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Prevalence of *Campylobacter*, *Enterococcus* and *Staphylococcus aureus* in slaughtered camels

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Abstract: The contribution of camels and their products (meat and offal) as potential reservoirs of foodborne pathogens is far from elucidated. Therefore, the purpose of this study was to investigate the contribution of camels as potential sources of different foodborne agents and to determine their antibiotic resistance profile. For this reason, one hundred apparently healthy camels admitted to the Zagazig abattoir (Sharkia province, Egypt) for slaughtering were studied. Three different specimens were collected from each camel including fresh faeces, raw meat and liver which were processed to determine the presence of different foodborne pathogens using standard bacteriological techniques. Antimicrobial susceptibility testing was also performed using the disc diffusion method. The occurrence of *Campylobacter* in the faeces, raw meat and liver were 20%, 33% and 15%, respectively, with the most prevalent *C. coli* (21%) followed by *C. jejuni* (0.7%) and *C. lari* (0.7%). *Enterococcus* spp. was isolated at 50%, 40%, and 43% from the examined faeces, meat and liver, respectively, with *E. faecalis* (24%) as the most widely identified bacterial spp. The respective specimens showed typical colonies of *S. aureus* with 15%, 45% and 25%, respectively, with an overall prevalence 28.3%. *S. aureus* was found to colonise workers hands (40%; 10/25), followed by *E. faecalis* (20%) while *Campylobacter* spp. was not detected in any of the tested workers' hands. All recovered foodborne agents were found to be susceptible to enrofloxacin and resistant to rifampicin. The high loads of the pathogenic, as well as indicator bacteria in the raw camel meat, could indicate unhygienic conditions at the abattoir.

Keywords: abattoir; *Camelus dromedarius;* raw meat; liver; offal; faeces; workers; hand swabs; foodborne disease

Camels play an important role in offsetting protein deficiencies worldwide and have received particular concern from several researchers in response to a drastic increase in the animal protein demand, particularly red meat protein. It has recently reported that camel meat has unique char-

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acteristics, such as having good quality protein, low fat and cholesterol contents with relatively high contents of polyunsaturated fatty acids when compared to other food animals (El-Badawi 2018). Although there has been growing attention being paid to camel meat globally, outbreaks of foodborne diseases in developing countries can be unrecognised (Schirone et al. 2017), probably because of the poverty, the lack of infrastructure and the lack of resources for food safety management and food control services.

Food, particularly meat, can serve as a potential source of foodborne illness although the inciting agents and the exact sources of infections are mostly unknown (Wang et al. 2016). Generally, meat can be prone to microbial spoilage and can harbour a wide variety of foodborne and zoonotic agents, such as *Campylobacter* spp., *Staphylococcus aureus,* and *Enterococcus* spp. All these pathogens can be harboured within the gastrointestinal tract of food-producing animals and, hence, contamination to meat during the processing at an abattoir, with subsequent human illnesses, is a rational expectation (Naas et al. 2017; Premarathne et al. 2017; Tyson et al. 2018). Several other bacterial zoonotic pathogens may exist and have been described already in different camel samples such as *Salmonella*, the Shiga toxin producing *E. coli* (O157:H7 and other serotypes), *Listeria* and *Clostridium difficile* (Bosilevac et al. 2015; Esfandiari et al. 2015; Stipetic et al. 2016).

In this context, campylobacteriosis is becoming one of the leading causes of diarrhoea in humans that have become a major public health concern (Gilliss et al. 2013). The disease is often caused by thermophilic *Campylobacter* spp. including *Campylobacter jejuni* and *Campylobacter coli*, which are widely spread in nature (Premarathne et al. 2017). The main reservoirs of those bacteria are the alimentary tract of wild and domesticated birds and mammals (Humphrey et al. 2007). These pathogens are simply transmitted to humans through the ingestion of contaminated foods of animal origin particularly meat from different livestock, as well as raw milk (Salihu et al. 2011; Premarathne et al. 2017).

Enterococci are, Gram-positive lactic acid bacteria, ubiquitous in the environment (in the soil, on plants, and in water), considered as common commensals of the gastrointestinal tract of mammals, birds, insects, and reptiles and can be found in foods, especially those of animal origin (Tyson et al. 2018). *Enterococcus faecalis* and *Enterococcus faecium*, have recently emerged as opportunistic pathogens and ranked third among the leading causes of nosocomial infection including endocarditis, urinary tract infections, central nervous system, intra-abdominal and pelvic infections (Naas et al. 2017). *Enterococci* have intrinsic resistance to several antibiotics and have the ability to exchange the genetic information between themselves and to non-pathogenic organisms by means of plasmids and transposon (Rozanska et al. 2015).

Staphylococcus (*S.*) *aureus* is considered a leading cause of gastroenteritis in humans due to the consumption of contaminated food and has the ability to produce several enterotoxins that cause different symptoms with varying severity (Jaradat et al. 2013). It has been reported that *S. aureus* could rank third amongst the reported foodborne illnesses (Zhang et al. 1998). Given that *Staphylococci* are usually found as a commensal microflora on the skin, nose and mucous membranes of healthy humans and animals, it can easily cause clinical illness with a subsequent variety of clinical signs ranging from skin and soft tissue infections to sepsis and toxic shock (Raji et al. 2016).

The emergence of antimicrobial resistance has been receiving growing attention globally and is currently regarded as public health potential. The development of drug resistance among these zoonotic agents has been associated with the intensive and uncontrolled usage of antibiotics in food-producing animals (Aarestrup 2015). Recent studies have shown that the resistance bacteria, from animal origins, could be regarded as highly or critically important in human therapy and significantly affect global public health and may add to the burden of antimicrobial resistance in humans (Aarestrup 2015; Tyson et al. 2018). The contribution of camels and their products (meat and offal) as potential reservoirs of foodborne pathogens is far from elucidated. Therefore, the present study is aimed at investigating the contribution of camels as potential sources of different foodborne agents and to determine their antibiotic resistance profile.

MATERIAL AND METHODS

Samples collection. The present study included one hundred seemingly healthy camels admitted

https://doi.org/10.17221/104/2019-VETMED

to the Zagazig slaughterhouse (Sharkia province, Egypt) from April, 2018 to December, 2018. Three different specimens were collected from each camel and included fresh faeces, raw meat and liver. For the former, the samples were collected aseptically from the bowel after evisceration. On the other side, hand swabs were collected from twenty-five slaughterhouse workers. Each sample was individually labelled, and packed in a separated sterile plastic bag and kept in a dedicated container and was transported to the laboratory as soon as possible for processing.

Samples preparation. Twenty-five grams from each meat and liver sample were aseptically transferred into a sterile stomacher bag and homogenised with 225 ml of 0.1% (w/v) sterile Buffer Peptone Water (BPW) (Oxoid, Basingstoke, Hampshire, UK) for 2 minutes. For the faecal samples, one gram was added to 9 ml of BPW. For the hand swabs, the sterile cotton swabs moistened with BPW were rubbed gently against the dorsal and palmar surfaces and the fingertips as well. The swabs were immediately inserted onto 10 ml of BPW. All the samples were transported to the laboratory on ice and were processed as soon as possible.

Isolation and identification of *Campylobacter* spp. The isolation and identification of *Campylobacter* spp. was carried out according to the International Organization for Standardization ISO 10272 (2006). Ten ml from the samples in BPW were added to 90 ml of Bolton broth supplemented with antibiotics (Oxoid, Basingstoke, Hampshire, UK) and incubated at 37 °C for 4 h followed by a second incubation at 41.5 °C for 40–48 h under microaerophilic conditions using a campy gas sachet (CampyGen, Oxoid, UK) in an anaerobic jar. After the combined incubation for 48 h, 100 µl of the broth culture was streaked onto a modified Cefoperazone charcoal deoxycholate agar (mCCDA, Oxoid Ltd., UK). The mCCDA plates were incubated under microaerophilic conditions at 42 ± 1 °C for 24 h to 72 h and then examined for typical colonies which were purified using a Columbia blood agar with 5% (v/v) defibrinated horse blood. The presumptive identification of *Campylobacter* colonies was based on the colony appearance. The colonies were tested for catalase, oxidase, Gram stain and nitrate reduction tests for genus specification. A maximum of three colonies exhibiting reactions typical for *Campylobacter* spp. were further characterised by determining growth at 25 °C, and for cephalothin sensitivity, hippurate and indoxyl acetate hydrolysis for the species characterisations. Additional confirmation of the most prevalent *Campylobacter* spp. was performed using PCR (polymerase chain reaction).

Isolation and identification of *Enterococcus* spp. The volume of 0.1 ml of the appropriate tissue homogenate was seeded on the surface of Slanetz-Bartley agar plates (Oxoid, Basingstoke, Hampshire, UK) and were incubated for 48 h at 35 °C. The phenotypic identification at the genus level of the recovered isolates was based on the Gram stain, catalase production, bile-aesculin and hyper saline tests, while identification to the species level was performed according to Facklam and Sahm (1995).

Isolation of *Staphylococcus aureus*. The amount of 100 ml from the samples in BPW was spread out on the surface of a Baird-Parker agar (Oxoid, Basingstoke, Hampshire, UK) supplemented with Egg Yolk Tellurite Emulsion (Oxoid, Basingstoke, Hampshire, UK) and incubated at 37 °C for 24–48 hours. One to three presumptive black colonies surrounded by an opaque halo were purified using a blood agar (Oxoid, Basingstoke, Hampshire, UK) and were confirmed by traditional biochemical tests such as catalase, nitrate reduction, haemolysis and coagulase tests (Gwida and El-Gohary 2013).

Molecular confirmation of *Campylobacter coli* from the examined samples. All the recovered *C. coli* strains (n = 64) were further confirmed with a PCR assay using primer sets specific to the gene *CeuE* in *C. coli* according to the method described by Shin and Lee (2009). The sequences of the oligonucleotide primer sets consisted of a forward primer (5' ATT TGA AAA TTG CTC CAA CTA TG 3') and a reverse primer (5'TGA TTT TAT TAT TTG TAG CAG CG 3') and the expected size was 462 bp (Figure 1). The genomic DNA was prepared by suspending the bacterial colonies in sterilised distal water and heated at 95 ºC in an Applied Biosystems 96-well thermal cycler (Applied Biosystems, Foster City, CA, USA) for 15 minutes. The supernatant was used as a template DNA after centrifugation, and a PCR was performed as recommended by the referenced authors (Shin and Lee 2009). The PCR products were run on a 1.5% agarose gel by electrophoresis. The separated bands were visualised and photographed under an ultraviolet trans-illuminator.

Antimicrobial susceptibility. The susceptibility profile of the recovered bacterial isolates to 18 antibiotics was determined using a disc diffusion tech-

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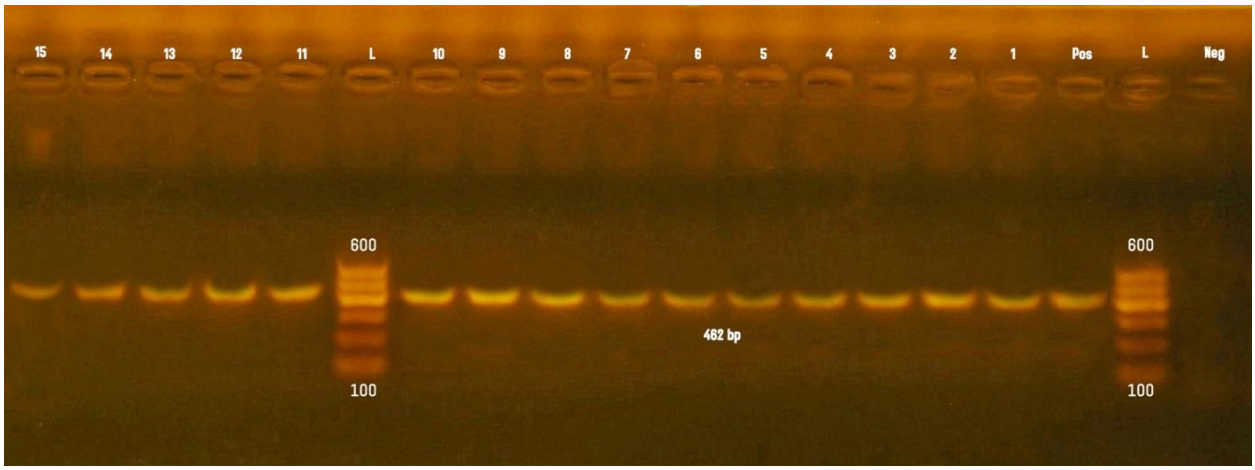

Figure 1. Agarose gel electrophoresis of PCR amplification of *C. coli* with expected amplicon size ~ 462 bp. Lane 1–15 positive samples

L = DNA ladder; Neg = negative controls; PCR = polymerase chain reaction; Pos = positive controls

nique. The used antibiotics included the following: Ampicillin (Amp; 10 µg), Cefadroxil (CFR; 30 µg), Chloramphenicol (C; 30 µg), Bacitracin (B; 10 IU), Enrofloxacin (ENR; 5 µg), Erythromycin (E; 15 µg), Flumequine (UB; 30 µg), Ceftriaxone (CRO; 30 µg), Kanamycin (K; 30 µg), Nalidixic (Na; 30 µg), Neomycin (N; 30 µg), Spiramycin (SP; 100 µg), Streptomycin (S; 10 µg), Amikacin (AK; 30 µg), Colistin sulphate (CT; 25 µg), Penicillin G (P; 10 IU), Oxacillin (OX; 1 µg) and Rifampicin (RD; 5 µg) (Oxoid, Basingstoke, Hampshire, UK). For *S. aureus* and *Enterococcus* spp., the plates were incubated at 37 °C for 24 h, while for *Campylobacter* spp., 5% defibrinated horse blood was added and the plates were incubated at 42 °C for 48 h in a microaerophilic atmosphere. The susceptibility categorisation was performed according to the Clinical and Laboratory Standards Institute guidelines (CLSI 2017).

RESULTS

The occurrence of *Campylobacter* in the faeces, raw meat and liver were 20/100 (20%), 33/100 (33%) and 15/100 (15%), respectively. The most prevalent *Campylobacter* species isolated from the examined samples were *C. coli* (64/300, 21%) followed by *C. jejuni* (2/300, 0.7%) and *C. lari* (2/300, 0.7%). A fragment of size ~ 462 bp was amplified from all the biochemically identified *C. coli* (Figure 1). *Enterococcus* spp. was isolated with the percentage of 50, 40, and 43, from the examined faeces, meat and liver, respectively. The most frequently identified species of *Enterococcus* was *E. faecalis* (73/300, 24%). The distributions of *Enterococcus* by the species found in the tested specimens were *E. faecalis* (30%, 20% and 23%), *E. faecium* (15%, 20% and 13%) and *E. durans* (5%, 0% and 7%), respective-

Table 1. The frequency distribution of the selected food-borne pathogens recovered from the camel specimens and slaughterhouse workers

Source of examined samples	*S. aureus*	*C. coli*	*C. jejuni*	*C. lari*	*Campylobacter* spp.	*E. faecium*	*E. faecalis*	*E. durans*	*Enterococcus* spp.
Camel faeces *n* = 100	15 (15%)	18	1	1	20	15	30	5	50
Camel meat *n* = 100	45 (45%)	32	1	0	33	20	20	0	40
Camel liver *n* = 100	25 (25%)	14	0	1	15	13	23	7	43
Total camel samples	85 (28%)	64	2	2	68 (22.7%)	48	73	12	133 (44%)
Hand swabs *n* = 25	10 (40%)	0	0	0	0	0	5 (20%)	0	5 (20%)

https://doi.org/10.17221/104/2019-VETMED

ly. The examined faeces, meat and liver specimens showed typical colonies of *S. aureus* on BPA (Baird Parker Agar) with the percentage of 15, 45 and 25, respectively with an overall prevalence of 28.3% (85/300) (Table 1). *S. aureus* was found to be colonising the workers hands (40%, 10/25), followed by *E. faecalis* (20%, 5/25) while *Campylobacter* spp. was not detected in any of the tested workers hands.

The resistant pattern of the obtained bacterial isolates to the antimicrobial agents used in this study is illustrated in Table 2. All the recovered foodborne agents were found to be susceptible to enrofloxacin; while all the isolates were resistant to rifampicillin. None of the identified *S. aureus, E. faecalis, E. faecium* showed resistance to chloramphenicol, but *C. coli* showed a low resistance rate (17%). The *S. aureus* strains were resistant to ampicillin, cefadroxil, bacitracin, ceftriaxone, amikacin, penicillin, oxacillin, and rifampicillin while the *C. coli* strains were resistant to erythromycin, kanamycin, neomycin, spiramycin, streptomycin, amikacin and colistin sulphate.

DISCUSSION

Camels are included in this study because of the growing demand for the consumption of their meat and offal in Egypt. Nevertheless, the data on the prevalence of antimicrobial-resistant foodborne pathogens from camel origins is yet to be

Table 2. The antibiotic resistance profiles of the different food-borne pathogens isolated from the camels and the slaughterhouse workers

Antibiotic used	*S. aureus* (*n* = 95)	*C. coli* (*n* = 64)	*E. faecalis* (*n* = 78)	*E. faecium* (*n* = 48)
Penicillin				
Ampicillin (Amp; 10 µg)	100	90	100	98
Penicillin G (P; 10 IU)	100	–	8	14
Oxacillin (OX; 1 µg)	100	–	88	93
Cephalosporins (First generation)				
Cefadroxil (CFR; 30 µg)	100	80	100	100
Cephalosporins (Third generation)				
Ceftriaxone (CRO; 30 µg)	100	75	100	100
Amphenicol				
Chloramphenicol (C; 30 µg)	0	17	0	0
Polypeptides				
Bacitracin (B; 10 IU)	100	–	75	70
Quinolone				
Enrofloxacin (ENR; 5 µg)	0	0	0	0
Nalidixic (Na; 30 µg)	–	75	90	78
Macrolides				
Erythromycin (E; 15 µg)	80	100	10	15
Spiramycin (SP; 100 µg)	70	100	0	0
Fluoroquinolone				
Flumequine (UB; 30 µg)	0	15	15	10
Aminoglycosides				
Kanamycin (K; 30 µg)	33	100	25	18
Neomycin (N; 30 µg)	80	100	15	10
Amikacin (AK; 30 µg)	100	100	90	85
Streptomycin (S; 10 µg)	70	100	18	20
Others				
Colistin sulphate (CT; 25 µg)	–	100	–	–
Rifampicillin (RD; 5 µg)	100	–	100	100

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elucidated. To our knowledge, the current study is the first report on the occurrence of *Campylobacter* spp., *Enterococcus* spp. and *S. aureus* from camels in our country. In the present study, twenty percent of the examined camel faecal samples were found to be contaminated with *Campylobacter* spp. particularly *C. coli* 90% (18/20). In the context, comparatively low detection rates (11.3% and 4.0%) were previously reported in Iran (Salihu et al. 2009a; Rahimi et al. 2017), respectively. The authors reported that *C. jejuni* was the most prevalent spp. in their studies. On the other hand, some authors identified *C. sputorum* in 2% of camel faecal samples *(*3 out of 145) (Baserisalehi et al. 2007). Nevertheless, isolation of *Campylobacter* spp. from animal faeces have been described from different countries at varying rates. For instance, a variable occurrence range of 5–49% has been reported in sheep and goats (Maridor et al. 2008; Salihu et al. 2009b), 0–80% in cattle, and 50–100% in pigs (Viola and DeVincent 2006; Silva et al. 2011).

Campylobacter spp. was recovered from the camel meat and liver specimens with 33% and 15%, respectively. A lower detection rate (17.49%, 19 out of 108) from meat processing facilities and retail stalls in Sokoto has been reported (Salihu et al. 2011). The authors detected *C. jejuni*, *C. coli* and *C. lari* in camel meat with 26.31%, 57.90% and 15.76%, respectively. In contrast, higher contamination rates (60% and 78%) were determined from poultry offal and beef liver (Cloak et al. 2001; Noormohamed and Fakhr 2013), respectively.

The frequencies of the *Campylobacter* recovery from camel meat (33%) was more than those from faeces (20%). Similar results were previously obtained by a Mpalang et al. (2014), Karikari et al. (2017), who identified the contamination rate of *Campylobacter* in carcasses (50% and 36.3%) compared to those from faecal specimens (20% and 28.7%), respectively. Our findings demonstrated that *C. coli* were the most commonly identified species among the other ones. This was in agreement with that reported by several authors (Bostan et al. 2009; a Mpalang et al. 2014; Karikari et al. 2017).

The overall incidence of *Enterococcus* spp. in the examined camel specimens was 44%. For the camel faecal specimens, 50% was identified with *Enterococcus* spp. A higher detection rate (92%) of *Enterococcus* spp. was identified from camels in Tunisia with nearly similar detection rate for *E. faecium* (11%) and *E. durans* (4 %), but lower for *E. faecalis* (11%) (Klibi et al. 2013). In another study from Spain, *Enterococcus* spp. was isolated from camel faeces with different occurrence rates, *E. faecium* (25.4%), *E. durans* (5.8%), *E. faecalis* (4.62%) (Tejedor-Junco et al. 2015).

A high detection rate (59%, 13 out 22) of *Enterococcus* spp. was identified in camel meat compared to the findings reported here (Naas et al. 2017). The different detection rates for *Enterococcus* spp. were determined in chicken and pork meat (58.3% and 31.6%, respectively) and in chicken and pig faeces (61.5% and 57%, respectively) (Vignaroli et al. 2011). In a recent study, the authors evaluated the presence of *Enterococci* in different retail meat commodities in the United States in the period between 2002 to 2014 and found that the overall occurrence was 92% and was distributed at 95.0% in retail chickens, 94.4% from ground turkey, 92.7% from ground beef, and 85.8% from pork chop products (Tyson et al. 2018). The most common *Enterococci* recorded in the present investigation were *E. faecalis* which was in agreement with previous studies (Jahan et al. 2013; Tyson et al. 2018). It has also reported that over 90% of food samples of animal origins are contaminated with *Enterococci* at the slaughterhouse, mostly with *E. faecalis*, followed by *E. faecium* (Boehm and Sassoubre 2014; Tyson et al. 2018). The results of our study have demonstrated that a high proportion of the examined samples were contaminated with *Campylobacter* spp. and *Enterococcus* spp. which indicates an inferior quality of the products due to cross and faecal contamination and referred to poor personal hygiene.

Here, we identified *S. aureus* in 15% of the examined camel faeces, which was comparable to the results obtained from apparently healthy goat and sheep faecal swabs with an overall rate of 12.5% (Ali et al. 2017). In contrast, a low detection rate (2%, 1/45) of *Staphylococci* was reported from camel faeces from Qatari farms (Al-Thani and Al-Ali 2012). However, the same authors identified *Staphylococcus* spp. with a percent of 23.8 (15/63) from different camel specimens including the buccal, vagina, oral, cloacal-uterine swabs, intestine, liver and pus samples.

Approximately half (45%) of the examined camel meat was found to be contaminated with *S. aureus* which matches a recent study (Raji et al. 2016) where they were able to detect *S. aureus* at a rate of (50%, 12/24) from Riyadh, Saudi Arabia. In contrast, a high level of *S. aureus* contamination

https://doi.org/10.17221/104/2019-VETMED

(97.27%, 143/147) of camel meat was previously obtained by Jaradat et al. (2013). On the other hand, a lower contamination rate was previously reported elsewhere (Quddoumi et al. 2006; Greeson et al. 2013) at the levels of 12.5% and 5.6%, respectively.

The occurrence of *S. aureus* in the examined liver samples was 25%. A nearly similar contamination rate (26.2%) was previously reported by Hamza et al. (2017) from camels in a Tambool slaughterhouse. In contrast, a high detection rate was previously reported from Sudan (Aljameel et al. 2014; Eldoma and Omar 2015). Detection of *S. aureus* from the examined camel meat indicates poor sanitary conditions, unsatisfactory handling and shows the importance of camel meat as potential sources for staphylococcal food poisoning. The discrepancy in the detection rates of foodborne pathogens which were observed in other studies could be attributed to the different sampling techniques used, seasonal effects and the laboratory methods employed in the various studies (Tyson et al. 2018). For the local situation, it could be clarified that the meat production in the country came through the traditional methods of slaughtering and the local slaughterhouses are still suffering from several administrative limitations (Hemmat et al. 2013). For instance, the carcasses remained on the ground for a long time during their preparation, thereby creating a potentially suitable media for cross-contamination of the carcasses with the intestinal contents. On the other hand, the camel meat could be contaminated during the different stages of skinning and evisceration without separation between a dirty and clean area and the bacteria transfer easily from the exposed surfaces to the sterile carcass (Karikari et al. 2017). Other potential possibilities for the high microbial load of the camel meat could be the knives, workers and their clothes, air and water supplies and the absence of any written sanitary measures at the slaughterhouse, the lack of worker training for these measures whereas, most of the workers in the slaughterhouses and meat industries are from low income and educational groups (Elsharawy and Mahran 2018).

Our results illustrated the high frequency for each of *S. aureus* (40%) and *E. faecalis* (20%) from the meat handlers. In a previous study from Kenya, some authors found that slaughterhouse workers' hand swabs were contaminated with *Enterococcus* spp. at the percent of 26.7%. In the same line, it has been mentioned that a high proportion (i.e., 30% to 35%) among healthy people is considered the principal habitat for *S. aureus* because they harboured the bacterium in the nasopharynx and on the skin and can easily contaminate foods (Acha and Szyfres 2003). Indeed, the relatively high prevalence of *S. aureus* in the raw meat and handlers could represent a great health hazard due to the potential toxin-mediated virulence and the possibility of invasiveness to consumers. Surprisingly, none of the examined hand swabs yielded a positive result; hence the risk to contract *Campylobacter* spp. from the infected animals cannot be excluded.

Here, the results of antimicrobial susceptibility profile indicated that most of the campylobacter isolates were susceptible to enrofloxacin, flumequine and chloramphenicol, while high prevalence of resistance were expressed against the remaining antibiotics. These findings were comparable to those previously reported by other researchers (Salihu et al. 2011; Karikari et al. 2017; Rahimi et al. 2017). Variable resistance rates were demonstrated by other investigators (Al-Thani and Al-Ali 2012; Greeson et al. 2013; Naas et al. 2017; Tyson et al. 2018). The widespread resistance of *C. coli*, *Enterococcus* spp. and *S. aureus* to ampicillin, cefadroxil, ceftriaxone, amikacin could be alarming and warrant possible risks of infection to people through the consumption of contaminated camel products or by direct contact with the animals and raise uncertainties about their effectiveness in the treatment with more serious consequences for human health. Additionally, these resistance agents can be passed from one bacterial strain to other ones by gene transfer.

The present study provides baseline data on the microbiological quality of camel meat at Zagazig slaughter house. The high loads of the pathogenic, as well as indicator bacteria in the raw camel meat, could indicate unhygienic conditions at the abattoir. The camel meat could be a significant source of food-borne pathogens to the consumer unless good hygienic practices and slaughtering processes are implemented in the abattoir. It is also suggested that municipal authorities should monitor and regulate the hygienic practices of the camel meat retail markets to safeguard the consumer and reduce the public health risk to a minimum. Further studies are needed to elucidate the genetic characterisation of the isolated bacteria reported here with special regards to their antimicrobial resistance genes and to their genetic linkages.

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