta-lactams by hydrolyzing the beta-lactam ring.

ESBLs cannot efficiently inactivate cephamycins, beta-lactamase inhibitors, and particularly carbapenems. So, carbapenems act as important therapeutic options against multiple-drug resistant (MDR) strains. However, recently the trend of carbapenemase producing Enterobacterales has increased all around the world, as well as in Iran.

According to the Ambler classification of beta-lactamases, two main classes of carbapenemases were introduced. One of them is class B Zinc metallo-beta-lactamase (MBL), susceptible to metallic ion chelator such as EDTA, in which New Delhi metallo-beta-lactamase (NDM) is the most important enzyme. Secondly come oxacillinase (OXA) enzymes or class D beta-lactamas, subclassified based on single amino acid substitutions or deletions that are responsible for their effective hydrolyzing activity.

The beta-lactamase production is mostly associated with achievement of resistance determinant genes carried on large plasmids whose dissemination by horizontal gene transfer among different species has become a serious global health problem.

In regard to the importance of epidemiological data on ESBLs and carbapenem producing strains, we aimed to analyze the molecular characteristics of uropathogenic E. coli and K. pneumoniae and its antibiotics resistance pattern in northern Iran.

Materials and Methods

Study Design and Bacterial Isolates

This cross-sectional study was performed at 5 teaching hospitals in the north of Iran within six months. This study has been designed in accordance with the declaration of Helsinki and also the regional approval obtained by University Ethics Committee (IR.GUMS.REC.1394.641). The presumptive E. coli and K. pneumoniae isolates were isolated from clean-catch urine specimens using standard microbiologic tests and API 20E strips (API-bioMérieux, France).

Antimicrobial Susceptibility Testing

The antibiotic susceptibility of isolates was tested by standard disk diffusion method on Mueller-Hinton agar medium (Merck, Germany) according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. The antibiotic disks were ampicillin (10 µg), amoxicillin-clavulanate (20/10 µg), cefepime (30 µg), aztreonam (30 µg), gentamicin (10 µg), nalidixic acid (30 µg), ofloxacin (5 µg), ciprofloxacin (5 µg), cefoxitin (30 µg), cefixime (5 µg), ceftazidime (30 µg), cefotaxime (30 µg), imipenem (10 µg), tetracycline (30 µg), trimethoprim/sulfamethoxazole (25 µg), and nitrofurantoin (300 µg). E. coli ATCC 25922 strain was employed for quality check purpose. Multiple-drug resistant (MDR) isolates were defined non-susceptible (resistant or intermediate) to at least 1 agent in ≥3 antimicrobial categories according to previously mentioned definitions.

ESBL testing was performed by double-disk synergy test using cefotaxime (30 µg) and ceftazidime (30 µg), alone and in combination with clavulanate (10 µg).

Escherichia coli ATCC 25922 and K. pneumoniae ATCC 700603 were used as negative and positive control strains, respectively.

Plasmid DNA Extraction and Molecular Assays

Plasmid DNA extraction from the fresh isolates was done using gene JET plasmid miniprep Kit (Fermentas, Lithuania) according to its instructions. PCR was performed to detect blashv, blaOXA-1, and blaNDM genes by a Veriti 96-well thermal cycler instrument (Applied Biosystems at Life Technologies, Foster City, CA) as previously described. Primers were provided by Metabion Co, Germany. The list of used primers is shown in Table 1. PCR was done in a final volume of 20 µL containing Master Mix (Bioneer, South Korea), primers at concentrations of 0.3–0.4 µM, 3µL DNA templates and ddH2O. All controls for PCR were kindly provided by Pasteur Institute, Tehran, Iran. The PCR setup was an initial denaturation step at 94°C for 3 min, followed by 30 cycles of DNA denaturation at 94°C for 30 s, primer

| Primer | Oligonucleotide Sequence (5' to 3') | Gene | Reference |
|--------|-----------------------------------|------|-----------|
| SHV-F  | ATGCGTTATATTGCGCTGTG              | blashv | 13        |
| SHV-R  | TGGTGTATTATCGGCGCAA               | blashv |           |
| NDM-F  | GGCAGCTTGCTCGCGATGTGCGGC         | blanmd | 14        |
| NDM-R  | GTCCGGGGAGGTGAGGCGGCA             | blanmd |           |
| OXA-F  | TTTTCTGTGTGGGTTGGTTT            | blaoxa-1 | 15       |
| OXA-R  | TTCTTGGCCTTTATGCTTG             | blaoxa-1 |           |
annealing for 45 sec. Temperatures varied based on the sequences of primers, and primer extension at 72°C for 50 sec, followed by a final extension at 72°C for 5 min. The products were separated by electrophoresis in 1% agarose gels with 1 X TAE (Tris/Acetate/EDTA) buffer, stained with safe stain load dye (CinnaGen Co., Iran), and visualized under ultraviolet illumination.

**DNA Sequencing**

To confirm PCR products, a purified amplicon of tested genes was sent for sequencing by the ABI capillary system (Macrogen Research, Seoul, Korea). Afterwards, sequences were confirmed by comparison with available sequences on NCBI database ([http://www.ncbi.nlm.nih.gov/BLAST/](http://www.ncbi.nlm.nih.gov/BLAST/)). These sequences were submitted in the GenBank nucleotide database under accession numbers: MG797557 (OXA-1, *E. coli*), KU985247.1 (OXA-1, *K. pneumoniae*), MG797558 (SHV-1, *E. coli*), MG797559 (SHV-1, *K. pneumoniae*), KU985246.1 (NDM-1, *E. coli*), and KU985245.1 (NDM-1, *K. pneumoniae*) available at National Center of Biotechnology Information website ([http://www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)). The mutations and homology among sequences were analyzed by the CLC sequence viewer (Qiagen, Denmark), and phylogenetic trees were constructed by the neighbor-joining method (Bootstrap: 1000 times).

**Statistical Analysis**

The distribution of antibiotic resistance and genes between groups was calculated by Chi-square and Fisher’s exact tests using SPSS™ software, version 21.0 (IBM Corp., USA). A P value of ≤0.05 was considered as statistically significant.

**Results**

Generally, 291 uropathogenic isolates, consisting of 223 *E. coli* and 68 *K. pneumoniae* isolates were included in our study. *E. coli* isolates were obtained from 169 (75.8%) female and 54 (24.2%) male subjects with a mean age of 35.8 ± 26.3 years. Also, *K. pneumoniae* isolates were obtained from 38 (55.9%) female and 30 (44.1%) male subjects with a mean age of 28.3 ± 26.7 years. In overall, the age range of included patients was from 1 month to 89 years.

The results revealed that *E. coli* isolates were mostly non-susceptible to ampicillin (84.8%) followed by nalidixic acid (78.5%) and tetracycline (65.5%) while the highest susceptibility belonged to imipenem (97.8%). Regarding antibiotic susceptibility among *K. pneumoniae* isolates, the lowest susceptibility rate was held by nalidixic acid (29.4%) followed by nitrofurantoin (47.1%), and the highest susceptibility belonged to imipenem (94.1%). Further analysis revealed that the rate of ESBL-producing *E. coli* and *K. pneumoniae* isolates were 37.7% and 32.4%, respectively. ESBL producers showed significantly higher antibiotic resistance compared to non-ESBLs (Tables 2 and 3). Moreover, the most effective in vitro agent against ESBL-producing in both uropathogenic isolates was imipenem. The distribution of ESBLs isolates according to patients age was 28 (26.4%) among patients less than 18 years, 55 (51.9%) among 19–64 years, and 23 (21.7%) among older than 65 years old.

The overall presence of *blaSHV*, *blaNDM-1*, and *blaOXA-1* genes was detected in 16 (5.5%), 12 (4.1%), and 48 (16.4%) of isolates, respectively. Full results of investigated genes separated by pathogen, MDR, ESBLs, and carbapenem resistance are presented in Table 4. The investigated genes were significantly more prevalent in ESBLs-producing isolates in both uropathogens whereas only the presence of *blaNDM-1* gene in *K. pneumoniae* was significantly associated with carbapenem-resistant isolates.

The neighbor-joining analysis for *E. coli* KU985246.1 strain indicated that the most related *blaNDM-1* sequences were from China, Singapore, UK, Thailand, and Bangladesh. However, *K. pneumoniae* KU985245.1 strains were mostly related to *blaNDM-1* sequences from Myanmar and China (Figure 1).

The pervasiveness of MDR isolates was estimated at 82.5% in *E. coli* and 60.3% in *K. pneumoniae* while the rate of MDR isolates was significantly higher in ESBLs-producing isolates, as 45.7% of *E. coli*, and 53.7% of *K. pneumoniae* isolates were MDR (P < 0.001).

The co-occurrence of β-lactamase genes in *E. coli* isolates was one *blaSHV*/*blaNDM-1*, and one *blaOXA-1*/*blaNDM-1* isolates. This pattern in *K. pneumoniae* isolates was one *blaSHV*/*blaNDM-1/*blaOXA-1, 3 *blaOXA-1/*blaNDM-1, and 7 *blaSHV*/*blaOXA-1 isolates.

**Discussion**

The emergence of MDR Enterobacteriales, particularly ESBLs-producing strains, is responsible for a large rate of nosocomial outbreaks, related to increased morbidity and mortality. Drug-resistant strains of *E. coli* and *K. pneumoniae* have acquired resistance to most—and in some cases to all antibiotics that are currently available in the clinic. This problem demands looking for novel antibiotics targeting drug-resistant Gram-negative pathogens.
Table 2 The Results of Antibiotic Susceptibility Pattern of *E. coli* Isolates

| Antibiotic                | Total No. 223 | ESBLs-Positive No. 84 | P value* |
|---------------------------|---------------|-----------------------|----------|
|                           | Susceptible | Intermediate | Resistant | Susceptible | Intermediate | Resistant |
| Amoxicillin               | 34 (15.2)    | 8 (3.6)     | 181 (81.2) | 1 (1.2)     | 1 (1.2)     | 82 (96.7) | <0.001 |
| Amoxicillin-clavulanate   | 98 (43.9)    | 58 (26)     | 67 (30)    | 19 (22.6)   | 35 (41.7)   | 30 (35.7) | <0.001 |
| Cefoxitin                 | 176 (78.9)   | 21 (9.4)    | 26 (11.7)  | 61 (72.6)   | 13 (15.5)   | 10 (11.9) | 0.073  |
| Cefotaxime                | 99 (44.4)    | 16 (7.2)    | 108 (48.4) | 1 (1.2)     | 0           | 83 (98.8) | <0.001 |
| Ceftriaxime               | 115 (51.6)   | 20 (9)      | 88 (39.5)  | 6 (7.1)     | 10 (11.9)   | 68 (81)   | <0.001 |
| Cefixime                  | 111 (49.8)   | 9 (4.0)     | 103 (46.2) | 21 (25)     | 15 (17.9)   | 48 (57.1) | <0.001 |
| Cefepime                  | 148 (66.4)   | 19 (8.5)    | 56 (25.1)  | 21 (25.0)   | 3 (3.6)     | 80 (95.2) | <0.001 |
| Ciprofloxacin             | 114 (51.1)   | 13 (5.8)    | 96 (43)    | 21 (25.0)   | 3 (3.6)     | 76 (90.5) | <0.001 |
| Oxacillin                 | 126 (56.5)   | 3 (1.3)     | 94 (42.2)  | 25 (29.8)   | 0           | 59 (70.2) | <0.001 |
| Nalidixic acid            | 48 (21.5)    | 16 (7.2)    | 159 (71.3) | 5 (6)       | 3 (3.6)     | 76 (90.5) | <0.001 |
| Aztreonam                 | 123 (55.2)   | 16 (7.2)    | 84 (37.7)  | 4 (4.8)     | 13 (15.5)   | 67 (79.8) | <0.001 |
| Tetracycline              | 77 (34.5)    | 3 (1.3)     | 143 (64.1) | 22 (26.2)   | 1 (1.2)     | 61 (72.6) | 0.042  |
| Gentamicin                | 191 (85.7)   | 7 (3.1)     | 25 (11.2)  | 63 (75)     | 4 (4.8)     | 17 (20.2) | <0.001 |
| Trimethoprim/sulfamethoxazole | 85 (38.1) | 0           | 138 (61.9) | 17 (20.2)   | 0           | 67 (79.8) | <0.001 |
| Nitrofurantoin            | 199 (89.2)   | 6 (2.7)     | 18 (8.1)   | 66 (78.6)   | 2 (2.4)     | 15 (17.9) | <0.001 |
| Imipenem                  | 218 (97.8)   | 5 (2.2)     | 0          | 82 (97.6)   | 2 (2.4)     | 0         | 0.91   |

Note: *Compared with antibiotic resistance pattern of non-ESBL-producing isolates.

Table 3 The Results of Antibiotic Susceptibility Pattern of *K. pneumoniae* Isolates

| Antibiotic                | Total No. 68 | ESBLs-Positive No. 22 | P value* |
|---------------------------|---------------|-----------------------|----------|
|                           | Susceptible | Intermediate | Resistant | Susceptible | Intermediate | Resistant |
| Amoxicillin-clavulanate   | 35 (51.5)    | 7 (10.3)     | 26 (38.2)  | 1 (4.5)     | 6 (27.3)     | 15 (68.2) | <0.001 |
| Cefoxitin                 | 55 (80.9)    | 2 (2.9)      | 11 (16.2)  | 16 (72.7)   | 2 (9.1)      | 4 (18.2)  | 0.24   |
| Cefotaxime                | 39 (57.4)    | 0            | 29 (42.6)  | 0           | 1 (4.5)      | 21 (95.5) | <0.001 |
| Cefixime                  | 38 (55.9)    | 2 (2.9)      | 28 (41.2)  | 0           | 1 (4.5)      | 21 (95.5) | <0.001 |
| Tetracycline              | 44 (64.7)    | 2 (2.9)      | 22 (32.4)  | 3 (13.6)    | 1 (4.5)      | 18 (81.8) | <0.001 |
| Gentamicin                | 47 (69.1)    | 8 (11.8)     | 13 (19.1)  | 9 (40.9)    | 3 (13.6)     | 10 (45.5) | <0.001 |
| Trimethoprim/sulfamethoxazole | 53 (77.9) | 2 (2.9)     | 13 (19.1)  | 12 (54.5)   | 1 (4.5)      | 9 (40.9)  | 0.001  |
| Nitrofurantoin            | 20 (29.4)    | 26 (38.2)    | 22 (32.4)  | 4 (18.2)    | 6 (27.3)     | 12 (54.5) | 0.16   |
| Aztreonam                 | 40 (58.8)    | 2 (2.9)      | 26 (38.2)  | 1 (4.5)     | 1 (4.5)      | 20 (90.9) | <0.001 |
| Gentamicin                | 42 (61.8)    | 0            | 26 (38.2)  | 9 (40.9)    | 0            | 13 (59.1) | 0.014  |
| Trimethoprim/sulfamethoxazole | 40 (69.1) | 1 (1.5)     | 19 (27.9)  | 9 (40.9)    | 1 (4.5)      | 12 (54.5) | <0.001 |
| Nitrofurantoin            | 30 (47.1)    | 12 (17.6)    | 24 (35.3)  | 5 (22.7)    | 5 (22.7)     | 12 (54.5) | 0.005  |
| Imipenem                  | 64 (94.1)    | 1 (1.5)      | 3 (4.4)    | 19 (86.4)   | 1 (4.5)      | 2 (9.1)   | 0.06   |

Note: *Compared with antibiotic resistance pattern of non-ESBL-producing isolates.

Table 4 The Full Results of Investigated Genes Separated by Pathogen, MDR, ESBLs, and Carbapenem Resistance

| Gene     | *E. coli* | *K. pneumoniae* |
|----------|-----------|-----------------|
|          | Total No. 223 | ESBLs No. 84 | MDR No. 184 | Total No. 68 | ESBLs No. 22 | MDR No. 41 |
| bla*SHV  | 6         | 6              | 0           | 6            | 9             | 9           |
| bldNDM   | 4         | 4              | 0           | 4            | 7             | 8           |
| bldOXA-1 | 33        | 31             | 0           | 33           | 32            | 31          |

Note: *P value compared to susceptible isolates was statistically significant (P < 0.05).

Abbreviations: MDR, multiple-drug resistant; IMI-R, imipenem-resistant.
Darobactin is an example of the current efforts that showed a reasonable activity against important drug-resistant pathogens, *E. coli* and *K. pneumoniae*, including polymyxin-resistant, ESBLs and carbapenem-resistant isolates with a minimum inhibitory concentration (MIC) of 2 μg mL⁻¹. The periodic surveillance for knowing the distribution and mechanisms of antibiotic resistance has an important role in preventing and overcoming the risk of complications attributed to ESBL-producing strains. In our study, 36.4% of all isolates were ESBL producers with a high rate of antibiotic resistance. Despite the great discrepancy in the rate of ESBLs-producing *Enterobacterales*, our finding is consistent with the median values (range 13.4% to 69.2%) reported in different uropathogens and regions of Iran. The variations in the occurrence of ESBL producers can be in account of different infection control measures, infection types and studied population.

Regarding the emergence of ESBL-producing strains, the main concern is the spread of resistance determinants due to the horizontal gene transfer. *bla*<sub>TEM</sub>, *bla*<sub>SHV</sub>, and *bla*<sub>CTX-M</sub> are the most frequent ESBLs encoding genes. In the present research, the proportion of *bla*<sub>SHV</sub> genotype was low and found in 5.5% (2.7% in *E. coli* vs 14.7% in *K. pneumoniae*) of isolates. The prevalence of ESBLs genes among *Enterobacterales* was varied. Previously, the rates of *bla*<sub>SHV</sub> containing *Enterobacterales* with a focus on uropathogenic isolates were reported 12.2% to 54.8% by Iranian authors. Meanwhile, several authors have shown the global spared of SHV type β-lactamases in uro-

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**Figure 1** The neighbor-joining dendrogram (Bootstrap: 1000) of two *bla*<sub>NDM-1</sub> harboring isolates.
pathogenic Enterobacterales from China,\textsuperscript{30} India,\textsuperscript{31} Saudi Arabia,\textsuperscript{32} Turkey,\textsuperscript{33} Ukraine,\textsuperscript{34} and Morocco.\textsuperscript{35}

In our results, 4.1\% of uropathogenic Enterobacterales contained \textit{blaNDM}-1, which to the best of our knowledge, is the first prevalence of this gene in Guilan province (North of Iran). Previously, the most reported origin of NDM-1 producing bacteria belonged to Asian countries, including China, India, Turkey, Pakistan and our neighboring countries in Persian Gulf region.\textsuperscript{10} Unfortunately, reports point out the increasing emergence of \textit{blaNDM}-1 harboring Enterobacterales in different regions of Iran. Concerning the emergence of \textit{blaNDM}-1 harboring Enterobacterales, there are some reports from the Capital (Tehran),\textsuperscript{6,36,37} central part (Isfahan),\textsuperscript{7} and southwest (Shiraz) of Iran.\textsuperscript{10}

In the present study, the most prevailing \(\beta\)-lactamases encoding genes, generally 16.4\% of isolates, and 44.4\% of ESBLs-producing isolates were \textit{blaOXA-1} positive. Previously, Alizadeh et al, in a study conducted in the southwest of Iran (Kerman), showed that 17.2\% of uropathogenic isolates were OXA-1 producers.\textsuperscript{20} Reviewing global reports such as Brazil (60\%),\textsuperscript{38} Portugal (55\%),\textsuperscript{39} Saudi Arabia (54.8\%, and 48.3\%),\textsuperscript{32,\textsuperscript{40}} and Bangladesh (47.5\%),\textsuperscript{41} indicate that the occurrence of OXA-1 \(\beta\)-lactamases can be varied based on type and source of isolates and the prevalence of ESBLs in each region.

The present work has some limitations: firstly, the \(\beta\)-lactamase expression was not assessed by real time-PCR, particularly concerning those isolates genetically positive for investigated genes yet phenotypically \(\beta\)-lactam susceptible. Secondly, other \(\beta\)-lactamases encoding genes reported in other Iranian studies should be further investigated. Finally, the availability of clinical features of the patient populations including treatments and outcomes of treatments could provide important information.

In summary, the prevalence of ESBL-producing uropathogenic Enterobacterales containing NDM-1 \(\beta\)-lactamases could be a major concern in our region. Carbapenems are still effective on our MDR isolates, but the co-occurrence of \(\beta\)-lactamases genes suggests restricted infection control policies and the rational prescription and use of antibiotics.

**Disclosure**

The authors report no conflicts of interest in this work.

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