

Prevalence and Antibiotic Resistance of *Escherichia coli* O157:H7 Isolated from Raw Meat Samples of Ruminants and Poultry

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Abstract *Escherichia coli* O157:H7 is one of the most dangerous zoonotic pathogens of meat. The present investigation was done to study the prevalence and antibiotic resistance of *E. coli* O157:H7 strains isolated from raw meat samples. A total of 458 meat samples were collected. Samples were cultured using what? After which sorbitol negative isolates were analyzed for *rfbO157* and *flicH7* genes. Thirty-six out of 458 meat samples were positive for sorbitol negative strains of *E. coli* (7.86%). All of the sorbitol negative strains were also positive for *rfbO157* and *flicH7* genes. Prevalence of *E. coli* O157:H7 strains were 7.86%. The prevalence of *E. coli* O157:H7 in chicken meat was higher than the other samples (16.25%). The genes that encode resistance to ampicillin (*CITM*) (100%), gentamicin (*aac(3)-IV*) (94.44%) and tetracycline (*tetA*) (61.11%) had the highest prevalence. *Escherichia coli* O157:H7 strains from raw meat samples from ruminants and poultry had the highest resistance to ampicillin (100%), tetracycline (83.33%) and gentamicin (83.33%) respectively. Strains of antibiotic resistant *E. coli* O157:H7 found in this present study are of public health importance.

Keywords: *Escherichia coli* O157:H7, raw meat, antibiotic resistance pattern, antibiotic resistance genes

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1. Introduction

Food pathogens cause more than three-hundred diseases from simple diarrhea to death [1,2]. Foodborne diseases cause about 75 million illnesses, 320,000 hospitalizations, and 4,000 deaths in the United States annually [2,3,4]. Access to hygienic and healthy food samples is an important issue particularly in Iran where basic principles of meat inspection are not applied in some slaughterhouses. Food samples with animal origin and especially meat play an important role in the transmission of foodborne pathogens to humans [5,6,7,8].

Escherichia coli (*E. coli*) O157:H7 is an important foodborne pathogen of public health importance [5,6,7,8]. *E. coli* is a gram-negative, non-sporulating, rod-shaped, facultative anaerobe and Shiga toxin-producing *E. coli* (STEC) is a subdivision of enterohemorrhagic *E. coli* (EHEC) [9,10,11]. Outbreak of food poisoning and foodborne diseases are associated with certain STEC O-serogroups and O157 is the most important serogroup associated with intensive clinical syndromes like lethal hemolytic uremic syndrome (HUS), bloody and non-bloody diarrhea, thrombotic thrombocytopenic purpura (TTP) and hemorrhagic colitis (HC) [9,10,11]. Human infection with *E. coli* O157:H7 serotype has been associated with contaminated food samples, water, and person-to person transmission [9,10,11]. Meats from ruminants and poultry are considered to be the primary

reservoirs of *E. coli* O157:H7 [9,10,11].

High levels of resistance in *E. coli* O157:H7 is an important factor which can increase the pathogenicity of bacterium. Food samples with animal origin and especially meat have been found to harbor *E. coli* O157:H7 with high levels of resistance against commonly used groups of antibiotics including quinolones, aminoglycosides, macrolides, cephalosporins, sulfonamides, fluoroquinolones and tetracycline [9-15]. Some antibiotic resistance genes including the genes that encode resistance to ampicillin (*CITM*), fluoroquinolone (*qnr*), gentamicin (*aac(3)-IV*), cephalothin (*blaSHV*), trimethoprim (*dfrAI*), sulfonamide (*sulI*), tetracycline (*tetA* and *tetB*), chloramphenicol (*catI* and *cmlA*) and aminoglycosides (*aadA1*) have been found to be responsible for antibiotic resistance in STEC strains [9-14,16,17,18].

Regarding an uncertain prevalence of *E. coli* O157:H7 in raw meat samples, the present research was carried out to study the prevalence and distribution of antibiotic resistance genes and antibiotic resistance pattern of *E. coli* O157:H7 strains isolated from raw bovine, ovine, caprine, camel, chicken, turkey and quail meat samples.

2. Materials and Methods

2.1. Ethical Considerations

Verification of this research project and the licenses related to sampling process were approved by Dr. Zohreh Mashak.

2.2. Samples

From September 2015 to December 2015, a total of 458 raw meat samples including cows (n= 70), sheep (n= 68), goats (n= 60), camel (n= 60), chicken (n= 80), turkey (n= 60), and quail (n= 60) were collected and immediately transferred to the laboratory in cooler with ice-packs. Samples were randomly collected from the various parts of Alborz province, Iran. All meat samples showed normal physical characters including odor, color and density.

2.3. *Escherichia coli* O157:H7 Isolation

Twenty-five grams of each meat sample was aseptically transferred to 225 ml of Trypticase Soy Broth (TSB, Merck, Frankfurt, Germany) supplemented with 0.5 mg/ml novobiocin and incubated at 37°C for 24 hrs [10,16]. Enriched culture was plated onto Sorbitol MacConkey agar (SMAC, Merck, Frankfurt, Germany) supplemented with cefixime (0.05 mg/ml) and potassium tellurite (2.5 mg/L). All plates were then incubated at 37°C for 24 hrs. Then, non-sorbitol fermented colonies were selected from the SMAC plates and streaked onto plates containing Eosin Methylene Blue agar (EMB, Merck, Frankfurt, Germany) and were incubated at 37°C for 24 hrs. These isolates, with typical *E. coli* green metallic shine on EMB agar were biochemically tested for growth on triple sugar iron agar (TSI, Merck, Frankfurt, Germany) and lysine iron agar (LIA, Merck, Frankfurt, Germany), oxidative/fermentative degradation of glucose, citrate utilization, urease production, indole production, tryptophan degradation, glucose degradation (methyl red test, Merck, Frankfurt, Germany), Voges Proskauer (VP, Merck, Frankfurt, Germany), lysine decarboxylase and motility tests [10,16].

2.4. PCR Confirmation of *Escherichia coli* O157:H7

Sorbitol negative *E. coli* strains were subjected to DNA extraction and PCR amplification of *rfbO157* and *flicH7* targets. Sorbitol negative colonies were sub-cultured on Luria-Bertani broth (LBB, Merck, Frankfurt, Germany) and further incubated for 48 h at 37 °C. Genomic DNA was extracted from bacterial colonies using the DNA extraction kit (Thermo Fisher Scientific, Frankfurt, Germany) according to manufacturer's instruction. The DNA extraction was done according 4 different stages of growth of bacteria, sample preparation, lysis of cell walls, purification of DNA and finally DNA condensation. The concentrations of extracted DNA of meat samples were

previously determined by measuring absorbance of the sample at 260 nm using spectrophotometer [19]. Table 1 shows the primer sequence and PCR cycling program used for the amplification of the *rfbO157* and *flicH7* genes. The PCR reactions were performed in a total volume of 25 µL, including 1.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 200 µM dNTPs each (Thermo Fisher Scientific, Frankfurt, Germany), 2.5 µL PCR buffer (10X), 25 pmoL of each primer (Table 1) [20,21], 1.5 U of Taq DNA polymerase (Thermo Fisher Scientific, Frankfurt, Germany) and 5 µL (40-260 ng/µL) of the extracted DNA template of the *E. coli* isolates. *Escherichia. coli* O157:H7 (ATCC 35150) and sterile distilled water were used as t positive negative controls respectively [20,21].

2.5. PCR Amplification of Antibiotic Resistance Genes

Escherichia. coli O157:H7 strains were tested for presence of antibiotic resistance genes using PCR method and Table 2 shows the list of primers, program and condition of each reaction used for detection of antimicrobial resistant genes [11,22]. Programmable DNA thermo-cycler (Eppendorf Flexrcycler, Eppendorf AG Barkhausenweg, Hamburg, Germany) was used in all PCR reactions. The PCR amplification products (15 µl) were subjected to electrophoresis in a 1.5% agarose gel in 1X TBE buffer at 80 V for 30 min, stained with SYBR Green (Thermo Fisher Scientific, Frankfurt, Germany). All runs included a negative DNA control consisting of PCR grade water and strains of *E. coli* O157:K88ac:H19, CAPM 5933 and *E. coli* O159:H20, CAPM 6006 were used as positive controls.

2.6. Antimicrobial Susceptibility Testing

Antibiogram test of *E. coli* strains against 13 commonly used antibiotics was determined according to the guidelines described by Clinical and Laboratory Standards Institute (950 West Valley Road, Suite 2500 Wayne, PA 19087 USA) [23]. For this purpose, tetracycline (30 µg), ampicillin (10 µg), cefotaxime (30 µg), gentamycin (10 µg), ciprofloxacin (5 µg), amikacin (30 µg), imipenem (30 µg), cotrimoxazole (30 µg), enrofloxacin (5 µg), sulfamethoxazole (25 µg), trimethoprim (5 µg), streptomycin (10 µg), and chloramphenicol (30 µg) (Oxoid, Wade Road Basingstoke Hampshire RG24 8PW, United Kingdom). Plates were incubated at 37°C for 18-24 h and results were interpreted as described by CLSI (2012) [23].

Table 1. Primer sequence and PCR program used for amplification of the *rfbO157* and *flicH7* genes

Target gene	Primer sequence (5'-3')	PCR product (bp)	PCR programs
<i>rfbO157</i>	CGGACATCCATGTGATATGG TTGCTATGTACAGCTAATCC	259	1 cycle: 94 ^{oC} ----- 5 min. 35 cycles: 94 ^{oC} ----- 60 s 56 ^{oC} ----- 30 s 72 ^{oC} ----- 60 s
<i>flicH7</i>	GCGCTGTCGAGTTCTATCGAG CAACGGTGACTTTATCGCCATTCC	625	1 cycle: 72 ^{oC} ----- 10 min

Table 2. The oligonucleotide primers and the PCR programs used for amplification of antibiotic resistance genes of *Escherichia coli* isolates of raw meat

Target gene	Primer sequence (5'-3')	PCR product (bp)	PCR programs	PCR Volume (50µL)
<i>aadA1</i>	F: TATCCAGCTAAGCGCGAACT R: ATTTGCCGACTACCTTGGTC	447		
<i>tetA</i>	F: GGTTCACTCGAACGACGTCA R: CTGTCCGACAAGTTGCATGA	577		
<i>tetB</i>	F: CCTCAGCTTCTCAACGCGTG R: GCACCTTGCTGATGACTCTT	634		
<i>dfrA1</i>	F: GGAGTGCCAAAGGTGAACAGC R: GAGGCGAAGTCTTGGGTAAAAAC	367		
<i>qnr</i>	F: GGGTATGGATATTATTGATAAAG R: CTAATCCGGCAGCACTATTTA	670	1 cycle: 94 °C ----- 8 min. 32 cycles: 95 °C ----- 60 s 55 °C ----- 70 s 72 °C ----- 2 min	5 µL PCR buffer 10X 2 mM MgCl ₂ 150 µM dNTP (Fermentas) 0.75 µM of each primers F & R 1.5 U Taq DNA polymerase (Fermentas)
<i>aac(3)-IV</i>	F: CTTCAGGATGGCAAGTTGGT R: TCATCTCGTTCTCCGCTCAT	286	72 °C ----- 2 min 1 cycle: 72 °C ----- 8 min	3 µL DNA template
<i>sul1</i>	F: TTCGGCATTCTGAATCTCAC R: ATGATCTAACCTCGGTCTC	822		
<i>blaSHV</i>	F: TCGCCTGTGTATTATCTCCC R: CGCAGATAAATCACCACAATG	768		
<i>CITM</i>	F: TGGCCAGAACTGACAGGCAAA R: TTTCTCCTGAACGTGGCTGGC	462		
<i>cat1</i>	F: AGTTGCTCAATGTACCTATAACC R: TTGAATTCATTAAGCATTCTGCC	547		
<i>cmlA</i>	F: CCGCCACGGTGTGTTGTATC R: CACCTTGCTGCCATCATTAG	698		

2.7. Statistical Analysis

Statistical analysis was performed using the SPSS/20.0 software and chi-square and fisher exact test for significant relationships. The prevalence of antibiotics resistance properties of *E. coli* O157:H7 isolated from various types of raw meat samples were statistically analyzed. Statistical significance was regarded at a *P* value < 0.05.

3. Results

Table 3 represents the prevalence of *E. coli* and also O157:H7 serotype in different types of raw meat samples. Thirty-six out of 458 (7.86%) raw meat samples were positive for sorbitol negative bacteria. All of the sorbitol negative bacteria harbored both *rfbO157* and *flicH7* genes in the PCR reaction. Therefore, the prevalence of the *E. coli* O157:H7 strains in raw meat samples were 7.86%.

Figure 1 shows the results of the gel electrophoresis for the *rfbO157* and *flicH7* genes. We found that chicken meat samples had the highest (16.25%) prevalence of *E. coli* O157:H7, while caprine meat samples had the lowest (3.33%). Statistically significant difference was seen between the prevalence of *E. coli* O157:H7 and type of samples (*P* < 0.05).

Table 4 represents the distribution of antibiotic resistance genes among the *E. coli* O157:H7 strains recovered from raw meat samples. We found that the genes that encode resistance against ampicillin (*CITM*) (100%), gentamicin (*aac(3)-IV*) (94.44%) and tetracycline (*tetA*) (61.11%) had the highest prevalence. *E. coli* O157:H7 strains isolated from chicken meat samples had the highest and the most diverse prevalence of antibiotic resistance genes. Statistically significant difference was seen between the prevalence of antibiotic resistance genes and type of samples (*P* < 0.05). *E. coli* O157:H7 strains isolated from chicken, bovine and turkey had the highest prevalence of antibiotic resistance genes.

Table 5 represents the total prevalence of antibiotic resistance among the *E. coli* O157:H7 strains isolated from various types of raw meat samples. We found that *E. coli* O157:H7 strains of our study harbored the highest levels of resistance against ampicillin (100%), tetracycline (83.33%), gentamicin (83.33%), amikacin (58.33%) and sulfamethoxazole (58.33%). *E. coli* O157:H7 strains isolated from chicken meat samples had the highest and the most diverse prevalence of antibiotic resistance. Statistically significant difference was seen between the prevalence of antibiotic resistance and type of samples (*P* < 0.05). Prevalence of resistance against imipenem (2.77%) and chloramphenicol (11.11%) antibiotics were low.

Table 3. Total prevalence of *E. coli* O157:H7 in various types of raw meat samples.

Types of meat samples	No. samples collected	No. sorbitol-negative strains (%)	No. <i>E. coli</i> O157:H7 strains (%)
Bovine	70	4 (5.71)	4 (5.71)
Ovine	68	3 (4.41)	3 (4.41)
Caprine	60	2 (3.33)	2 (3.33)
Camel	60	2 (3.33)	2 (3.33)
Chicken	80	13 (16.25)	13 (16.25)
Turkey	60	8 (13.33)	8 (13.33)
Quail	60	4 (6.66)	4 (6.66)
Total	458	36 (7.86)	36 (7.86)

Table 4. Total distribution of antibiotic resistance genes among the *E. coli* O157:H7 strains isolated from various types of raw meat samples.

Samples (No. O157:H7 strains)	Distribution of antibiotic resistance genes (%)										
	<i>dfrA1</i>	<i>aac(3)-IV</i>	<i>tetA</i>	<i>tetB</i>	<i>qnr</i>	<i>aadA1</i>	<i>blaSHV</i>	<i>CITM</i>	<i>cat1</i>	<i>cmlA</i>	<i>sul1</i>
Bovine (4)	2 (50)	4 (100)	3 (75)	-	2 (50)	2 (50)	2 (50)	4 (100)	-	-	2 (50)
Ovine (3)	1 (33.33)	3 (100)	2 (66.66)	1 (33.33)	1 (33.33)	1 (33.33)	1 (33.33)	3 (100)	-	-	1 (33.33)
Caprine (2)	-	2 (100)	2 (100)	-	1 (50)	1 (50)	1 (50)	2 (100)	-	-	1 (50)
Camel (2)	-	2 (100)	2 (100)	-	-	1 (50)	1 (50)	2 (100)	-	-	1 (50)
Chicken (13)	5 (38.46)	12 (92.30)	8 (61.53)	3 (23.07)	7 (53.84)	6 (46.15)	5 (38.46)	13 (100)	4 (30.76)	1 (7.69)	7 (53.84)
Turkey (8)	2 (25)	8 (100)	5 (62.50)	2 (25)	2 (25)	2 (25)	2 (25)	8 (100)	1 (12.50)	-	2 (25)
Quail (4)	1 (25)	3 (75)	2 (50)	1 (25)	2 (50)	1 (25)	1 (25)	4 (100)	-	-	1 (25)
Total (36)	11 (30.55)	34 (94.44)	22 (61.11)	7 (19.44)	15 (41.66)	14 (38.88)	13 (36.11)	36 (100)	5 (13.88)	1 (2.77)	15 (41.66)

Table 5. Antibiotic resistance pattern of *E. coli* O157:H7 strains isolated from various types of raw meat samples.

Samples (No. O157:H7 strains)	Pattern of antibiotic resistance (%)												
	Tet*	Amp	Cef	Gen	Cip	Amk	Imp	Cot	Enr	Sul	Trp	S10	C30
Cow (4)	4 (100)	4 (100)	2 (50)	4 (100)	2 (50)	2 (50)	-	2 (50)	2 (50)	2 (50)	2 (50)	2 (50)	-
Sheep (3)	2 (50)	3 (100)	1 (33.33)	2 (66.66)	1 (33.33)	2 (66.66)	-	1 (33.33)	2 (66.66)	2 (66.66)	2 (66.66)	1 (33.33)	-
GoatCaprine (2)	2 (100)	2 (100)	-	2 (100)	1 (50)	1 (50)	-	1 (50)	1 (50)	1 (50)	1 (50)	1 (50)	-
Camel (2)	1 (50)	2 (100)	-	1 (50)	-	-	-	-	-	-	-	1 (50)	-
Chicken (13)	11 (84.61)	13 (100)	7 (53.84)	11 (84.61)	7 (53.84)	9 (69.23)	1 (7.69)	7 (53.84)	8 (61.53)	8 (61.53)	8 (61.53)	5 (38.46)	3 (23.07)
Turkey (8)	7 (87.50)	8 (100)	2 (25)	7 (87.50)	2 (25)	5 (62.50)	-	2 (25)	4 (50)	6 (75)	5 (62.50)	2 (25)	1 (12.50)
Quail (4)	3 (75)	4 (100)	1 (25)	3 (75)	1 (25)	2 (50)	-	-	2 (50)	2 (50)	2 (50)	1 (25)	-
Total (36)	30 (83.33)	36 (100)	13 (36.11)	30 (83.33)	14 (38.88)	21 (58.33)	1 (2.77)	13 (36.11)	19 (52.77)	21 (58.33)	20 (55.55)	13 (36.11)	4 (11.11)

*Tet: tetracycline (30 u), amp: ampicillin (10 u), cef: cefotaxime (30 µg), gen: gentamicin (10 µg), cip: ciprofloxacin (5 µg), amk: amikacin (30 u), imp: imipenem (30 u), cot: cotrimoxazole (30 µg), enr: enrofloxacin (5 µg), sul: sulfamethoxazole (25 µg), trp: trimethoprim (5 µg), s10: streptomycin (10 µg), c30: chloramphenicol (30 µg).

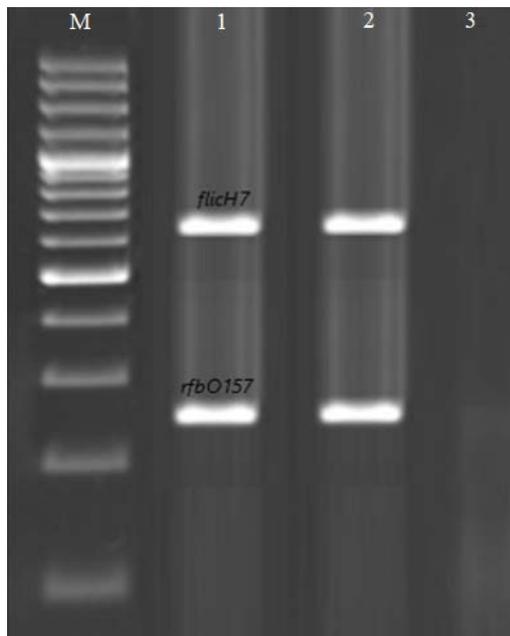


Figure 1. Results of the gel electrophoresis for the *rfbO157* and *flicH7* genes. M: 100 bp ladder, 1: Positive sample for *rfbO157* (259 bp) and *flicH7* (625 bp) genes, 2: Positive controls and 3: Negative control

4. Discussion

E. coli O157:H7 is the most commonly isolated serotype of EHEC group from ill persons and also cases of food infection in the Japan, United States and the United Kingdom [23,24]. The Centers for Disease Control and Prevention (CDC) has appraised that *E. coli* O157:H7 infections cause 75,000 illnesses, 2,500 hospitalizations,

and 50 deaths annually in the United States [24]. The annual cost of illness due to *E. coli* O157:H7 infections was 400 million dollars [24].

Raw ruminant and poultry meat are considered as substantial sources of *E. coli* O157:H7. Results of the present investigation showed that 36 samples out of 458 samples (7.86%) were contaminated with *E. coli* O157:H7 which was entirely high. Some of the most important causes for the high prevalence of *E. coli* O157:H7 in raw meat samples of our study are I: close contact of meat carcasses with each other and easily transmission of *E. coli* O157:H7; II: possibility for transmission of *E. coli* O157:H7 from the contents of digestive tract, blood, wool and external surface of body through the slaughter process; III: transmission of *E. coli* O157:H7 from the hands of the infected butchers and meat inspector to meat; IV: transmission of *E. coli* O157:H7 from animals like rats, cats, fox and birds which have been entered from outside the slaughterhouse to meat and environment; V: using from infected water for washing of meat carcasses; VI: transmission of *E. coli* O157:H7 from the contaminated equipment like knife and yeah used for cutting the head, skin and divided the carcasses to meat; VII: lack of attention to detailed meat inspection in some Iranian slaughterhouses.

Zarei et al. (2013) [25] reported that the prevalence of *E. coli* O157:H7 in the meat samples of beef, buffalo and lamb were 2.8%, 1.4% and 0%, respectively which was entirely lower than our findings. Hessain et al. (2015) [26] reported that the prevalence of *E. coli* O157:H7 in raw beef, chicken and mutton meat samples were 2%, 2.5% and 2.5%, respectively which was lower than our findings. They showed that the prevalences of *E. coli* O157:H7 in ground beef, beef burgers, beef sausage, ground chicken

and chicken burgers were 5%, 10%, 0.0%, 5% and 0.0%, respectively. Momtaz et al. (2013) [10] indicated that 238 out of 820 meat samples (29.02%) were positive for presence of *E. coli* and of which 153 samples (64.28%) were STEC. They showed that sheep meat (35.45%) had the highest prevalence of *E. coli*, while camel meat (19.56%) had the lowest. They showed that the prevalence of O157 serogroup in the meat samples of beef, sheep, goat and camel were 31.34%, 28.57%, 36% and 25%, respectively. Previous study which was conducted in China [27] showed that of 551 samples studied, 21 (3.81%) were positive for *E. coli* O157 and seven (1.27%) for O157:H7. They showed that the highest prevalence rate was found in beef (13.32%), pork (6.90%), chicken (3.28%) and duck (2.54%). Bekele et al. (2014) [28] reported that of 384 meat samples collected from Addis Ababa, 39 (10.2%) were positive to *E. coli* O157:H7. They reported that beef (13.30%), sheep (9.40%) and goat (7.80%) meat samples had the highest prevalence of *E. coli* O157:H7. *E. coli* O157:H7 can colonize the intestinal tract of many livestock and during slaughtering may contaminate the carcass, work surfaces and material used for processing of meat products. With good hygienic practices during skinning and eviscerating, the rate of carcass contamination should be significantly below the carriage rate. High differences of the prevalence of *E. coli* O157:H7 strains in different studies is due to the fact that maybe types of samples, number of samples collected, method of sampling, method of experiment, place of sampling and weather and climate of geographical zone of sampling were different. Differences in the levels of health care and hygiene, accuracy in meat inspection, hygiene of the slaughterhouses and finally levels of personal hygiene are other factors which may affected the prevalence of *E. coli* O157:H7 in each region.

Another important issue which is not proper observed in some Iranian farms is antibiotic prescription. Unfortunately, Iranian veterinary practitioners prescribed antibiotics in a highly irregular and unauthorized manner without any attentions to the results of disk diffusion method. Therefore, it was not surprising that the *E. coli* O157:H7 strains of our investigation had the high prevalence of resistance against ampicillin, tetracycline, gentamicin, amikacin and sulfamethoxazole antibiotics, which was covered by presence of antibiotic resistance genes. Goncuoglu et al. (2010) [29] showed that prevalence of resistance of *E. coli* O157:H7 isolated from meat in Turkey against cephalothin, streptomycin, sulfamethoxazole and sulfonamides were 36.36%, 9.09%, 14.28% and 7.14%, respectively. Zhang et al. (2015) [27] reported that *E. coli* O157:H7 isolates of raw meat in China were highly resistant to penicillin (100%), chloramphenicol (64.29%) and ampicillin (57.14%) which was similar to our findings. Momtaz et al. (2013) [10] reported that the most commonly detected antibiotic resistance genes in the raw beef meat samples were blaSHV (70.14%), aac(3)-IV (64.17%), tetA (58.20%), aadA1 (49.25%), CITM (46.26%) and dfrA1 (43.28%) which was similar to our findings. They showed that resistance against penicillin and tetracycline were high, while resistance against ciprofloxacin and nitrofurantoin were low. Our results showed that all of the *E. coli* O157:H7 strains harbored resistance at-least against two antibiotic agents. Our

results were similar with those of South Africa [30], Korea [31] and Mexico [32]. Momtaz et al. (2013) [22] reported that aac(3)-IV (68.03%), sul1 (82.78%), blaSHV (56.55%), aadA1 (60.65%) and tetA (51.63%) and also resistance against tetracycline (86.88%), penicillin (100%), gentamycin (62.29%) and streptomycin (54.91%) were the most commonly reported antibiotic resistance-based finding of STEC strains of diarrheic patients which was similar to our results.

Chloramphenicol is a forbidden antibiotic. The high presences of resistance against chloramphenicol showed its irregular and unauthorized use in veterinary treatment and especially field of poultry in Iran. We found that the prevalence of resistance against chloramphenicol in the *E. coli* O157:H7 strains isolated from chicken and turkey meat samples were 23.07% and 12.50%, respectively with was entirely high. Practitioners of the field of poultry use from chloramphenicol antibiotic as a basic one. Therefore, in a very short period of time, antibiotic resistance will appear. High prevalence of resistance against chloramphenicol in the *E. coli* O157:H7 strains of meat samples have been reported from Iran [10,22], USA [33], Turkey [28], UK [34] and Nigeria [35]. High differences of the prevalence of antibiotic resistance in the *E. coli* O157:H7 strains in different studies is due to the fact that maybe availability of antibiotics, their cost and even idea of veterinarian for antibiotic prescription are different in each region. Therefore, various investigations reported different prevalence for antibiotic resistance. High prevalence of the tetA, CITM and aac(3)-IV antibiotic resistance genes and also high prevalence of resistance against tetracycline, ampicillin and gentamicin have also reported by other Iranian researchers [36,37].

In conclusions, we identified a large number of antibiotic resistance genes and also antibiotic resistance in the *E. coli* O157:H7 strains isolated from bovine, ovine, caprine, camel, chicken, turkey and quail raw meat. The strains isolated from chicken, turkey and bovine meat samples, resistance against ampicillin, gentamicin and tetracycline antibiotics and finally presence of CITM, aac(3)-IV and tetA antibiotic resistance genes were the most commonly detected characters in the *E. coli* O157:H7 strains of raw meat. High prevalence of resistant *E. coli* O157:H7 bacteria in the samples showed insufficiency of meat inspection and also presence of cross contamination in Iranian slaughterhouses. Because of low levels of bacterial resistance against imipenem, cefotaxime, cotrimoxazole and streptomycin antibiotics, occurrence of food infections via consumption of meat contaminated with *E. coli* O157:H7 can be treated with their regular prescription. Complete cooking of meat before consumption can prevent from occurrence of *E. coli* O157:H7 infection in human.

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