Estimation of potential bacteriological hazards and their genetic virulence determinants in beef meals provided to intensive care patients


Department of Bacteriology, Immunology and Mycology, Faculty of Veterinary Medicine, Suez Canal University, Egypt

Department of Food Hygiene, Faculty of Veterinary Medicine, Suez Canal University, Egypt

Department of Biology, College of Science, University of Jeddah, Saudi Arabia

Department of Food Hygiene, Faculty of Veterinary Medicine, New Valley University, Egypt

Article history:
Received: 19 July 2021
Received in revised form: 12 August 2021
Accepted: 15 August 2021
Available Online: 8 April 2022

Abstract

Meat is a good source of protein which makes it a good substrate for microbial growth. In this study, the prevalence, antibiogram and virulence genes of some foodborne pathogens from hospital beef meals provided to intensive care patients were evaluated. Therefore, a total of 60 beef meat samples (30 raws and 30 cooked samples) were randomly collected from different hospital kitchens in Ismailia province, Egypt. Samples were subjected to bacteriological evaluation for Staphylococcus aureus, Escherichia coli and Salmonella. The obtained results revealed that S. aureus, E. coli and Salmonella were isolated by a prevalence of 38.3% (23/60), 16.6% (10/60), and 8.3% (5/60), respectively. S. aureus was highly resistant to penicillin and streptomycin. Escherichia coli was highly resistant to amoxicillin, streptomycin, ciprofloxacin, gentamicin and ampicillin. Salmonella was highly resistant to amoxicillin, penicillin and cefpodoxime, ampicillin, gentamicin, ciprofloxacin and streptomycin. Staphylococcus aureus harboured sea, seb, sec and sed enterotoxin genes with a prevalence of 13.04%, 4.34%, 13.04 % and 4.34%, respectively. Escherichia coli isolates harboured stx1 and stx2 with a prevalence of 83.33% and 66.66%, respectively. Escherichia coli was serotyped as O128, O142, O26 and O157. Salmonella harboured invA and hilA genes by 100% and 80%, respectively. In conclusion, the application of good manufacturing practices with well-trained food handlers is necessary to control and prevent contamination of hospitable meals by foodborne bacteria in order to protect and save intensive care patients.

1. Introduction

Meat is an important source of protein, essential amino acids, B complex vitamins and minerals. Therefore, it offers a highly favourable environment for the growth of pathogenic bacteria. The importance of food safety for hospitalized patients and the detrimental effect that contaminated food could have on their recovery have been emphasized (Hassan et al., 2015).

In hospitals, outbreaks of foodborne infections are preventable but encouraged by many factors, including personnel carriers, poor kitchen hygiene conditions, carelessness, and lack of food handler training. In hospitals, the risk of tainted food is that such food is provided to customers in poor health (Teffo and Frederick, 2020; Young et al. 2020). This risk varies according to numerous parameters such as the microorganism’s nature, the contamination level, the food nature and especially the consumer’s physiological state. Therefore, the causes of foodborne illness and/or collective food poisoning may be microbiological food contamination by infected raw materials, insufficient cooking temperatures, improper preservation, contaminated facilities, cross-contamination and poor personal hygiene (Ndraha et al., 2018).

Foodborne illness occurs when a pathogen is ingested with food and establishes itself in the human host, or when a toxigenic pathogen establishes itself in a food product and produces a toxin, which is then ingested by the human host. Thus, foodborne illness is generally classified into foodborne infection and foodborne intoxication. Foodborne pathogens are biological agents that can cause a foodborne illness event. A foodborne disease outbreak is defined as the
occurrence of two or more cases of a similar illness resulting from the ingestion of a common food (CDC, 2012)

The most important bacterial pathogens in beef meat that are responsible for foodborne infections include *Escherichia coli*, *Salmonella* and coagulase-positive *Staphylococcus aureus* (Abdaslam et al., 2014). *E. coli* is mostly non-virulent, but pathogenic variants of *E. coli* (pathovars or pathotypes) cause much morbidity and mortality worldwide; many of these pathotypes are a major public health concern and are transmitted through ubiquitous mediums, including food and water (Croxon et al., 2013).

Transmission of *E. coli* occurs when food or water that is contaminated with faeces of infected humans or animals is consumed. Contamination of animal products often occurs during the slaughter and processing of animals (Garcia et al., 2010). *Salmonella* is one of the most widely implicated microorganisms in food-borne disease outbreaks. The most common causes of *Salmonella* food poisoning are meat products. Furthermore, *S. aureus* is one of the most causative agents of foodborne disease outbreaks causing gastroenteritis and is rarely acquired directly from raw meat but mostly occurs due to either excessive handling or contamination during or after cooking of meat and meat products (Addis and Sisay, 2015; Bou-Mitri et al., 2018; De Freitas et al. 2019).

The presence of *S. aureus* in food may be considered a public health hazard because of its ability to produce enterotoxin and the risk of subsequent food poisoning. Although there are nine identified staphylococcal enterotoxins, designated as A, B, C1, C2, C3, D, E, F, and G, types A and D are responsible for the majority of the outbreaks (Mossel et al., 1995).

Therefore, the present study was performed to analyze sanitary-hygienic conditions and evaluate the microbiological status of hospital beef meals and investigate the prevalence of foodborne bacteria in hospital meat meals, perform antimicrobial susceptibility testing of bacterial isolates and detection of some virulence genes of the isolated foodborne pathogens.

2. Materials and methods

2.1 Sample collection

A total of 60 random raw and cooked beef meat samples (30 each) were randomly collected from different hospital kitchens in Ismailia province from September 2020 to March 2021 for bacteriological evaluation. All samples were prepared according to techniques recommended by APHA (2001).

2.2. Isolation and identification of *Staphylococcus aureus*, *Escherichia coli* and *Salmonella*

For isolation of *S. aureus*, a loopful from meat samples mixed with buffered peptone water was streaked on Baird-Parker agar media (Bioline, Italy) and incubated at 37°C for 24-48 hrs. The suspected *S. aureus* colonies were identified according to their colonial characters, hemolytic activity on blood agar, microscopical examination using Gram staining, biochemical reactions (catalase, coagulase, mannitol fermentation, oxidation fermentation and Voges–Proskauer test) as described by Cowan and Steel (1974).

For isolation of *E. coli*, a loopful from meat samples mixed with buffered peptone water was streaked on MacConkey’s agar (Oxoid, Hampshire, UK) and eosin methylene blue (EMB) agar (Oxoid, Hampshire, UK) then incubated at 37°C for 24 hrs. The suspected colonies were identified according to colonial characters, microscopical examination by Gram’s staining, motility test, hemolytic activity on blood agar, and biochemical reactions (oxidase, catalase, indole, lactose fermentation, methyl-red, citrate-utilization, H2S, Voges-Proskauer, and urease tests) as described by Quinn et al. (2019).

For isolation of *Salmonella*, pre-enrichment of samples was done using Rapport–Vassiliadis broth (Oxoid, Hampshire, UK) then cultivation at 37°C for 18-24 hrs then selective cultivation from pre-enriched broth on Salmonella–Shigella (SS) agar (Oxoid, Hampshire, UK) and xylose lysine deoxycholate (XLD) agar (Oxoid, Hampshire, UK) then incubation at 37°C for 18-24 hrs. The suspected colonies were identified according to colonial characters, microscopical examination by Gram staining and biochemical reactions (oxidase test, catalase test, indole, methyl-red, citrate-utilization, H2S, urease and Voges-Proskauer).

2.3 Serotyping of *Escherichia coli* and *Salmonella*

*Escherichia coli* isolates were serotyped by slide agglutination test for detection of somatic (O) antigen with the aid of standard polyvalent and monovalent commercial *E. coli* antisera (Denka Seiken Co., Ltd., Tokyo, Japan) as described by Starr (1986). *Salmonella* isolates were serotyped according to Kauffman – White scheme Kauffman (1974) for the determination of Somatic (O) and flagellar (H) antigens using *Salmonella* antiserum.

2.4 Antimicrobial susceptibility of *Staphylococcus aureus*, *Escherichia coli* and *Salmonella*

Isolates were tested against 12 antibacterial agents (Oxoid Hampshire, UK) including amoxicillin/clavulanic acid, amoxicillin, cefpodoxime, ampicillin,
ciprofloxacin, erythromycin, gentamicin, flumequine, cefotaxime, cefradine, enrofloxacin and streptomycin. Antibiogram was performed using Kirby Bauer disk diffusion method on Muller Hinton agar (Oxoid Hampshire, UK) as described before by Bauer et al. (1996). Briefly, 4-5 colonies from re-enriched preserved identified isolates, were inoculated in 5 mL Muller Hinton broth (Oxoid Hampshire, UK) and incubated for 4-5 hrs until turbidity was observed. The inoculated broth was then adjusted to a density equivalent to 0.5 MacFarlane standards. Sterile swabs were used to streak the bacterial suspension in different directions to wet the entire surface of labelled Muller Hinton agar plates and left for 30 mins. Antibiotic discs were then applied on the surface of the streaked plates using sterile forceps and the antibiotic dispenser. After overnight incubation, the inhibition zone was measured for each antibiotic using a calibre. The size of the inhibition zone was interpreted according to the prescribed guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2015).

2.5 Molecular detection of some virulence genes in Staphylococcus aureus, Escherichia coli and Salmonella isolates

PCR was used for detection of sea, seb, sec and sed enterotoxin genes of S. aureus additionally detection of stx1 and stx2 of E. coli and detection of invA and hilA genes of Salmonella according to the previously published protocols (Table 1). QIAamp DNA Mini kit (Qiagen, GmbH, Germany/Catalogue No.51304) was used for DNA extraction according to the manufacturer’s recommendations. DNA amplification of S. aureus was performed in a thermal cycler using the following conditions: initial denaturation for 5 mins at 94°C followed by 30 cycles of denaturation (94°C for 2 mins), annealing (50°C for 1 min), and extension (72°C for 1 min). A final extension step (72°C for 5 mins) was performed after the completion of the cycles. DNA amplification of E. coli virulence genes, stx1 and stx2 were detected by the following program, initial denaturation (3 mins at 94°C), followed by 35 cycles of denaturation (1 min at 94°C), annealing (1 min at 55°C) and extension (1 min at 72°C), as well as a final extension at 72°C for 7 mins. Concerning DNA amplification of Salmonella as the following conditions, initial denaturation at 94°C for 60 s, followed by 35 cycles of denaturation at 94°C for 60 s, annealing at 64°C for 30 s and extension at 72°C for 30 s, followed by a final extension at 72°C for 7 mins. The reaction volume (25 μL) consisted of 6 μL of genomic DNA, 12.5 μL of 2x Master Mix and 20 pmol of each primer (Biobasic, Canada), and the final volume was completed to 25 μL by DNase RNase free water. Positive controls and negative controls (DNase free water) were included in all reactions.

3. Results and discussion

3.1 Prevalence of foodborne pathogens in hospital beef meals

Isolates were identified as S. aureus based on their morphology and biochemical characteristics. Microscopically, the bacteria appeared as Gram-positive small size, non-motile and non-sporulated cocci arranged in grape-like clusters. On Baired-Parker agar suspected S. aureus colonies appeared as dark grey to black colonies surrounded by a clear zone. On blood agar, the colonies were hemolytic. S. aureus was identified on the basis of coagulase test, catalase test, indole production, methyl red test, Voges-proskauer reaction, urease production, citrate utilization and sugar fermentation.

<table>
<thead>
<tr>
<th>Microorganism</th>
<th>Gene</th>
<th>Primer sequence (5’-3’)</th>
<th>Length of amplified product</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. aureus</td>
<td>sea</td>
<td>TTGGAAACGGTTAAAAACGAA GAACTTCCCCATCCAAAAACA</td>
<td>120</td>
<td>Rall et al. (2008)</td>
</tr>
<tr>
<td></td>
<td>seb</td>
<td>TCGCATAAAACGTGAAAAACGC GGGTACTCTATATTGAGCC</td>
<td>478</td>
<td></td>
</tr>
<tr>
<td></td>
<td>sec</td>
<td>GACATAAAAGCTAGGAATT AAATCGGATTTAACATTATCC</td>
<td>257</td>
<td></td>
</tr>
<tr>
<td></td>
<td>sed</td>
<td>CTAGTTTGGATATATCTCTCT TAATGCTATATCTATAGG</td>
<td>317</td>
<td></td>
</tr>
<tr>
<td>E. coli</td>
<td>stx1</td>
<td>ACACCTGGATGATCTCAGTTG CTGAACTCCCTCCCATATG</td>
<td>614</td>
<td>Dipinetto et al. (2006)</td>
</tr>
<tr>
<td></td>
<td>stx2</td>
<td>CCATGCAACGGACACGGACTTT CCGTCATACCAGCAGACCTTGG</td>
<td>779</td>
<td></td>
</tr>
<tr>
<td>Salmonella</td>
<td>invA</td>
<td>GTGAAATATCGCCACCGTGCGGCA TCATCGCCACGTCAAAAAGGAACC</td>
<td>284</td>
<td>Shanmugasamy et al. (2011)</td>
</tr>
<tr>
<td></td>
<td>hilA</td>
<td>CTGCCGCAGTGTATTAAGGATA CTGTCGCCCTTAATCGCATGT</td>
<td>497</td>
<td>Guo et al. (2000)</td>
</tr>
</tbody>
</table>
Isolates were identified as E. coli based on their morphology and biochemical characteristics. Microscopically, the bacteria appeared as Gram-negative moderate size, motile, and non-sporulated rods. On MacConkey’s agar, E. coli gave characteristic pink colonies due to lactose fermentation. On blood agar, the colonies were hemolytic, while on EMB the bacteria gave characteristic metallic sheen colonies. Biochemically, all isolates were positive for catalase, lactose fermentation, indole, and methyl-red tests. Simultaneously, they were negative for cytochrome oxidase, Voges-Proskauer, citrate-utilization, H₂S production, and urease tests.

Salmonella appeared as Gram-negative moderate size, motile, and non-sporulated rods microscopically. On XLD, Salmonella appeared as red colonies with a black centre while on SS agar appeared as colourless colonies with a black centre. Biochemically, all isolates were positive for catalase, methyl-red, citrate-utilization and H₂S production tests. Simultaneously, they were negative for oxidase, indole, Voges-Proskauer and urease tests.

The prevalence of S. aureus, E. coli and Salmonella species in examined beef samples were 38.3% (23/60), 16.6% (10/60), and 8.3% (5/60), respectively, as shown in Table 2. Foodborne diseases persist to be an inclusive public health crisis with an estimated 600 million people falling ill annually (Faour et al., 2015). In 2013, 160 Egyptian students have been recorded ill after consumption of food contaminated with Salmonella (Herriman, 2019).

Staphylococcus aureus was the most prevalent isolate from both raw and cooked beef meals, where it was isolated from raw beef by a percentage of 60% (18/30), while it was isolated from cooked beef by a percentage of 16.6% (5/30). Escherichia coli was isolated from raw beef meals by a percentage of 26.6% (8/30), while it was isolated from cooked beef meals by a percentage of 6.6% (2/30). Salmonella was isolated from raw meat and cooked meat meals by a percentage of 13.3% (4/30) and 3.3% (1/30), respectively as described in Table 2.

According to the obtained results, it could be confirmed that raw meat was the most contaminated with S. aureus than other samples. S. aureus inhabits the human skin and mucous membranes, where they exist mostly as commensal flora. Humans are the natural carriers of S. aureus, and the organism can be found in a healthy human population (Collins et al., 2012).

The hospital feedings, sterile ready-to-use ones are exempted from the potential microbial contamination (Patchell et al., 1998). Clinical consequences of contaminated feedings are abdominal pain, vomiting, diarrhoea, infection, fever, bacteremia, septicemia, and pneumonia (Oliviera et al., 2000; Desport et al., 2004). Since the microbial population receives the limit which causes food poising that is mainly affected by suppressed immune function and is often at high risk of developing and/or progressing malnutrition (Mokhalalati et al., 2004).

The current results agreed with Wu et al. (2018) who isolated S. aureus from meat hospital meals by 35.0%. In addition, Shaltout et al. (2020) isolated E. coli from hospital meat meals by 13.33% and 11.7%, respectively. On the other hand, Jakabi et al. (2002) isolated Salmonella by 9%. The presence of these pathogens in hospital meals may reflect the bad hygienic practices during different stages of food chains from slaughtering, handling, transportation and excessive handling during preparation and serving of the meals.

3.2 Serotyping of Escherichia coli and Salmonella isolates

The results in Table 3 revealed that 10 (16.7%) E. coli isolates (8 from raw beef, 2 from cooked beef) were serologically typed. Where, 4 isolates (3 from raw beef, one from cooked beef) were typed as O128 (40%), 3 isolates were O142 (30%) in raw beef only, and one isolate was O26 (10%) in raw beef only. Finally, 2 isolates (one from raw beef, one from cooked beef) were typed as O157 (20%).

Serotyping is a common way to characterize Shiga toxin-producing Escherichia coli (STEC) strains and is based on the O antigen (somatic antigen) and H antigen (flagellar antigen) (Gyles, 2007). In concern to E. coli serovars, O128, O142, O26 and O157 were the detected serotypes. Similar results were observed by Saad et al. (2018). Detection of different E. coli O-serogroups in

Table 2. Prevalence of different foodborne pathogens from raw (n = 30) and cooked (n = 30) beef meals

<table>
<thead>
<tr>
<th>Bacterial isolates</th>
<th>No. of positive samples</th>
<th>Percentage (%)</th>
<th>Beef meals (n = 60)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Raw (n = 30)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>No. of positive samples</td>
</tr>
<tr>
<td>S. aureus</td>
<td>23</td>
<td>38.30%</td>
<td>18</td>
</tr>
<tr>
<td>E. coli</td>
<td>10</td>
<td>16.60%</td>
<td>8</td>
</tr>
<tr>
<td>Salmonella</td>
<td>5</td>
<td>8.30%</td>
<td>4</td>
</tr>
</tbody>
</table>
food are an indication of great public health hazards. Beef serves as a potential vehicle for transmitting _E. coli_ O157:H7. The importance of proper handling and cooking of beef is probably as important in preventing _E. coli_ O157:H7 infections. These include the application of Good Agricultural Practice (GAP) and Good Manufacturing Practice (GMP), followed by the implantation of the Hazard Analysis of Critical Control Points (HACCP) system at all food chains serving hospitable meals (Hiko et al., 2008).

Table 3. Prevalence of _E. coli_ serotypes (n = 10) in hospital beef meals

<table>
<thead>
<tr>
<th><em>E. coli</em> strains</th>
<th>Beef meals</th>
<th>Strain Characteristic</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Raw no. (%)</td>
<td>Cooked no. (%)</td>
</tr>
<tr>
<td>O128</td>
<td>3 (30)</td>
<td>1 (10)</td>
</tr>
<tr>
<td>O142</td>
<td>3 (30)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>O26</td>
<td>1 (10)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>O157</td>
<td>1 (10)</td>
<td>1 (10)</td>
</tr>
<tr>
<td>Total</td>
<td>8 (80)</td>
<td>2 (20)</td>
</tr>
</tbody>
</table>

ETEC: Enterotoxigenic _E. coli_, EPEC: Enteropathogenic _E. coli_, EHEC: Enterohemorrhagic _E. coli_

The results in Table 4 revealed that five isolates of _Salmonella_ were serologically identified as follows, _Salmonella enterica_ serovar Typhimurium by 40% (2/5) in raw beef meals. While _Salmonella enterica_ serovar Enteritidis by 20% (1/5) in raw beef meals and 20% (1/5) in cooked beef meals. _Salmonella enterica_ serovar Infantis by 20% (1/5) in raw beef meals. The obtained results came in to agree with those obtained by Saad et al. (2018) who detected _S. enterica_ ser. _Typhimurium_ and _S. enterica_ ser. _Enteritidis_ in beef and hamburger.

_Salmonella enterica_ serovar Infantis was confirmed as the cause of human salmonellosis in several countries and is the third most frequently isolated serovar of _Salmonella_ after _S. enterica_ ser. _Enteritidis_ and _S. enterica_ ser. _Typhimurium_ (Ishihara et al., 2009). _Salmonella enterica_ ser. _Typhimurium_ was not detected in cooked beef samples, this is attributed to many stress factors which injured these bacteria, such as heat, which inhibits the repair mechanisms (Varnum and Evans, 1991).

Table 4. Prevalence of _Salmonella_ serotypes (n = 5) in hospital beef meals

<table>
<thead>
<tr>
<th>Identified Group</th>
<th>Antigenic structure</th>
<th>Beef meals</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>S. enterica</em> ser. Typhimurium</td>
<td>B 1,4,5,12 i : 1.2</td>
<td>Raw: 2 (40%) Cooked: 0 (00.0)</td>
</tr>
<tr>
<td><em>S. enterica</em> ser. Enteritidis</td>
<td>D1 1,9,12 g,m</td>
<td>1 (20%)</td>
</tr>
<tr>
<td><em>S. enterica</em> ser. Infantis</td>
<td>C1 6,7 r : 1.5</td>
<td>1 (20%)</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>4 (80%)</td>
</tr>
</tbody>
</table>

O: Somatic antigen, H: Flagellar antigen

3.3 Antimicrobial resistance of the isolated pathogens

The results of antimicrobial susceptibility testing of isolated pathogens are shown in Table 5. The antimicrobial susceptibility testing of _S. aureus_ (n = 23) from raw and cooked beef meals were as follows: antibiotics of choice against _S. aureus_ were gentamicin and ciprofloxacin at 60.9%, followed by amoxycillin at 56.5%, enrofloxacin at 52.2%, cefotaxime and cefpodoxime at 43.5%, erythromycin and ampicillin at 21.7%, flumequine at 13.1% and cephadine at 8.7%. While _S. aureus_ was highly resistant to penicillin, chloramphenicol (100% for each) was followed by streptomycin (78.3%). _S. aureus_ was resistant to penicillin and streptomycin this nearly agreed with those detected by Akanbi et al. (2017).

The results of antimicrobial susceptibility testing of _E. coli_ (n = 10) from raw and cooked beef meals were as follows; antibiotics of choice against _E. coli_ were cefpodoxime 80% and cefotaxime 70%, while, _E. coli_ was highly resistant to the following antibiotics, amoxycillin (100%), streptomycin and ciprofloxacin (80% for each) and ampicillin (60%). _Escherichia coli_ was highly resistant to amoxycillin, streptomycin, ciprofloxacin, gentamicin and ampicillin, this was in agreement with Kibret and Abera (2011).

The findings of antimicrobial susceptibility testing of _Salmonella_ isolates (n = 4) from raw and cooked beef meals were as follows; antibiotics of choice against _Salmonella_ spp. were flumequine and cefotaxime by 75% for each. While _Salmonella_ spp. were highly resistant to the following antibiotics, amoxycillin (100%), streptomycin and ciprofloxacin (80% for each) and ampicillin (60%). _Escherichia coli_ was highly resistant to amoxycillin, streptomycin, ciprofloxacin, gentamicin and ampicillin, this was in agreement with previous studies by Miko et al. (2005).

The careless use of antibiotics in veterinary practice is the main cause of the development of multidrug-resistant bacteria. Moreover, it is important to highlight that the use of any antimicrobial agent should not substitute good hygiene practices and, wherever possible, alternative management methods should be sought and used. In addition, veterinarians should respect and follow the sanitary legislation concerning the use of antimicrobial agents in their country.

3.4 Prevalence of virulence genes of _Staphylococcus aureus_, _Escherichia coli_ and _Salmonella_

PCR proved that the tested _S. aureus_ isolates (n = 23) were harboured the virulence genes (Table 6) _sea, seb, sec_ and _sed_ enterotoxin genes with a prevalence of...
which inhibits the repair mechanisms (Varnum and
stress factors which injured these bacteria, such as heat,
was not detected in cooked beef this is attributed to many
Typhimurium and
S. enterica
producing gastroenteric illness in humans (Chaudhary
Thung
et al.

The current results proved that E. coli isolates (n = 6)
were harbourd the virulence genes stx1 and stx2 with a
prevalence of 83.33% (5/6) and 66.66% (4/6), respectively. Concerning invA
and hilA genes of
Salmonella, the tested isolates (n = 5) were harboured
invA gene by 100% (5/5) while hilA by 80% (4/5).

The present data in Table 6 show that
Salmonella (n = 5) was harbourd invol and hilA genes. These findings were
in accordance with previous data detected by
Thung et al. (2018) and
Salam
et al. (2014). Salmonella
harbouring invol and hilA virulence genes is capable of producing gastroenteric illness in humans (Chaudhary
et al., 2015). On the other hand, Salmonella serotyped as S. enterica ser. Typhimurium, S. enterica ser. Enteritidis and S. enterica ser. Infantis and this was in accordance with
doja and burger. Salmonella enterica ser. Typhimurium was not detected in cooked beef this is attributed to many stress factors which injured these bacteria, such as heat, which inhibits the repair mechanisms (Varnum and
Evans, 1991).

In conclusion, the presence of S. aureus, E. coli and
Salmonella in hospital meat meals presents a great
danger to public health as a result of the ability of these
bacteria to produce foodborne poisoning, especially in
immunosuppressed persons as intensive care patients.
The application of good manufacturing practices with
well-trained food handlers is necessary to control and
prevent contamination of the hospitable meals by
foodborne bacteria in order to protect and save intensive care patients.

Table 6. Prevalence of virulence genes in the isolated
foodborne pathogens

<table>
<thead>
<tr>
<th>Genes</th>
<th>No. (%)</th>
<th>Genes</th>
<th>No. (%)</th>
<th>Genes</th>
<th>No. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>seb</td>
<td>1 (4.34)</td>
<td>stx2</td>
<td>4 (66.67)</td>
<td>hilA</td>
<td>4 (80)</td>
</tr>
<tr>
<td>sed</td>
<td>3 (13.04)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Conflict of interest

The authors declared that the present study was
performed in absence of any conflict of interest.

References

Escherichia coli O157 and other food borne pathogens from meat products and their
susceptibility to different antimicrobial agents. Current Research in Microbiology and
Biotechnology, 2(3), 391-397.

dorne bacterial illnesses. Journal of Tropical
Diseases, 3(4), 1–7.


CLSI. (2015). M100-S25, Performance standards for antimicrobial susceptibility testing. Twenty-fifth informational supplement. Wayne, USA: CLSI.


