

**How to Cite:**

Shahreza, M. S., & Afshari, H. (2022). Ribotyping and assessment of toxigenic genes of clostridium difficile strains isolated from raw meat. *International Journal of Health Sciences*, 6(S6), 4853–4863. <https://doi.org/10.53730/ijhs.v6nS6.11471>

## **Ribotyping and assessment of toxigenic genes of clostridium difficile strains isolated from raw meat**

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**Abstract**---*Background:* *Clostridium difficile* is an anaerobic, spore forming, rod shaped bacterium that can produce toxins and may transmit through some types of food samples. The present survey was done to assess the prevalence, toxigenic gene profile and ribotyping of *C. difficile* strains isolated from raw bovine and ovine meat samples. *Methods:* Two hundred and fifty raw meat samples were collected from Isfahan, Iran and analyzed for presence of *C. difficile* using the microbial culture. Genomic DNA was extracted from *C. difficile* isolates. Extracted DNA samples were subjected to PCR for determination of *tcdA*, *tcdB*, and *cdtA* toxigenic genes. Ribotyping was done using the 16S and 23S rRNA genes amplification in a separated PCR assay. *Results:* Fifteen out of 250 (6%) raw meat samples were contaminated with *C. difficile*. Prevalence of *C. difficile* strains amongst the raw bovine and ovine meat samples were 8% and 4%, respectively. The most commonly detected toxigenic genes were *tcdA* (33.33%) and *cdtA* (20%). Distribution of *tcdB* was 13.33%. Amongst the combined toxigenic genes, *tcdA+cdtA* had the highest distribution (13.33%). Among isolates of bovine meat samples, 027 ribotype was the most prevalent (40%). Among isolates of raw ovine meat samples, both 027 and 078 ribotypes had equal prevalence (20%). *Conclusion:* Role of raw meat as a source of toxigenic *C. difficile* strains, particularly 027 and 078 ribotypes was determined. Well-cooking of raw meat samples before consumption may diminish the risk of foodborne *C. difficile* infections.

**Keywords**---clostridium difficile, toxigenic genes, ribotypes, raw meat.

## Introduction

*Clostridium difficile* is a gram-positive, obligate anaerobic, spore-forming and cytotoxin producing bacterium with optimum growth temperature at 35–40°C (1). It is recognized as a major cause of antimicrobial-associated and hospital-associated diarrhea, and the cause of almost all cases of pseudomembranous colitis (2). Foods maybe responsible in transmission of *C. difficile* into the human population (3). It is considered that *C. difficile* can be transmitted to human by foods since it is disseminated by oral-fecal route and isolated from food animals including poultry and in some lower cases raw bovine and ovine meat samples (4). Meat can be contaminated by *C. difficile* through infected animals or food handlers during slaughtering (5). Several studies determined that *C. difficile* spore contamination level is generally low (6). However, the spores of this pathogen, if present in meat or other foods, may not be killed by cooking and can survive at 71°C for two hours (7).

Some toxigenic genes are responsible for the pathogenesis of *C. difficile* infections (8). The two virulence factors associated with the *C. difficile* infection are toxin A (*tcdA*) and toxin B (*tcdB*), which are an enterotoxin and a cytotoxin, respectively (9). The binary toxin (*cdt*) is encoded by the genes *cdtA* and *cdtB* located outside PaLoc (10). *Cdt* is frequently observed in *C. difficile* strains associated with increased severity of *C. difficile* infection (CDI) (10). The epidemiology of CDI in humans have been changed as a consequence of the emergence and dissemination of new strains of *C. difficile* called ribotype 027 and 078 (11). Roles of these two ribotype in the epidemiology of *C. difficile* strains in food samples and the cases of foodborne diseases is not determined yet. According to the high importance of the *C. difficile*, the present survey was done to assess the ribotyping and toxigenic gene profiles of the *C. difficile* strains isolated from raw meat.

## Materials and Methods

### Samples

From march to August 2021, a total of 250 raw meat samples (100 g, tight muscle), including bovine (n= 125) and ovine (n= 125), were collected from butchers of the Isfahan province, Iran. Samples were collected separately using the sterile plastic bags. Samples were transferred to laboratory in cooler with ice packs at the day of sampling.

### C. difficile isolation and identification

About 5 g of each sample was cultured in 25 mL of *C. difficile* moxalactam norfloxacin (CDMN) (Oxoid SR0048) and fortified with *C. difficile* selective supplement (Oxoid, SR0173) including 500 mg cysteine hydrochloride, 12 mg norfloxacin and 35 mg moxalactam per liter. The samples were incubated anaerobically for 7 days at 37 °C. Subsequently, 2 mL of enriched culture were

added to 2 mL of 98% ethanol (Merck, Germany) and kept for 2 h at room temperature. The tubes were centrifuged for 10 min at 10000 rpm. The sediment was streaked onto CDMN agar and then incubated under anaerobic conditions at 37 °C for 24-48 h. All *C. difficile* isolates were confirmed by morphology and L-proline- aminopeptidase test (prodisk, hardy diagnostics, Santa Maria, USA). Positive strains were recultured on blood agar and incubated at 37 °C for 36 h in anaerobic conditions (12).

### DNA extraction

*C. difficile* isolates were sub-cultured on the CDMN broth and further incubated for 7 days at 37 °C. In addition, genomic DNA was extracted from bacterial colonies using the DNA extraction kit (Fermentas, Germany), according to the manufacturer's instructions (13-17). Furthermore, the purity (A260/A280) and concentration of the extracted DNA were checked (NanoDrop, Thermo Scientific, Waltham, MA, USA) (18-22). The truth of the DNA was assessed on a 2% agarose gel stained with ethidium bromide (0.5 µg/mL) (Thermo Fisher Scientific, St. Leon-Rot, Germany) (23-25).

### Detection of toxigenic genes

Table 1 shows the PCR conditions used for detection of toxigenic genes (26). A programmable DNA thermal cycler (Eppendorf Mastercycler 5330, Eppendorf-Nethel-Hinz GmbH, Hamburg, Germany) was used for all PCR reactions. Next, 10 µL of the PCR product was exposed to electrophoresis in a 2% agarose gel in a 1X TBE buffer at 80 V for 30 min, which was stained with SYBR Green (27-30). Besides, the UVI doc gel documentation system (Grade GB004, Jencons PLC, London, UK) was utilized for the analysis of images (31-33).

Table 1  
PCR conditions used for detection of toxigenic genes (26)

Target genes	Primer sequence (5'-3')	Product size (bp)	Thermal procedure	Volumes (50 µl)
<i>tcdA</i>	GCATGATAAGGCAACTT CAGTGGTA AGTTCCTCCTGCTCCATC AAATG	629	1 cycle: 94 °C ----- 10 min.	5 µL PCR buffer 10X
<i>tcdB</i>	CCAAARTGGAGTGTTAC AAACAGGTG GCATTCTCCATTCTCAG CAAAGTA	410	35 cycles: 94 °C ----- 50 s 54 °C ----- 40 s 72 °C ----- 50 s	2 mM MgCl <sub>2</sub> 150 µM dNTP 0.75 µM of each primers F & R 1.5 U Taq DNA polymerase 3 µL DNA template
<i>cdtA</i>	GGGAAGCACTATATTTAA GCAGAAGC CTGGGTTAGGATTATTTA CTGGACCA	221	1 cycle: 72 °C ----- 3 min	

### Ribotyping of *C. difficile* isolates

For PCR ribotyping was done according to using two pairs of primers including 3'-GTGCGGCTGGATCACCTCCT-5' (16S *rRNA*) and 3'-CCCTGCACCCTTAATAACTTGACC-5' (23S *rRNA*) (34). The ribotype pattern was obtained by electrophoresis on 3% agarose gel at 80 v for 6 h and stained with ethidium bromide and then compared with ribotype patterns 027 and 078 recorded in reference laboratories.

### Statistical analysis

Statistical analysis was performed using SPSS Statistics 21.0 (SPSS Inc., Chicago, IL, USA). Besides, chi-square and Fisher's exact two-tailed tests were employed to assess any significant relationships between the data obtained from the present study (35, 36). P-value < 0.05 was considered statistically significant as well.

### Results

#### *C. difficile* prevalence

Table 2 shows the prevalence of *C. difficile* strains isolated from raw meat samples. Fifteen out of 250 (6%) raw meat samples were contaminated with *C. difficile*. Prevalence of *C. difficile* strains amongst the raw bovine and ovine meat samples were 8% and 4%, respectively. Statistically significant differences were found between types of samples and *C. difficile* prevalence ( $P < 0.05$ ).

Table 2  
Prevalence of *C. difficile* strains isolated from raw meat samples

Type of meat samples	N. collected	N. positive for <i>C. difficile</i> (%)
Bovine	125	10 (8)
Ovine	125	5 (4)
Total	250	15 (6)

#### *C. difficile* toxigenic genes

Table 3 shows the prevalence of toxigenic genes amongst the *C. difficile* strains isolated from raw meat samples. The most commonly detected toxigenic genes were *tcdA* (33.33%) and *cdtA* (20%). Distribution of *tcdB* was 13.33%. Amongst the combined toxigenic genes, *tcdA+cdtA* had the highest distribution (13.33%). Statistically significant differences were found between types of samples and distribution of *C. difficile* toxigenic genes ( $P < 0.05$ ).

Table 3  
Prevalence of toxigenic genes amongst the *C. difficile* strains isolated from raw meat samples

Type of meat samples	N. positive	Distribution of toxigenic genes (%)					
		<i>tcdA</i>	<i>tcdB</i>	<i>cdtA</i>	<i>tcdA+tcdB</i>	<i>tcdA+cdtA</i>	<i>tcdB+cdtA</i>
Bovine	10	4 (40)	2 (20)	2 (20)	1 (10)	2 (20)	1 (10)
Ovine	5	1 (20)	-	1 (20)	-	-	-
Total	15	5 (33.33)	2 (13.33)	3 (20)	1 (6.66)	2 (13.33)	1 (6.66)

### C. difficile ribotyping

Figure 1 shows the 027 and 078 ribotypes distribution amongst the *C. difficile* strains isolated from raw meat samples. Among isolates of bovine meat samples, 027 ribotype was the most prevalent (40%). Among isolates of raw ovine meat samples, both 027 and 078 ribotypes had equal prevalence (20%).



Figure 1. 027 and 078 ribotypes distribution amongst the *C. difficile* strains isolated from raw meat samples.

### Discussion

Medical sciences have been developed in recent years (37-48). However, infections remain a big issue. In this regard, *C. difficile* is considered prevalent cause of gastrointestinal infections (1, 2). In the present survey, 6% of raw bovine and ovine meat samples were contaminated with *C. difficile* strains. Probable reasons for the prevalence of *C. difficile* strains in examined meat samples are meat contamination through hand manipulation by meat inspectors in slaughterhouses and also butchers. Additionally, transmission of *C. difficile* strains through the contaminated environment of the slaughterhouses should be considered. A relatively high incidence of *C. difficile* contamination was observed

in the United States, where 42% of different retailed meat products and raw meats were found to be contaminated with *C. difficile* (49). Another study in the United States showed 8% *C. difficile* prevalence in ground meat samples (50). *C. difficile* has also been detected in experiments run in Canada with an incidence of 20% meat samples analyzed by Rodriguez-Palacios et al. (51).

Previous survey showed a collection of 12 ribotypes from *C. difficile* isolates in meat samples through PCR-ribotyping. Overall, eight (67%) of the 12 isolates hadn't previously been identified and designated as belonging to the ribotype M31. The other identified ribotypes were 014, 077 and M26 (51). Furthermore, these authors cited the genetic diversity of *C. difficile* in retail raw meat in another study, including ribotypes 014, 077, M26, C, F, H, K and J (52). In contrast, some different studies showed a link between the presence of similar ribotypes in meat samples and clinical ones. For example, ribotype 012, 027, 078 identified in meat samples in Iran, USA and Europe (53-56).

Toxigenic genes had the high distribution among isolates. We found the distribution of *tcdA*, *tcdB* and *cdtA* as 33.33%, 13.33%, and 20%, respectively. Razmyar et al. (2017) (57) reported that out of 65 packed chicken samples, 10 (15.30%) samples were positive for *C. difficile* and 7 (10.70%) samples were *tcdA* and *tcdB* positive, one sample had only shown harboring *tcdA*, and two (3%) of them were binary toxin positive. Muratoglu et al. (2020) (58) stated that the distribution of *tcdA*, *tcdB*, and *cdtA* toxigenic genes amongst the *C. difficile* strains isolated from meat products samples were 100%, 100%, and 86.40%, respectively, which was much higher than our findings. The impact of veterinary and food hygiene in medical sciences has been determined before (59-67).

## Conclusion

As shown, toxigenic *C. difficile* strains were isolated from raw meat samples of ovine and bovine species. This study may show the role of raw meat samples of animal species in transmission of toxigenic *C. difficile* strains, particularly 027 and 078 ribotypes. As these two ribotypes are mainly associated with severe gastrointestinal diseases, the consumption of raw meat samples contained these ribotypes may cause several foodborne infections. However, supplementary studies should be done to assess the main risk of these ribotypes in the *C. difficile* strains isolated from raw meat samples.

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