



***Escherichia coli* in Iran: An Overview of Antibiotic Resistance: A Review Article**

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Abstract

Background: *Escherichia coli* is the most prominent cause of infectious diseases that span from the gastrointestinal tract to extra-intestinal sites such as urinary tract infection, septicemia, and neonatal meningitis. The emergence and spread of antibiotic resistance in *E. coli* is an increasing public health concern across the world. Rising resistance in *E. coli* isolates is also observed in Iran. This review summarizes the status of antibiotic resistance of *E. coli* isolates in Iran from 2007 to 2016.

Methods: The data of the prevalence of *E. coli* antibiotic resistance were collected from databases such as Web of Science, PubMed, Scopus, Embase, Cochrane Library, Google Scholar and Scientific Information Database.

Results: Antibiotic resistance in *E. coli* is on the rise.

Conclusion: Prevalence of antibiotic resistance of *E. coli* varies from region to region in Iran.

Keywords: *Escherichia coli*, Antibiotic resistance, *E. coli* infections

Introduction

Over the past decade increasing antibiotic resistance among isolates of Enterobacteriaceae has become a main public health concern (1). In the most recent estimates of global antibiotic resistance published by the WHO in 2014, *Escherichia coli* was named as one of the biggest concerns associated with hospital and community-acquired infections (2).

Pathogenic *E. coli* is one of the major causes of infectious diseases that span from the gastrointestinal tract to extra-intestinal sites such as the urinary tract, bloodstream, and central nervous system (3,4).

E. coli is the most common producers of Extended-Spectrum Beta-Lactamases (ESBLs) (5). The presence of ESBLs enzymes compromises the efficacy of all β -lactams, excepting

cephamycins and carbapenems, by hydrolysis of the β -lactam ring, and play a major role in the inhibition of the penicillin-binding protein targets (6). More than 300 different ESBL enzymes have been recognized so far (7). Since the early 2000s, CTX-M enzymes have been increasingly detected, and these enzymes have now replaced other ESBLs such as TEM and SHV as the most common type of ESBL (6, 8). Other enzymes having ESBL have also been described (e.g. PER, VEB-1, BES-1, CME-1, SFO-1, and GES-1) (9). Due to the rising percentage of bacteria-carrying ESBL genes, there has been a corresponding increase in the clinical use of antibiotics of the carbapenem group. The hallmark of carbapenemases enzymes is its ability to inactivate carbapenems and extended-spectrum cephalosporins (10).

Metallo- β -lactamase (MBLs) enzymes are now widespread and found in Asia, Europe, Canada, Australia, and South and North America (11). The fluoroquinolones are potent antibiotic agents used in the prophylaxis and treatment of infections caused by *E. coli*. Fluoroquinolone-resistant *E. coli* strains often indicate resistance to all main classes of available antimicrobials such as gentamicin, tetracycline, ampicillin, chloramphenicol, and trimethoprim/sulfamethoxazole (12). The aminoglycosides are powerful bactericidal agents often used along with a spectrum beta-lactams. Resistance to aminoglycosides is most commonly caused by aminoglycoside modifying enzymes such as phosphorylate (aminoglycoside phosphoryl transferase [APH]), acetylate (aminoglycoside acetyltransferase [AAC]) or adenylate (aminoglycoside nucleotidyltransferase [ANT]) (13).

The genes encoding resistance to sulfonamide-class antibiotics such as *sul1*, *sul2*, and *sul3*, which competitively inhibit dihydropteroate synthetase activity, are highly prevalent among Gram-negative bacteria isolated from human samples (14). Unfortunately, the *sul* genes have the highest prevalence in *E. coli* isolates (14, 15).

Trimethoprim (TMP) inhibits dihydrofolate reductase that catalyses the formation of tetrahydrofolate from dihydrofolate. The most prevalent of the *dhfr* genes, *dhfrI* and variants of *dhfrII*, mediate high-level resistance to TMP and are most frequently found in Gram-negative enteric bacteria (16).

The purpose of this review was assessing the exact magnitude of *E. coli* antibiotic resistance in peer-reviewed published literature in Iran over the last nine years.

Methods

Literature search strategy

From 2007 to 2016, all published literature addressing antibiotic resistance of *E. coli* in Iran were collected from databases Web of Science, PubMed, Scopus, Embase, Cochrane Library, Google Scholar and Scientific Information Database. The following keywords containing Medical Subject Headings or keywords in titles or ab-

stracts were used “*E. coli*” [MeSH] AND “antibiotic resistance” [MeSH] AND “Iran” [MeSH].

Inclusion and exclusion criteria

All original articles that presented cross-sectional or cohort studies and reported the prevalence of antibiotic resistance of *E. coli* in Iran were considered.

Data analysis

The analysis for the descriptive data was carried out using SPSS software (Chicago, IL, USA, ver. 19).

Results and Discussion

Epidemiology of antibiotic resistance

In 2015 the Eastern Mediterranean regional office of WHO reported that none of the participating countries had a national action plan for antimicrobial resistance, considered a priority and an outcome indicator for control measures (17). In Iran, like other Eastern Mediterranean countries, antibiotics can easily be obtained over the counter. Antimicrobial medicines are often prescribed at the request of patients, and pharmacies do not necessarily comply with regulations. Many people in the Eastern Mediterranean region believe that antibiotics help in most ailments with fever. Poor-quality and counterfeit antimicrobial medicines are a particular problem with respect to antimicrobial resistance in these regions (17-19).

In Iran antibiotic resistance in Gram-negative bacteria is on the rise, particularly in *E. coli* (20-23). Different patterns of antibiotic resistance is seen in various regions across the Iran: For example, more than 90% of *E. coli* isolates were resistant to penicillin (ampicillin or amoxicillin) in Tehran (capital) (24, 25) (Table 1).

The rate of resistance of *E. coli* isolates in four countries to third-generation cephalosporins was 22%-63% (2). Many studies conducted in Iran have also revealed a similar resistance rate of *E. coli* isolates to third-generation cephalosporins in various regions (26, 28-32) (Table 1). In Iran, cephalosporins are widely used because of their low rate of side effects. This may be related to the increased resistance to these antibiotics (33).

Table 1: Antibiotic resistance pattern of *E. coli* strains isolated from human sources based on disk diffusion method in various regions of Iran

City	Source	AMG	PCN	CEPH	FLQ	MAC	IMP	SXT	TET	CAM	NAL	ESBL	Ref
Babol (north)	Urine	36.80	-	45.60	24.60	-	38.60	64.90	-	-	-	-	(71)
Rasht (north)	Urine	59.9	68.2	41.8	43.6	-	-	60	60	-	47.3	-	(29)
Rasht (north)	Urine, MDR	33.33	-	60.60	36.36	-	36.36	-	78.78	45.45	-	24.00	(30)
Rasht (north)	Urine	36.36	-	51.51	33.33	-	33.33	-	81.81	45.45	-	24.00	(31)
Karaj (north)	UTI	73.69	73.69	38.16	26.32	9.22	15.79	69.74	-	-	60.53	-	(47)
Tabriz (north west)	Clinical sample	45.70	99.30	46.40	47.60	12.90	1.40	75.00	72.80	20.70	60.70	-	(26)
Zanjan (north west)	Clinical sample	28.50	68.50	31.50	52.20	-	0.00	46.50	-	-	-	33.00	(32)
Zanjan (north west)	EAEC, children	10.70	18.60	15.00	12.10	25.70	0.70	5.70	17.10	-	-	-	(44)
Zanjan (north west)	Stool, children	18.60	55.70	47.80	25.00	74.30	1.40	15.70	52.10	-	-	-	(44)
Tabriz (north west)	Clinical sample	67.90	-	63.30	40.80	-	6.30	61.90	-	-	54.90	66.20	(48)
Kermanshah (west)	UTI, ESBL	30.60	93.90	73.50	42.90	4.10	0.00	75.50	-	-	-	24.50	(28)
Sanandaj (west)	Diarrhea children	-	79.80	30.30	30.30	20.20	-	70.70	89.90	88.90	36.40	-	(72)
Sanandaj (west)	Clinical sample, MDR	49.00	-	68.60	64.70	47.00	47.00	88.20	29.40	-	56.80	-	(58)
Sanandaj (west)	Urine	45.03	84.97	32.54	19.97	19.97	10.03	75.02	89.89	86.00	75.02	19.02	(51)
Hamadan (west)	Diarrhea	35.00	-	85.00	32.50	10.00	-	50.00	-	-	62.50	-	(73)
Hamadan (west)	UTI	53.30	-	87.00	39.10	23.90	-	66.00	-	-	59.00	-	(73)
Hamedan (west)	Stool	27.50	87.50	75.00	5.00	-	-	72.50	75.00	35.00	22.50	-	(22)
Hamadan (west)	UTI, children	-	-	30.00	-	0.00	-	70.00	-	-	47.00	-	(61)
Hamadan (west)	UTI, children	17.50	33.30	35.00	15.00	0.00	2.50	70.80	-	-	40.90	27.3	(38)
Mashhad (north east)	Clinical sample	-	-	52.00	43.00	-	-	-	-	-	-	42.50	(60)
Semnan (north east)	Urine	25.20	99.10	28.30	40.20	-	-	63.40	67.70	-	54.90	29.20	(27)
Semnan (north east)	Clinical sample	27.60	98.50	18.90	25.80	-	-	58.20	53.50	20.00	-	17.45	(27)
Kashan (central)	Clinical sample	-	-	-	-	-	-	-	-	-	-	46.60	(74)
Kashan (central)	Clinical sample	38.80	76.10	30.60	21.60	-	0.00	-	-	-	-	-	(75)
Isfahan (central)	UTI	14.84	69.53	59.76	55.46	19.40	0.00	25.00	-	-	23.43	43.67	(59)
Isfahan (central)	UTI	-	-	34.00	39.00	6.00	-	29.00	-	-	63.00	-	(52)
Isfahan (central)	UTI	-	94.53	51.66	45.83	11.85	1.20	-	-	-	-	36.11	(76)
Arak (central)	Clinical sample	-	-	-	-	-	-	-	-	-	-	80.50	(34)
Kashan	EPEC, EPEC,	43.10	100	39.20	35.30	-	0.00	-	-	-	62.70	-	(54)

(central) Tehran	children Stool,	51.29	89.60	-	28.60	-	-	38.96	83.10	59.74	-	-	(42)
(capital) Tehran	children UTI	-	100	2.60	-	-	-	-	-	-	-	2.40	(24)
(capital) Tehran	STEC	62.29	36.06	-	2.45	1.63	-	-	86.88	1.63	-	-	(50)
(capital) Tehran	UTI	17.07	36.58	-	19.51	5.69	-	-	73.98	25.20	-	-	(68)
(capital) Tehran	Clinical sample	36.20	91.50	39.50	39.00	94.00	0.00	57.00	58.50	-	-	70.00	(25)
(capital) Tehran	UTI	40.00	81.30	56.70	61.30	17.30	0.70	64.70	-	-	71.30	-	(53)
(capital) Tehran	UTI	-	28.00	69.30	19.33	-	-	-	-	-	-	28.00	(40)
(capital) Tehran	EPEC, children	0.00	5.70	2.80	1.40	-	-	4.20	18.50	2.80	1.40	-	(45)
(capital) Tehran	EPEC, children	-	61.90	19.00	16.70	-	0.00	54.80	38.10	2.38	-	21.40	(71)
(capital) Tehran & Ilam	UTI	-	81.25	40.97	-	3.47	-	60.41	58.33	-	-	50.00	(14)
(capital & west) Central, western & northern	Diarrhea	6.00	62.00	7.00	3.00	-	-	39.00	63.00	31.00	4.00	-	(57)
Jahrom (south)	Urine, children	15.60	80.20	10.40	8.30	3.10	0.00	76.00	70.80	35.40	25.00	-	(62)
Jahrom (south)	Urine	11.70	-	20.00	21.70	3.30	-	45.00	-	-	41.70	-	(77)
Shiraz (south)	Diarrhea	8.33	36.11	16.67	8.33	5.56	5.56	41.67	41.67	13.89	-	12.96	(41)
Yasouj (south west)	UTI	15.50	76.00	40.50	29.00	-	1.00	62.00	50.00	13.00	48.50	-	(78)
Kerman (south east)	Diarrhea	-	-	40.77	-	-	2.77	-	-	-	-	25.92	(39)
Kerman (south east)	Clinical sample	-	-	37.00	-	-	0.00	-	-	-	-	68.00	(35)
Kerman (south east)	Clinical sample	39.30	91.40	31.00	44.90	-	0.00	93.40	83.70	-	71.90	43.70	(65)
Kerman (south east)	Urine	36.45	-	-	29.18	6.25	0.00	60.42	-	-	54.16	-	(79)
Bam (south east)	Clinical sample	52.30	-	28.70	24.30	-	-	39.70	-	-	59.70	-	(80)
Zabol (south east)	UTI	-	-	-	-	-	-	-	-	-	-	44.40	(81)
Zabol (south east)	Cervico- vaginal	77.27	94.69	61.36	31.81	-	34.93	67.42	92.42	-	88.63	-	(46)
Zahedan (south east)	Urine	76.60	93.30	54.40	-	-	-	73.30	90.00	-	67.70	62.70	(43)

AMG: aminoglycoside, PCN: penicillin, CEPH: Third-generation cephalosporine, FLQ: fluoroquinolone, MAC: macrolide, IMP: imipenem, SXT: co-trimoxazole, TET: tetracycline, CAM: chloramphenicol, NAL: nalidixic acid, ESBL: extended spectrum beta-lactamase, MDR: multi-drug-resistant

β -lactamase enzymes production in *E. coli* is the most important mediator of resistance to a broad spectrum of β -lactams antibiotics (6, 7). Based on previous reports from various regions in Iran, high prevalence of ESBL phenotype of *E. coli* was detected in Arak (central) (34), Kerman (south-east) (35) and Tabriz (north-west) (36) (Table 1) (Fig. 1).



Fig. 1: Prevalence of ESBLs-producing *E. coli* clinical isolates in Iran

Among ESBL gene families, *bla_{CTX-M}*, *bla_{TEM}*, and *bla_{SHV}* are the most common in *E. coli* ESBL-producing isolates obtained from various clinical samples (37). A high prevalence of *bla_{CTX-M}* (66.70%) (38) and *bla_{CTX-M-1}* (61.08%) (25) were detected in *E. coli* isolates. Moreover, *bla_{CTX-M-1}* and *bla_{CTX-M-15}* were present in 95.30% (34) and 91.07% (39) *E. coli* ESBL-producing isolates. *bla_{TEM}* gene was reported in 95.20% (40) and 83.33% (41) of *E. coli* isolates from Tehran (capital) and Shiraz (south), respectively. Gene carriage for ampicillin resistance gene (CITM) was observed in 90.25% (highest distribution) (42)

and 5.00% (lowest distribution) (43) of the *E. coli* isolates.

Unfortunately, there is very little data concerning carbapenem resistance of *E. coli* isolates in Iran. The presence of *bla_{IMP}*, *bla_{VIM}*, and *bla_{NDM-1}* genes from EAEC isolates in children were reported and none of the isolates possessed these genes (44).

None of the ESBL-producing *E. coli* isolates were positive for *bla_{IMP}* and *bla_{VIM}* in Kerman, south-eastern Iran (39). The distribution of resistance genes among *E. coli* isolates is summarized in Table 2.

Table 2: Prevalence of antibiotic resistance genes in *E. coli* strains (percentage) isolated from human source in Iran

Antimicrobial agent	Target gene	Ref
Beta-lactams	<i>bla</i> _{TEM} (19.00), <i>bla</i> _{SHV} (40.50), <i>bla</i> _{CTX-M-1} (19.04), <i>bla</i> _{CTX-M-2} (0.00), <i>bla</i> _{CTX-M-9} (0.00), <i>bla</i> _{CTX-M-15} (19.04)	(82)
	<i>bla</i> _{TEM} (49.00), <i>bla</i> _{SHV} (44.00), <i>bla</i> _{CTX-M} (28.00), <i>bla</i> _{VEB} (8.00), <i>bla</i> _{GES} (0.00)	(63)
	<i>bla</i> _{CTX-M-1} (95.30), <i>bla</i> _{CTX-M-2} (35.10), <i>bla</i> _{CTX-M-8} (16.60), <i>bla</i> _{CTX-M-9} (45.30)	(34)
	<i>bla</i> _{TEM} (85.20), <i>bla</i> _{SHV} (53.20), <i>bla</i> _{CTX-M} (26.10)	(14)
	<i>bla</i> _{TEM} (83.33), <i>bla</i> _{SHV} (31.48), <i>bla</i> _{CTX-M} (20.37)	(41)
	<i>bla</i> _{TEM} (43.50), <i>bla</i> _{SHV} (34.80), <i>bla</i> _{CTX-M} (15.90)	(32)
	<i>bla</i> _{TEM} (40.80), <i>bla</i> _{SHV} (20.80), <i>bla</i> _{CTX-M} (66.70)	(35)
	<i>bla</i> _{CTX-M-15} (91.07), <i>bla</i> _{OXA-1} (1.78), <i>bla</i> _{PER-1} (0.00)	(39)
	<i>bla</i> _{CTX-M-1} (61.08), <i>bla</i> _{CTX-M-2} (0.00), <i>bla</i> _{CTX-M-9} (0.00)	(20)
	<i>bla</i> _{TEM} (49.10), <i>CITM</i> (5.00), <i>bla</i> _{fox} (0.00)	(25)
	<i>bla</i> _{TEM} (46.96), <i>bla</i> _{SHV} (56.00)	(32)
	<i>bla</i> _{TEM} (12.14), <i>bla</i> _{SHV} (7.47)	(59)
	<i>bla</i> _{SHV} (27.64), <i>CITM</i> (39.83)	(68)
	<i>bla</i> _{SHV} (56.55), <i>CITM</i> (48.36)	(50)
	<i>bla</i> _{SHV} (57.79), <i>CITM</i> (90.25)	(42)
	<i>bla</i> _{TEM} (76.47), <i>bla</i> _{SHV} (27.00)	(60)
	<i>bla</i> _{TEM} (60.00), <i>bla</i> _{SHV} (26.00)	(24)
	<i>bla</i> _{TEM} (63.00), <i>bla</i> _{SHV} (7.00)	(75)
	<i>bla</i> _{TEM} (95.20), <i>bla</i> _{SHV} (26.10)	(40)
	<i>bla</i> _{CTX-M} (14.70)	(65)
	<i>CITM</i> (38.59)	(67)
	<i>AmpC</i> (24.00)	(24)
	<i>bla</i> _{IMP} (0.00), <i>bla</i> _{VIM} (0.00), <i>bla</i> _{NDM-1} (0.00)	(44)
<i>bla</i> _{IMP} (0.00), <i>bla</i> _{VIM} (0.00)	(42)	
Aminoglycoside	<i>aac</i> (3)-IIa (78.87), <i>ant</i> (2)-Ia (47.88)	(49)
	<i>aadA1</i> (52.84), <i>aac</i> (3)-IV (22.76)	(68)
	<i>aadA1</i> (60.65), <i>aac</i> (3)-IV (68.03)	(50)
	<i>aadA1</i> (96.10), <i>aac</i> (3)-IV (54.54)	(42)
Quinolone	<i>qnrA</i> (31.50), <i>qnrB</i> (17.00), <i>qnrS</i> (7.00)	(60)
	<i>qnrA</i> (37.50), <i>qnrB</i> (20.80), <i>qnrS</i> (0.00)	(40)
	<i>qnrA</i> (0.00), <i>qnrB</i> (6.66), <i>qnrS</i> (5.00)	(38)
	<i>qnr</i> (46.34)	(68)
	<i>qnr</i> (12.29)	(50)

	<i>qnr</i> (72.07)	(42)
	<i>qnr</i> (15.78)	(67)
Tetracycline	<i>tetA</i> (85.06), <i>tetB</i> (84.41)	(42)
	<i>tetA</i> (43.80), <i>tetB</i> (36.58)	(68)
	<i>tetA</i> (51.63), <i>tetB</i> (38.52)	(50)
	<i>tetA</i> (10.52)	(67)
Chloramphenicol	<i>cat1</i> (59.74), <i>cmlA</i> (60.38)	(42)
	<i>cat1</i> (15.44), <i>cmlA</i> (15.44)	(68)
	<i>cat1</i> (0.81), <i>cmlA</i> (0.81)	(50)
Co-trimoxazole	<i>sul1</i> (81.60), <i>sul2</i> (66.70), <i>sul3</i> (2.30), <i>dfrA1</i> (39.10), <i>dfrA5</i> (5.70)	(14)
	<i>dfrA1</i> (51.94), <i>Sul1</i> (40.25)	(42)
	<i>dfrA1</i> (63.15), <i>Sul1</i> (17.54)	(67)
	<i>dfrA1</i> (21.95), <i>Sul1</i> (36.58)	(68)
	<i>dfrA1</i> (36.06), <i>Sul1</i> (82.78)	(50)
Integrans	<i>IntI1</i> (22.03), <i>IntI2</i> (5.08), <i>IntI3</i> (0.00)	(26)
	<i>IntI1</i> (6.25), <i>IntI2</i> (10.41), <i>IntI3</i> (0.00)	(62)
	<i>IntI1</i> (78.26), <i>IntI2</i> (76.81), <i>IntI3</i> (26.09)	(83)
	<i>IntI1</i> (52.00), <i>IntI2</i> (2.50), <i>IntI3</i> (0.00)	(78)
	<i>IntI1</i> (47.05), <i>IntI2</i> (3.92)	(58)
	<i>IntI1</i> (78.20)	(14)
	<i>IntI1</i> (97.00)	(31)

The prevalence of isolates resistant to aminoglycosides ranged from 0.00% among EPEC isolated from children (Tehran, capital) (45) to 77.27% among *E. coli* isolated from Cervico-vaginal (Zabol, south-eastern Iran) (46). The percentage is also higher in Zahedan (south-east) (43), Karaj (north) (47), and Tabriz (north-west) (48). Among aminoglycoside-modifying enzymes, resistance against gentamicin, kanamycin, cidomycin, and tobramycin in *E. coli* is mediated by ANT (2'')-Ia enzyme, coded by *ant(2'')-Ia* gene. *aac (6')-Ib* gene is more common and leads resistance to kanamycin, tobramycin, and amikacin; Simultaneous resistance to gentamycin and tobramycin mediated by AAC(3)-IIa enzyme coded by *aac(3)-IIa* gene (49). The prevalence of different resistance genes varied—96.10% for the *aadA1* gene (42), 68.03% for the *aac(3)-IV* gene

(50), 78.87% for the *aac(3)-IIa* gene, and 47.88% for the *ant(2)-Ia* gene (49).

Nalidixic acid is an antibiotic from the first generation of quinolones. Nowadays resistance to this antibiotic has increased substantially across Iran (26, 43, 46, 47, 51-54).

Fluoroquinolones are highly efficacious antimicrobial agents, often preferred as initial agents for empirical therapy of UTIs. Unfortunately, urinary tract *E. coli* isolates in both hospitalized and outpatients are becoming increasingly resistant to commonly used fluoroquinolones (55, 56). The prevalence of fluoroquinolone-resistant isolates ranged from about 1%–3% (45, 50, 57) to more than 50% in Iran (32, 55, 58, 59). *qnr* genes (*qnrA*, *qnrB*, and *qnrS*) may facilitate the spread and increase the prevalence of quinolone-resistant strains. To date, *qnr* genes have been widely iden-

tified in Southern and Eastern Asia (82, 60). In earlier studies in Iran, the most prevalent gene among all isolates was *qnrA*, followed by *qnrB* and *qnrS* (40, 60). *qnrS* has been reported previously from clinical isolates of *E. coli* in Mashhad (60) and has also been detected in UTI isolated from children *E. coli* isolates from Hamadan (38). Our pooled evidence showed that the prevalence of macrolide resistance among *E. coli* clinical isolates varied from 0%–3% in Tehran (sample source: STEC), Hamadan (UTI from children), and Jahrom (urine from children) to 94% in Tehran (various clinical samples) (25, 50, 61, 62) (Table 1).

In a study in Tehran, 39% of *E. coli* isolates were resistant to aztreonam (25). Resistance against aztreonam may be related to the production of ESBL enzymes by ESBL-producing strains (53). Uropathogenic *E. coli* strains showed high sensitivity to nitrofurantoin (47, 50, 53). Susceptibility to nitrofurantoin may result from decreasing the use of this drug in Iran (53).

The rate of colistin-resistant ESBL-Producing *E. coli* with the MIC test was 82% (63). Increasing use of colistin for treatment of various infections due Gram-negative bacteria has led to the emergence of colistin resistance in several countries Asia (especially Korea and Singapore) (64).

Percentages of *E. coli* isolates resistant to cotrimoxazole vary with the geographical location of the patients: 93.40% in Kerman (65) and 4.20% in Tehran (45). Among clinical *E. coli* isolates resistance to TMP varies greatly, ranging from 10% to 70% depending on geographical locations (66). A high prevalence of clinical resistance to TMP (*dfrA1* gene) was reported in enteric bacteria (14, 42, 50, 67). Only one city (Tehran) reported a decreasing trend (21.95%) (68).

Resistance to sulfonamide was one of the most common resistances detected by previous studies and is often associated with the acquisition of the resistance genes *sul1* and *sul2* (14, 50).

High prevalence of tetracycline resistance has been observed in *E. coli* isolated from human and animals around the world (69). Prevalence of *tetA*

is higher than *tetB* gene in *E. coli* strains isolated from clinical samples (42, 50, 68).

The most developed countries have sufficient control of over-the-counter sales, while many drugs, including antibiotics, are easily available in many developing countries. In Iran, as in other developing countries, almost any antibiotic can be acquired over the counter without a prescription (19). In other cases, doctors might not advise laboratory tests to confirm bacterial infection and hence the antibiotic might be unnecessarily prescribed (70).

Conclusion

Over the years, antimicrobial resistance in Iran has increased markedly in Gram-negative bacteria such as *E. coli*. This prevalence of antibiotic resistance of *E. coli* varies from region to region in Iran. However, it cannot fully represent the prevalence of antibiotic resistance of *E. coli* in Iran, because the extent of resistance to different antibiotic categories is yet to be examined in many areas of the country.

Ethical considerations

Ethical issues (Including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double publication and/or submission, redundancy, etc.) have been completely observed by the author.

Conflict of Interests

The author declares that there is no conflict of interest.

References

1. Gayathri D, Eramma NK, Devaraja TN (2012). New Delhi metallo beta-Lactamase; Incidence and threats. *Int J Biol Med Res*, 3: 1870–4.
2. WHO (1983). Antimicrobial resistance. *Bull World Health Organ*, 61: 383–94.

3. Piatti G, Mannini A, Balistreri M, Schito AM (2008). Virulence factors in urinary *Escherichia coli* strains: Phylogenetic background and quinolone and fluoroquinolone resistance. *J Clin Microbiol*, 46: 480–7.
4. Alizade H, Ghanbarpour R, Aflatoonian MR (2014). Molecular study on diarrheagenic *Escherichia coli* pathotypes isolated from under 5 years old children in southeast of Iran. *Asian Pac J Trop Dis*, 4(Suppl 2): S813-S817.
5. Alizade H, Fallah F, Ghanbarpour R et al (2015). Genotyping of ESBL producing uropathogenic and diarrheagenic *Escherichia coli* in southeast of Iran. *Infect Disord Drug Targets*, 15: 118–24.
6. Barguigua A, El Otmani F, Talmi M et al (2011). Characterization of extended-spectrum β -lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* isolates from the community in Morocco. *J Med Microbiol*, 60 (Pt 9): 1344–52.
7. Ahmed OB, Omar AO, Asghar AH, Elhassan MM (2013). Prevalence of *TEM*, *SHV* and *CTX-M* genes in *Escherichia coli* and *Klebsiella* spp urinary isolates from Sudan with confirmed ESBL phenotype. *Life Sci J*, 10: 191–5.
8. Alizade H, Fallah F, Ghanbarpour R et al (2014). Phylotyping of *bla_{CTX-M-15}* gene in extended spectrum beta lactamase producing *Escherichia coli* isolates from clinical samples in Iran. *Hum Vet Med*, 6: 169–73.
9. Bradford P (2001). Extended spectrum beta lactamase in the 21 century: characterization, epidemiology, and detection of this important resistant threat. *Clin Microbiol Rev*, 14: 933–51.
10. Blair JMA, Webber MA, Baylay AJ et al (2015). Molecular mechanisms of antibiotic resistance. *Nat Rev Microbiol*, 13: 42–51.
11. Bonomo RA (2011). New Delhi metallo- β -lactamase and multidrug resistance: A global SOS? *Clin Infect Dis*, 52: 485–7.
12. Kuntaman K, Lestari ES, Severin JA et al (2005). Fluoroquinolone-resistant *Escherichia coli*, Indonesia. *Emerg Infect Dis*, 11: 1363–9.
13. Poole K (2005). Aminoglycoside resistance in *Pseudomonas aeruginosa*. *Antimicrob Agents Chemother*, 49: 479–87.
14. Arabi H, Pakzad I, Nasrollahi A et al (2015). Sulfonamide resistance genes (*sul*) in extended spectrum beta lactamase (ESBL) and non-ESBL producing *Escherichia coli* isolated from Iranian hospitals. *Jundishapur J Microbiol*, 8: e19961.
15. Bean DC, Livermore DM, Hall LMC (2009). Plasmids imparting sulfonamide resistance in *Escherichia coli*. Implications for persistence. *Antimicrob Agents Chemother*, 53: 1088–93.
16. Huovinen P (2001). Resistance to trimethoprim-sulfamethoxazole. *Clin Infect Dis*, 32: 1608–14.
17. WHO (2015). Worldwide country situation analysis: response to antimicrobial resistance. http://apps.who.int/iris/bitstream/10665/163468/1/9789241564946_eng.pdf?ua=1&ua=1
18. Habibzadeh F (2013). Editor's page use and misuse of antibiotics in the Middle East. *Lancet*, 382.
19. Sharifi A, Sharifi H, Karamouzian M et al (2013). Topical ocular anesthetic abuse among Iranian welders: time for action. *Middle East Afr J Ophthalmol*, 20: 336–40.
20. Moradi J, Hashemi FB, Bahador A (2015). Antibiotic resistance of *Acinetobacter baumannii* in Iran: A Systemic review of the published literature. *Osong Public Health Res Perspect*, 6: 79–86.
21. Kazemnia A, Ahmadi M, Dilmaghani M (2014). Antibiotic resistance pattern of different *Escherichia coli* phylogenetic groups isolated from human urinary tract infection and avian colibacillosis. *Iran Biomed J*, 18: 219–24.
22. Alikhani MY, Hashemi SH, Aslani MM, Farajnia S (2013). Prevalence and antibiotic resistance patterns of diarrheagenic *Escherichia coli* isolated from adolescents and adults in Hamedan, Western Iran. *Iran J Microbiol*, 5: 42–7.
23. Soltani J, Poorabbas B, Miri N, Mardaneh J (2016). Health care associated infections, antibiotic resistance and clinical outcome: A surveillance study from Sanandaj, Iran. *World J Clin Cases*, 4: 63–70.
24. Hosseini-Mazinani SM, Eftekhari F, Milani M, Ghandili S (2007). Characterization of β -lactamases from urinary isolates of *Escherichia coli* in Tehran. *Iran Biomed J*, 11: 95–9.
25. Najari Peerayeh S, Eslami M, Memariani M, Siadat SD (2013). High prevalence of *bla_{CTX-M-1}* group extended-spectrum β -lactamase genes in *Escherichia coli* isolates from Tehran. *Jundishapur J Microbiol*, 6: e6863.

26. Ahangarzadeh Rezaee M, Sheikhalizadeh V, Hasani A (2011). Detection of integrons among multi-drug resistant (MDR) *Escherichia coli* strains isolated from clinical specimens in northern west of Iran. *Braz J Microbiol*, 42: 1308–13.
27. Irajian G, Moghadas AJ (2010). Frequency of extended-spectrum beta lactamase positive and multidrug resistance pattern in Gram-negative urinary isolates, Semnan, Iran. *Jundishapur J Microbiol*, 3: 107–13.
28. Mohajeri P, Darfarin G, Farahani A (2014). Genotyping of ESBL producing uropathogenic *Escherichia coli* in West of Iran. *Int J Microbiol*, 2014:276941.
29. Issazadeh K, Naghibi SN, Khoshkholgh-pahlaviani MRM (2015). Drug resistance and serotyping of uropathogenic *Escherichia coli* among Patients with urinary tract infection in Rasht, Iran. *Zabedan J Res Med Sci*, 29–33.
30. Babaei Hemmati T, Mehdipour Moghaddam MJ, Salehi Z, Habibzadeh SM (2015). Prevalence of CTX-M-Type β -lactamases in multi-drug resistant *Escherichia coli* isolates from north of Iran, Rasht. *Biol J Microorg*, 3: 69–78.
31. Mehdipour Moghaddam MJ, Mirbagheri AA, Salehi Z, Habibzade SM (2015). Prevalence of class 1 integrons and extended spectrum beta lactamases among multi-drug resistant *Escherichia coli* isolates from north of Iran. *Iran Biomed J*, 19: 233–9.
32. Gashgi F, Zeighami H, Haghi F (2015). Frequency of *E. coli* clinical isolates producing *bla_{SHV}* and *bla_{TEM}* extended-spectrum beta-lactamases. *Hormozgan Med J*, 19: 218–224.
33. Mohammadi-Mehr M, Feizabadi M (2011). Antimicrobial resistance pattern of Gram-negative bacilli isolated from patients at ICUs of Army hospitals in Iran. *Iran J Microbiol*, 3: 26–30.
34. Safari M, Shojaipour M, Akbari M, Pourbabae A, Abtahi H (2013). Dissemination of CTX-M-type beta-lactamase among clinical isolates of *Enterobacteriaceae* in Markazi Province, Iran. *Jundishapur J Microbiol*, 6: e7182.
35. Kalantar D, Mansouri S (2010). Emergence of multiple β -lactamases produced by *Escherichia coli* clinical isolates from hospitalized patient in Kerman, Iran. *Jundishapur J Microbiol*, 3: 137–45.
36. Shams F, Hasani A, Ahangarzadeh Rezaee M et al (2015). Carriage of class 1 and 2 integrons in quinolone, extended-spectrum- β -lactamase-producing and multi drug resistant *E. coli* and *K. pneumoniae*: High burden of antibiotic resistance. *Adv Pharm Bull*, 5: 335–42.
37. Bush K, Jacoby GA (2010). Updated functional classification of beta-lactamases. *Antimicrob Agents Chemother*, 54: 969–76.
38. Sedighi I, Arabestani MR, Rahimbakhsh A et al (2015). Dissemination of extended-spectrum β -lactamases and quinolone resistance genes among clinical isolates of uropathogenic *Escherichia coli* in children. *Jundishapur J Microbiol*, 8: e19184.
39. Alizade H, Fallah F, Ghanbarpour R et al (2015). Phylogenetic groups, extended-spectrum beta-lactamases and metallo-beta-lactamase in *Escherichia coli* isolated from fecal samples of patients with diarrhea in Iran. *Gastroenterol Hepatol Bed Bench*, 8: 207–14.
40. Pakzad I, Ghafourian S, Taherikalani M et al (2011). *qnr* Prevalence in extended spectrum beta-lactamases (ESBLs) and none-ESBLs producing *Escherichia coli* isolated from urinary tract infections in central of Iran. *Iran J Basic Med Sci*, 14: 458–64.
41. Ghorbani-dalini S, Kargar M, Doosti A et al (2015). Molecular epidemiology of ESBL genes and multi-drug resistance in diarrheagenic *Escherichia coli* strains isolated from adults in Iran. *Iran J Pharm Res*, 14: 1257–62.
42. Heidary M, Momtaz H, Madani M (2014). Characterization of diarrheagenic antimicrobial resistant *Escherichia coli* isolated from pediatric patients in Tehran, Iran. *Iran Red Crescent Med J*, 16: e12329.
43. Shayan S, Bokaeian M, Shahraki S (2014). Prevalence and molecular characterization of AmpC-Producing clinical isolates of *Escherichia coli* from Southeastern Iran. *Microb Drug Resist*, 20: 104–7.
44. Khoshvaght H, Haghi F, Zeighami H (2014). Extended spectrum beta-lactamase producing Enterococcal *Escherichia coli* from young children in Iran. *Gastroenterol Hepatol Bed Bench*, 7: 131–6.
45. Shahcheraghi F, Ghezelgeh FR, Nobari S et al (2014). Identification and characterization of class 1 integrons among atypical

- enteropathogenic *Escherichia coli* isolated from children under 5 years of age. *Iran J Microbiol*, 6: 156–62.
46. Rashki A (2014). Cervico-vaginopathogenic *Escherichia coli* in Iran: Serogroup distributions, virulence factors and antimicrobial resistance properties. *Microb Pathog*, 75: 29–34.
 47. Khoshbakht R, Salimi A, Shirzad Aski H, Keshavarzi H (2013). Antibiotic susceptibility of bacterial strains isolated from urinary tract infections in Karaj, Iran. *Jundishapur J Microbiol*, 6: 86–90.
 48. Shams F, Hasani A, Pormohammad A et al (2014). *qnrA* implicated quinolone resistance in *Escherichia coli* and *Klebsiella pneumoniae* clinical isolates from a University Teaching Hospital. *Life Sci J*, 11(12s): 1032–5.
 49. Soleimani N, Aganj M, Ali L et al (2014). Frequency distribution of genes encoding aminoglycoside modifying enzymes in uropathogenic *E. coli* isolated from Iranian hospital. *BMC Res Notes*, 7: 842.
 50. Momtaz H, Dehkordi FS, Hosseini MJ et al (2013). Serogroups, virulence genes and antibiotic resistance in Shiga toxin-producing *Escherichia coli* isolated from diarrheic and non-diarrheic pediatric patients in Iran. *Gut Pathog*, 5:39.
 51. Mobaleghi J, Salimizand H, Beiranvand S et al (2012). Extended spectrum β -lactamases in urinary isolates of *Escherichia coli* in five Iranian hospitals. *Asian J Pharm Clin Res*, 5 (Suppl 2): 35–6.
 52. Mirzarazi M, Rezatofghi SE, Pourmahdi M, Mohajeri MR (2013). Antibiotic resistance of isolated gram negative bacteria from urinary tract infections (UTIs) in Isfahan. *Jundishapur J Microbiol*, 6: e6883.
 53. Neamati F, Firoozeh F, Saffari M, Zibaei M (2015). Virulence genes and antimicrobial resistance pattern in uropathogenic *Escherichia coli* isolated from hospitalized patients in Kashan, Iran. *Jundishapur J Microbiol*, 8: e17514.
 54. Motallebi M, Piroozmand A, Rohani M et al (2011). Multiple drug resistance of enteropathogenic *Escherichia coli* isolated from children with diarrhea in Kashan, Iran. *Afr J Microbiol Res*, 5: 3305–9.
 55. Nakhjavani FA, Mirsalehian A, Hamidian M et al (2007). Antimicrobial susceptibility testing for *Escherichia coli* strains to fluoroquinolones, in urinary tract infections. *Iran J Public Health*, 36: 89–92.
 56. Zahraei Salehi T, Farashi Bonab S (2006). Antibiotics susceptibility pattern of *Escherichia coli* strains isolated from chickens with colisepticemia in Tabriz province, Iran. *Int J Poult Sci*, 5: 677–84.
 57. Aslani MM, Salmanzadeh-ahrabi S, Alikhani YM et al (2008). Molecular detection and antimicrobial resistance of diarrheagenic *Escherichia coli* strains isolated from diarrheal cases. *Saudi Med J*, 29: 388–92.
 58. Lavakhamseh H, Mohajeri P, Rouhi S et al (2016). Multidrug-resistant *Escherichia coli* strains isolated from patients are associated with class 1 and 2 integrons. *Chemotherapy*, 61: 72–6.
 59. Gholipour A, Soleimani N, Shokri D et al (2014). Phenotypic and molecular characterization of extended-spectrum β -lactamase produced by *Escherichia coli*, and *Klebsiella pneumoniae* isolates in an educational hospital. *Jundishapur J Microbiol*, 7: e11758.
 60. Harifi Mood E, Meshkat Z, Izadi N et al (2015). Prevalence of quinolone resistance genes among extended-spectrum β -lactamase-producing *Escherichia coli* in Mashhad, Iran. *Jundishapur J Microbiol*, 8: e16217.
 61. Sedighi I, Solgi A, Amanati A, Alikhani MY (2014). Choosing the correct empirical antibiotic for urinary tract infection in pediatric: Surveillance of antimicrobial susceptibility pattern of *Escherichia coli* by E-Test method. *Iran J Microbiol*, 6: 387–91.
 62. Farshad S, Japoni A, Hosseini M (2008). Low distribution of integrons among multidrug resistant *E. coli* strains isolated from children with community-acquired urinary tract infections in Shiraz, Iran. *Pol J Microbiol*, 57: 193–8.
 63. Rezaei MS, Salehifar E, Rafiei A et al (2015). Characterization of multidrug resistant extended-spectrum beta-lactamase-producing *Escherichia coli* among uropathogens of pediatrics in north of Iran. *BioMed Res Int*, 2015:309478.
 64. Zahedi Bialvaei A, Samadi Kafil H (2015). Colistin, mechanisms and prevalence of resistance. *Curr Med Res Opin*, 31: 707–21.
 65. Mansouri S, Kalantar Neyestanaki D, Shokoohi M et al (2014). Characterization of AmpC,

- CTX-M and MBLs types of β -lactamases in clinical isolates of *Klebsiella pneumoniae* and *Escherichia coli* producing extended spectrum β -lactamases in Kerman, Iran. *Jundishapur J Microbiol*, 7: e8756.
66. Seputienė V, Povilonis J, Ruzauskas M et al (2010). Prevalence of trimethoprim resistance genes in *Escherichia coli* isolates of human and animal origin in Lithuania. *J Med Microbiol*, 59 (Pt 3): 315–22.
 67. Moghni M, Barati S (2013). Antibiotic resistance in food poisoning caused by *Escherichia coli* O157: H7 in hospitalized patients at 5 years in Iran. *Res J Pharm Biol Chem Sci*, 4: 436–42.
 68. Momtaz H, Karimian A, Madani M et al (2013). Uropathogenic *Escherichia coli* in Iran: serogroup distributions, virulence factors and antimicrobial resistance properties. *Ann Clin Microbiol Antimicrob*, 12: 8.
 69. Karami N, Nowrouzian F, Adlerberth I, Wold AE (2006). Tetracycline resistance in *Escherichia coli* and persistence in the infantile colonic microbiota. *Antimicrob Agents Chemother*, 50: 156–61.
 70. Centers for Disease Control and Prevention (2013). Antibiotic resistance threats in the United States (2013). <https://www.cdc.gov/drugresistance/threat-report-2013/index.html>
 71. Ferdosi Shahandashti E, Javanian M, Moradian-Kouchaksaraei M et al (2015). Resistance patterns of *Escherichia coli* causing urinary tract infection. *Caspian J Intern Med*, 6: 148-51.
 72. Kalantar E, Soheili F, Salimi H, Soltan Dallal MM (2011). Frequency, antimicrobial susceptibility and plasmid profiles of *Escherichia coli* pathotypes obtained from children with acute diarrhea. *Jundishapur J Microbiol*, 4: 23-8.
 73. Hemati Z, Ghanbarpour R, Alizade H (2014). The distribution of beta lactamase genes in *Escherichia coli* phylotypes isolated from diarrhea and UTI cases in northwest Iran. *Adv Clin Exp Med*, 23: 523–9.
 74. Khorshidi A, Rohani M, Akbari M, Motallebi M (2013). Molecular detection of *bla*_{TEM} and *bla*_{SHV} genes among clinical isolates of *Escherichia coli* from Kashan, Iran. *Afr J Microbiol Res*, 7: 751-4.
 75. Sadat Moini A, Soltani B, Taghavi Ardakani A et al (2015). Multidrug-resistant *Escherichia coli* and *Klebsiella pneumoniae* isolated from patients in Kashan, Iran. *Jundishapur J Microbiol*, 8: e27517.
 76. Moayednia R, Shokri D, Mobasherizadeh S et al (2014). Frequency assessment of β -lactamase enzymes in *Escherichia coli* and *Klebsiella* isolates in patients with urinary tract infection. *J Res Med Sci*, 19(Suppl 1):S41-5.
 77. Asadi S, Kargar M, Solhjoo K et al (2014). The association of virulence determinants of uropathogenic *Escherichia coli* with antibiotic resistance. *Jundishapur J Microbiol*, 7: e9936.
 78. Khoramrooz SS, Sharifi A, Yazdanpanah M et al (2016). High frequency of class 1 integrons in *Escherichia coli* isolated from patients with urinary tract infections in Yasuj, Iran. *Iran Red Crescent Med J*, 18: e26399.
 79. Adib N, Ghanbarpour R, Solatzadeh H, Alizade H (2014). Antibiotic resistance profile and virulence genes of uropathogenic *Escherichia coli* isolates in relation to phylogeny. *Trop Biomed*, 31: 17-25.
 80. Ayatollahi J, Vahidi A, Shahcheraghi SH et al (2013). Investigating the resistance of *Escherichia coli* against some selected antimicrobials in Bam. *Jundishapur J Microbiol*, 6: e7407.
 81. Javadian F, Sepehri Z, Khaje H et al (2014). Detection, susceptibility and molecular characterisation of ESBL-producing *E. coli* causing urinary tract infection. *J Bio Env Sci*, 5: 291-9.
 82. Memariani M, S Najari-Peerayeh, Salehi TZ, Mostafavi SKS (2015). Occurrence of *SHV*, *TEM* and *CTX-M* β -lactamase genes among enteropathogenic *Escherichia coli* strains isolated from children with diarrhea. *Jundishapur J Microbiol*, 8: e15620.
 83. Kargar M, Mohammadalipour Z, Doosti A et al (2014). High prevalence of class 1 to 3 integrons among multidrug-resistant diarrheagenic *Escherichia coli* in southwest of Iran. *Osong Public Health Res Perspect*, 5: 193–8.