Prevalence and Characterization of Shiga Toxin-Producing Escherichia coli Isolated from Slaughtered Qurban Animal in Jakarta Province

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ABSTRACT

This study was conducted to investigate the presence of shiga toxin producing Escherichia coli (STEC) and the possibility of carrying rfbE gene and H7 flagellar on meat, liver, and stool samples collected from Jakarta Province of Indonesia. A total of 51 samples collected from meat, liver, and stool of slaughtered cattle from qurban festival were tested using conventional culture and multiplex PCR methods. STEC non O157 were detected in meat (5.3%) and stool (8.3%) with one isolate from stool carried H7 flagellar. However, all isolates were lacking of rfbE gene. In antimicrobial susceptibility tests, the STEC isolates showed antibiotic resistance to erythromycin and oxacillin. Overall, the result shows that meat and liver of this origin activity represents a potential risk to human health.

Key words: STEC, multiplex PCR, meat, feces, antimicrobial

INTRODUCTION

Shiga toxin-producing Escherichia coli (STEC) are major food-borne pathogens, which are well known of producing Shiga toxin type 1 (Stx1), type 2 (Stx2), or both, encoded by the genes of stx1 and stx2, respectively (Sharma, 2006; Torres et al., 2006). The Stxs are AB5 toxins that inhibit protein synthesis in the host cell. This process may lead to an apoptotic cell death, especially to a damage of renal glomerular endothelial cells (Melton-Celsa et al., 2012; Xicohtencatl-cortes et al., 2007). Stx2 is the toxin type most related to hemolytic uremic syndrome (HUS). Hemolytic uremic syndrome is characterized by acute renal failure, thrombocytopenia, and microangiopathic hemolytic anemia and is a poten-

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the slaughter process. Therefore, at present no information is available about pathogenic bacteria, especially STEC contamination in Qurban festival. Cattle are the main reservoir of STEC, where the organism typically colonizes the lower gastrointestinal tract and shed the bacteria through their feces (Inat & Siriken, 2010; Perera et al., 2015). Also, cattle has a significant proportion of beef become contaminated during slaughter (Kundu et al., 2014). In Indonesia, satay is a popular undercooked meat and will become a problem when the meat is contaminated by STEC. It is suggested that meat may be an important transmission vehicle for this food-borne pathogen. Previous study (Selim et al., 2013) also indicated that an increasing number of strains are showing a multiresistance to a number of antibiotics. To address this, the present study was designed to investigate the presence of STEC in the meat, liver and bovine stools sample in Qurban festival in Jakarta Province of Indonesia by considering the possibility of STEC O157:H7 presence. The above isolates were additionally studied for virulence characteristics and antimicrobial susceptibility.

**MATERIALS AND METHODS**

**Bacterial Strains**

This study used 2 E. coli O157:H7 strains as control. Both strains, producing Stx1 and Stx2 were obtained from American Type Culture Collection (ATCC) 35150 and Bogor Agricultural University (BAU), respectively.

**Study Design for Purposive Sampling**

Purposive sampling was chosen in this study. A total of 51 samples including 19 meat, 20 liver and 12 fecal samples were collected from five different mosques in Jakarta in October 2014. The geographical distribution of the five mosques is depicted in Figure 1. At each mosque, all cattle were selected. It was made to ensure that fecal, liver, and meat samples were from exactly the same animals. The investigations on this study are minor influenced by the sampling method adopted (Wang et al., 1996).

**Sampling and Bacterial Culture Methods for Feces, Liver and Meat**

The procedure of culture method was based on a previous method with minor modification (Selim et al., 2013). As many as 250 g of meat, liver and fecal samples respectively, were taken into an aseptic plastic bag and placed in an ice box. Upon arrival at the laboratory, the samples were held at 4°C, not longer than 24 h before analysis. About 25 g of each sample was placed aseptically in a stomacher bag with 225 mL phosphate buffered saline (PBS) 0.1% (Oxoid, UK) and mixed for 1 min. Each sample (1 mL) was transferred into 50 mL of brain heart infusion (BHI) broth (Oxoid, UK) for enrichment and incubated at 37°C for 24 h. After the enrichment procedure, one loop of the broth was inoculated onto eosin methylene blue agar (EMB) (Oxoid, UK) for selective and differential procedures. After 24 h incubation at 37°C, up to two purple coloured colonies with green metallic sheen were transferred onto cefixime-tellurite sorbitol MacConkey (CT-SMAC) (Oxoid, UK) agar and incubated at 37°C for 24 h. SMAC agar is recommended for the isolation of pathogenic STEC O157. STEC O157 does not ferment sorbitol and therefore produces colourless colonies. In contrast, most of non STEC O157 ferment sorbitol and form pink colonies. Those identified as STEC O157 in CT-SMAC were subjected for the presence of virulence genes by multiplex PCR.

**Characterization of STEC**

The E. coli strains isolated in this study and the STEC O157 reference were cultured on 7% sheep blood agar (Oxoid, UK) for cultivation. After overnight culture, colonies from each plate were inoculated into BHI, and the broth was incubated at 37°C for 24 h prior to nucleic acid extraction. The broth cultures were centrifuged at 4,500 g for 15 min in a Biofuge pico (Heraweus, Hanau, Germany), the supernatant was discarded, the pellet was washed three times with 10 mL of phosphate buffered saline (PBS; pH 7.4). The cell pellet was resuspended in 200 µL of PBS. Total purified genomic bacterial DNA was extracted with a genomic DNA mini kit (QiAgen, DNeasy®, USA) according to manufacturer’s instruction. All the extracted DNA of the standard strains and of the sample isolates were examined using multiplex PCR for molecular typing of the virulence genes (rfbE, stx1, stx2, fliC) using specific nucleotide primers are listed in Table 1 (Hu et al., 1999). Amplification condition was carried out according to Inat and Siriken (2010) with a modification. The reaction mixture consisted of 4.8 µL of aquadest (DNAse, RNAse free), 10 µL of Maxima hot start green PCR master mix (2x) (Thermo Scientific™), and 0.4 µL of each primer.

![Geographical distribution of mosques A-E in Jakarta from which the samples were collected. Total number of samples= 51.](image-url)
Temperature conditions consisted of an initial 95°C denaturation step for 4 min followed by 35 cycles of 95°C for 30 s, 50°C for 30 s, and 72°C for 1 min. The final cycle was followed by 1 cycle at 72°C for 5 min in the thermal cycling system. Agarose gel electrophoresis was carried out according to Sanam (2015) with minor modification to evaluate the amplified fragments using standard PCR markers.

Antibiotic Susceptibility

It was determined by the standardized agar diffusion test on MüllerHinton agar (MHA, Difco, USA) using the following disks (Oxoid, UK): erythromycin (15 µg), cefepime (30 µg), oxacillin (30 µg), azithromycin (15 µg) and tetracyclines (30 µg). Isolates were categorized as susceptible, intermediate and resistant based upon interpretative criteria developed by the guideline of Clinical and Laboratory Standards Institute (CLSI, 2014).

RESULTS

Characterization of STEC Isolates by Multiplex PCR for stx1, stx2, rfbE and Flagellar H7 Gene

As shown in Table 2, two isolates (isolate number 11 and 14) were confirmed as STEC because they all carried stx genes. The isolates (n= 30) were also applied to a multiplex PCR assay to confirm the presence of flagellar gene. In flagellar H7 PCR assay, 1 isolate (isolate number 11) was found harboring H7 genes (Table 2). However, all isolates are lacking the rfbE gene (Table 2).

Antibiotic Resistance

The antibiotic resistance profiles of the STEC isolates against 5 antimicrobial agents are presented in Table 3, respectively. The results indicated that E. coli and STEC isolated from qurban festival in Jakarta were resistant to erythromycin (100%) and oxacillin (100%) (Figure 2). Resistance to cefepime, azithromycin, and tetracycline was rare.

DISCUSSION

In this study, 2 of STEC were detected in meat and feces samples as shown in Table 2. Meat sample (5.3%) and feces sample (8.3%) showed stx1 gene and stx2 gene in multiplex PCR (Figure 3), respectively. No STEC was detected in the liver samples. Ruminants are considered as an important source of STEC and cattle were identified as the primary reservoir of STEC (Akanbi et al., 2011). Intestinal carriages of STEC in ruminants cause fecal shedding and the release of STEC into the environment (Forano et al., 2013).

The non-O157 populations of E. coli have been shown to vary in their distribution among bovine and clinical sources (Borgatta et al., 2012). In the study, all isolates were lacking rfbE gene, which is well known as characteristic of O157 strains. On the other hand, gene flic, a characteristic of H7 strain was detected. From 51 isolates, 1 (8.3%) isolate was confirmed the presence of flic genes i.e isolates no. 11 in feces sample. The pathogenic potential of STEC isolates has also been shown to be associated with the presence of Stx genotypes (Rahal

Table 1. Primer sequences used in the multiplex PCR assay and the expected sizes of the products

| Target gene | Size (bp) | Primer | Sequence |
|-------------|-----------|--------|----------|
| rfbE        | 292       | RfbF   | 5'-GTGTCATTTTACCGACATCCATG-3' |
|             |           | RfbR   | 5'-CCTATAACGTGCAATTGACCCG-3' |
| flIC        | 625       | FLICh7-F | 5'-GCCGTGCTGAGTCTATCGAGC-3' |
|             |           | FLICh7-R | 5'-CAACGTCGATCTCGCCATTCGC-3' |
| stx1        | 210       | SLT-IF  | 5'-TGTAACGTGAAAGGTAAGTATAAC-3' |
|             |           | SLT-IR  | 5'-GCTAATGCTAGTAAACAAGAATAAC-3' |
| stx2        | 484       | SLT-IIF | 5'-GTTTGTCGATATTGCTATGGAG-3' |
|             |           | SLT-III  | 5'-GATGATCTTGGAATGATGGG-3' |

Table 2. Results of multiplex PCR

| Samples     | rfbE gene n (%) | fliC gene n (%) | stx1 gene n (%) | stx2 gene n (%) |
|-------------|-----------------|-----------------|-----------------|-----------------|
| Meat (n=19) | 0 (0)           | 0 (0)           | 1 (5.3)         | 0 (0)           |
| Liver (n=20)| 0 (0)           | 0 (0)           | 0 (0)           | 0 (0)           |
| Feces (n=12)| 0 (0)           | 1 (8.3)         | 0 (0)           | 1 (8.3)         |
| Total       | 0 (0)           | 1 (8.3)         | 1 (5.3)         | 1 (8.3)         |

Table 3. Antibiotic resistance profiles of the STEC non O157

| Isolate number | Antimicrobial agent | Diameter of killing zone (mm) | Interpretative criteria |
|----------------|---------------------|-------------------------------|-------------------------|
| 11             | Erythromycin        | 0                             | R                       |
|                | Cefepime            | 23                            | S                       |
|                | Oxacillin           | 0                             | R                       |
|                | Azithromycin        | 23                            | S                       |
|                | Tetracycline        | 24                            | S                       |
| 14             | Erythromycin        | 0                             | R                       |
|                | Cefepime            | 24                            | S                       |
|                | Oxacillin           | 0                             | R                       |
|                | Azithromycin        | 21                            | S                       |
|                | Tetracycline        | 18                            | S                       |

Note: R (Resistant), S (Susceptible)
In this study, one STEC isolate produced Stx2 i.e isolate no. 11 in feces sample. Stx2 are known to be more toxic and are more often associated with HC or HUS in human infections than Stx1 (Etienne-Mesmin et al., 2011; Lim et al., 2010; Melton-Celsa et al., 2012). One isolate obtained from meat of an animal investigated in the present study was positive for Stx1. In this study, STEC O:H7 isolate carried Stx2 indicating the high pathogenic potential for human. Previous study (Koitabashi et al., 2006) also suggested that Stx2 positive E. coli seem to be widely distributed in the Asian environment. This finding implies that humans were now exposed to STEC non-O157 from food of animal origin. Despite STEC non-O157 have lower virulence, this strain may be capable of causing disease when a high inoculum is ingested or in particularly susceptible individuals.

According to Gould et al., (2013); Luna-Gierke et al. (2014), the number of reported STEC non-O157 infections increased in the United States recently. In Indonesia, the case reports are not well established. However, nephrotic syndrome is one of the most frequent glomerular diseases seen in children. Approximately, there are six case of NS per year for every 100,000 child aged less than 14 years old in Indonesia (Mamesah et al., 2016). Interestingly, the etiology is unknown.

In this study, the antibiotic resistance profiles of two STEC isolates against 5 antimicrobial agents are presented in Table 3. These findings showed the STEC isolates were 100% of resistance to erythromycin and oxacillin. Meanwhile, previous study found E. coli pathogen were resistant to streptomycin, chloramphenicol, sulfamethoxazole and gentamicin (Nugraha et al., 2013). Currently, the treatment of STEC infections with antibiotics is controversial (Pacheco & Sperandio 2012). However, many clinicians still used antimicrobial therapy as an option for the treatment of STEC infection. Thus, the use of oxacillin and erythromycin both in human and animals may select for resistance among STEC. The presest study provides initial data for the presence of STEC non-O157 in Qurban festival in Jakarta. These findings might help to lessen the risk of transmission of STEC non-O157 in public health.

Figure 2. The killing zone performed by STEC non-O157 (left; isolate number 11) (right; isolate number 14)

Figure 3. The determination of rfbE (O157), stx1, stx2, fliC (H7) genes of E. coli by multiplex PCR. Lane M: Marker (100~3,000 bp), Lane K1: positive control (E. coli O157:H7 35150), Lane K2: positive control (E. coli 1-AN), Lanes 1 to 31: samples isolated from qurban animal origin.
CONCLUSION

STEC non-O157 was detected in feces (8.3%) and meat (5.3%) both isolated from cattle slaughtered in Qurban festival. However, no STEC were found in the liver. In antimicrobial susceptibility tests, the STEC isolates showed antibiotic resistance to erythromycin and oxacillin. The result showed that meat and feces of this origin represent a potential risk to human health.

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