Emergence of $\text{bla}_{\text{CTX-M-15}}$ Gene and Its Transferability in Enterobacter spp. Isolated From the Hospitals of Tehran, Iran

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Accepted: May 11, 2015; Accepted: June 30, 2015

**Background:** Enterobacter spp. is increasingly recognized as an important nosocomial pathogen and implicated in many episodes of hospital acquired infections. The current study aimed to describe distribution and transferability of $\text{bla}_{\text{CTX-M-15}}$ gene, and the antibiotic susceptibility pattern in the clinical isolates of Enterobacter spp.

**Objectives:** The current study aimed to describe the antibiotic susceptibility pattern of the clinical isolates of Enterobacter spp.

**Materials and Methods:** A total of 110 Enterobacter isolates were collected from five hospitals in Tehran, Iran from May 2012 to April 2013. Enterobacter species were identified by API 20E system. Antibacterial susceptibility was determined by disk diffusion method, and extended spectrum beta lactamase (ESBL) production was confirmed by combined disk method. The $\text{bla}_{\text{CTX-M-15}}$ gene was identified by PCR with specific primers. The transferability of the $\text{bla}_{\text{CTX-M-15}}$ gene was tested by conjugation with broth matting method.

**Results:** The prevalence of Enterobacter species was $\text{E. cloacae}$ (78.2%), $\text{E. aerogenes}$ (61.3%) and $\text{E. sakazakii}$ (8.2%). They were from different clinical sources. Maximal resistance in Enterobacter isolates was noticed against Augmentin®, trimethoprim - sulfamethoxazole and cefoxitin 75.5%, 64.5%, and 59.1%, respectively. Fourteen isolates showed ESBL phenotype. The $\text{bla}_{\text{CTX-M-15}}$ gene frequency in Enterobacter isolates was 11.8%. Three conjugative plasmids containing $\text{bla}_{\text{CTX-M-15}}$ were found in one Enterobacter isolate.

**Conclusions:** It was the first report on the $\text{bla}_{\text{CTX-M-15}}$ gene emergence in clinical Enterobacter spp. in Iran. The current study demonstrated the predominant presence of the gene encoding CTX-M-15 among ESBL producing Enterobacter spp. commonly with a large plasmid, in the setting.

**Keywords:** Conjugation; Drug Resistance; ESBLs; Enterobacter

1. Background

The genus Enterobacter includes the facultative anaerobic gram-negative bacteria belonging to Enterobacteriaceae family and widely found in the environment. Recently, the Enterobacter spp. has taken on clinical significance and has emerged as nosocomial pathogens, especially, from intensive care units (1, 2). Enterobacter species are significant causes of nosocomial infections and are intrinsically resistant to amoxicillin/clavulanate, cefazolin and cefotixin due to the production of constitutive chromosomal AmpC β-lactamases (3).

ESBLs (Extended-Spectrum Beta-Lactamases) are typically inhibitor-susceptible β-lactamases that hydrolyze penicillins, cephalosporins and aztreonam and are mostly encoded by mobile genes. The most frequently encountered ESBLs belong to the CTX-M, SHV, and TEM families (4). In clinical strains, CTX-M-encoding genes are commonly located on plasmids which vary in size from 7 - 200 kb (5). Many of these plasmids are conjugative with transfer frequencies ranging from $10^{-2}$ - $10^{-7}$ (6). To date, more than 60 types CTX-M ESBLs belonging to five evolutionary groups are described. In most clinical isolates CTX-M-15 is the most frequent CTX-M type, and is reported in Enterobacteriaceae isolates from many regions of the world (7-9). It is necessary to know the frequency of ESBL positive strains in hospitals to formulate a policy of empirical therapy in high risk units where infections due to resistant organisms are much higher (8-10).

2. Objectives

The current study aimed to describe the antibiotic susceptibility pattern of the clinical isolates and $\text{bla}_{\text{CTX-M-15}}$ gene distribution in clinical isolates of Enterobacter spp., and the transferability of the $\text{bla}_{\text{CTX-M-15}}$ by conjugation.

3. Materials and Methods

3.1. Bacterial Isolates and Identification

A total of 110 Enterobacter isolates were collected from hospitals in Tehran from May 2012 to April 2013. Isolates were identified by conventional methods or the API 20E system (bioMerieux, Inc., Hazelwood, MO).
3.2. Antibiotic Susceptibility Testing

The antibiotic susceptibility of integron positive isolates, was determined by disk diffusion method on Mueller-Hinton agar plates (Merck, Darmstadt, Germany) as recommended by the clinical laboratory standards Institute (CLSI) (11). The disks contained the following antibiotics (Mast, UK): Augmentin® (30 μg), imipenem (10 μg), co-trimoxazole (25 μg), tetracycline (30 μg), chloramphenicol (30 μg), ciprofloxacin (5 μg), aztreonam (30 μg), cefotaxime (30 μg), ceftazidime (30 μg), cefotixin (30 μg), tobramycin (10 μg), amikacin (30 μg), gentamicin (10 μg), and cepheim (50 μg). They were obtained from mast Pharmaceutical Inc. U.K. E.coli ATCC 25922 was used as control for antimicrobial susceptibility test.

3.3. ESBL Confirmation by Combination Disk Method

The isolates showing reduced susceptibility to cefazidime or cefotaxime were tested for ESBLs production by the combination disk method according to CLSI guidelines (CLSI). Combination disk method was performed using four disks: cefotaxime (CTX) (30 μg), cefotaxime (30 μg) + clavulanic acid (10 μg), ceftazidime (CAZ) (30 μg), and ceftazidime (30 μg) + clavulanic acid (10 μg). A 5 mm increase in a zone diameter for the tested antimicrobial agent (CAZ or CTX) in combination with clavulanic acid versus its zone when tested alone was considered as ESBLs positive. Quality control for ESBL production was performed using E. coli ATCC 25922 as negative control. Minimum inhibitory concentrations (MICs) of ceftazidime and cefotaxime were determined for ESBLs isolates by the E-test (AB Biodisk, Solna, Sweden) according to CLSI guidelines.

3.4. Polymerase Chain Reaction Analysis

The DNA of ESBL-producing isolates were extracted by boiling method and used as template in PCR assay. Amplification reactions were performed in a total volume of 25 μl of reaction mixture containing 5 μl of 10 × PCR buffer, 2.5 mM MgCl₂, 200 mM dNTP, and 1.25 units of Taq polymerase, 10 pmol of each primer and 1 μl of the sample DNA. The following specific primers with 850 bp length were designed for the PCR reactions (F): 5’-AGAATAAGGAAATCCGATGGT and (R): 5’-GCAAGACCTCAACCTTTGCC (12). Cycling conditions were as follows: Initial denaturation at 94°C for 5 minutes; 35 cycles of 94°C for iminute, 55°C for 45 seconds, and 72°C for 1 minute followed by a final extension at 72°C for 7 minutes. Klebsiella pneumoniae TMU4 was used as positive control.

3.5. Conjugation Experiments

The isolates with blaCTX-M-15 gene were used as donor strains in conjugation experiments. Conjugation transfer assay was performed in broth culture with E. coli 15ARr (ceftaxime sensitive and rifampicin resistant) as the recipient. Before conjugation transfer assay, donor strains were tested for sensitivity to rifampicin and resistance to cefotaxime on nutrient agar containing rifampicin (50 mg/mL) and cefotaxime (100 mg/mL). Donor and recipient cells were mixed at a ratio of 1:10. The trans-conjugants were selected on nutrient agar containing cefotaxime (100 mg/mL) supplemented with rifampicin (50 mg/mL) (13).

3.6. Conjugation Frequency

Conjugation frequency was also expressed as the percentage of transconjugants per added donor cell in 1 mL (13-15). Colony forming unit per mL (cfu/mL) was used instead of the number of cells. The CFU of donors and trans-conjugants from the dilution plates were measured with selective antibiotics (ceftaxime and rifampicin) (13-15). Donor number was determined by plating 10⁶, 10⁵ and 10⁴ dilutions. For trans-conjugants all dilutions (from 1-10⁶) were plated.

3.7. PCR Analysis and Determination of MIC of Transconjugants

DNA of trans-conjugants were obtained by the plasmid extraction kit (BIONEER®) and screened for blaCTX-M-15 gene. MICs of ceftazidime and cefotaxime were determined for trans-conjugants by the E-test (AB Biodisk, Solna, Sweden) according to CLSI guidelines (CLSI 2012).

4. Results

It was observed that 74.55% of the isolates were from the urine culture, 13.64% from the chip throat, 6.36% from wound, 3.64% from the blood culture and 0.91 % from the eye infection. Enterobacter cloacae (78.2%), E. aerogenes (61.3%) and E. sakazakii (8.2%) were determined. The frequency of clinical Enterobacter spp. isolates was higher in females (60%) than males (40%). Analysis of the antimicrobial susceptibility profile of the isolates showed that they were all susceptible to imipenem. Of the 110 isolates, 95.5% were resistant to Augmentin®, 64.5% resistant to trimethoprim-sulfamethoxazole, 22.7 % resistant to ceftazidime, and 23.6% resistant to cefotaxime (Table 1).

Of the 110 Enterobacter isolates, 1 (0.9%) was susceptible to all of the tested antimicrobials and 85 (77.3%) were multidrug-resistant and showed resistance to more than two antimicrobial families. Combined disc test was performed on 29 isolates. Fourteen Enterobacter isolates showed ESBL phenotype. All of the fourteen Enterobacter isolates had the blaCTX-M-15 gene (Figure 1).

The transferability of the blaCTX-M-15 was tested by conjugation. A conjugative plasmid containing blaCTX-M-15 was found in three Enterobacter isolates. Antibiotic susceptibility profile of transconjugant strains and donor strains are showed in Table 2. Conjugation frequency was calculated by the number of transconjugants in 1 mL per the number of donor cells in 1 mL which was 0.9 × 10⁶.

These results were confirmed by PCR. The MIC of parental isolates and transconjugants were similar and included ceftaxime 256 and for ceftazidime.
Enterobacter spp. is increasingly identified as a cause of serious nosocomial infections. In recent years, ESBL production among these isolates is becoming a major clinical concern because of its ability to develop resistance to several classes of antimicrobial agents and has high potential for transmission of resistance to other bacterial species (16). In the current study, the most prevalent clinical Enterobacter species was E. cloaceae (78.2%) that showed the important role of this species in human infections, which was in agreement with other reports (17-20).

In the current study, the frequency of ESBL-producing clinical Enterobacter spp. was 12.73% which was different from the other results in Pakistan (50%, 14.93%) (21, 22), Nigeria (37.5%) (10) and Pennsylvania, the USA (33.33%) (9).

Three of the fourteen isolates with blacTX-M-15 gene (21.4%), had a conjugative large plasmid. The low frequency is perhaps due to the type of conjugation method employed in the current study.

Based on these findings, larger multi-center studies are needed to determine the molecular epidemiology of Enterobacter isolates, the distribution of CTX-M ESBL as well as the presence of conjugative plasmids among Enterobacteriaceae in the hospital populations. The current study results showed that the MIC of the transconjugants and parental strains to CAZ and CTX were similar and the resistance determinants to CAZ and CTX were transferred on a conjugative large plasmid. As a result, third-generation of cephalosporin, fluoroquinolones, and imipenem are suggested to be used as frontline remedial antibiotics to treat Enterobacter infections. Careful monitoring and employing appropriate infection control policy are necessary to prevent further emergence and spread of resistant organisms in the hospitals.

Acknowledgements
Authors sincerely thank the staff members of depart-

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ment of bacteriology, TMU, and medical laboratory department of hospitals in Tehran, Iran.

**Authors’ Contributions**

Kobra Salimian Rizi performed the laboratory work. Shahin Najar Peerayeh designed the work study, and Bita Bakhshi advised the work study.

**Funding/Support**

This study was supported by a grant from Tarbiat Modares University, Faculty of Medical Sciences, Tehran, IR Iran.

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