scientific reports

Check for updates

OPEN

Identification and antimicrobial susceptibility profiles of *Campylobacter* isolated from camel at municipal abattoirs in eastern Ethiopia

Metages Yirgalem[1], Jelalu Kemal[2]✉, Takele Wolkaro[3], Misgana Bekele[2] & Yitagele Terefe[2,4]

Campylobacteriosis is an infectious zoonotic disease caused by the genus Campylobacter. The disease is transmitted from animals to humans predominantly through the consumption of contaminated food and water. However, the lack of information on the status of Campylobacter makes it difficult to quantify the role of camel meat in the dissemination of the pathogen. A cross-sectional study was conducted from June 2022 to August 2023 to investigate the occurrence of Campylobacter and associated risk factors and to determine the antimicrobial susceptibility profiles of Campylobacter species from camels slaughtered at municipal abattoirs in the towns of Harar, Babile, Jigjiga and Dire Dawa in eastern Ethiopia. A total of 324 (146 carcass swabs, 146 camel feces and 32 abattoir environmental swab samples) were collected and analyzed using TaqMan real-time PCR and culture techniques following standard procedures. In addition, antimicrobial susceptibility tests were performed using the disk diffusion method for eight antimicrobial agents according to the Clinical Laboratory Standards Institute. The overall prevalence of Campylobacter was 7.7%. Campylobacter was more frequently detected from carcasses and surface contact environmental swabs. We isolated Campylobacter at the genus level from approximately half of the PCR-positive samples, representing 54.2% (13 out of 24) of the total. The isolation levels of *C. jejuni* and *C. coli* were also 5.56% and 2.2%, respectively, which varied significantly (p = 0.037) based on sample type and site. The odds of occurrence of *C. jejuni* in samples collected from abattoir environments was 7.52 times greater than those in carcass and fecal samples. We detected resistance to chloramphenicol (78.6%), followed by amoxicillin (71.4%). However, 93%, 78.6%, and 71.4% of the isolates were susceptible to ceftriaxone, ciprofloxacin, and nalidixic acid, respectively. Multidrug resistance (MDR) was detected in 60% of the isolates. Of these MDR isolates, 9 (75%) were *C. jejuni* and 3 (25%) were *C. coli*. This study revealed that a considerable proportion of multidrug-resistant Campylobacter species circulate in both camel meat and abattoir environments. This indicates possible carcass cross-contamination by Campylobacter during slaughtering that can pose a threat to humans and limit therapeutic options, which could be prevented by applying good hygienic practices at abattoirs. Therefore, abattoir workers need to be aware of abattoir hygienic standard operating procedures. Regular coordinated actions should be implemented for the rational use of veterinary and medical drugs at the national level, together with training and awareness of hygienic practices.

Keywords Antimicrobial resistance, Camel carcass, *C. Coli*, *C. Jejuni*, Eastern Ethiopia

Camel is one of the most important livestock species in arid and semiarid areas of Ethiopia which are crucial for addressing global protein shortages caused by the sharp increase in demand for animal proteins[1]. However, food of animal origin, particularly meat, can be prone to microbial spoilage and can harbor a wide variety of

[1]Department of Animal Science, Wolkite University, P.O. Box 07, Wolkite, Ethiopia. [2]College of Veterinary Medicine, Haramaya University, P.O. Box 138, Dire Dawa, Ethiopia. [3] School of Animal and Range Land Sciences, Haramaya University, Dire Dawa, Ethiopia. [4]Department of Veterinary Medical Sciences, Alma Mater Studiorum University of Bologna, Ozzano dell'Emilia, Bologna, Italy. ✉email: jelaluk@gmail.com

foodborne and zoonotic microorganisms[2]. *Campylobacter*is a genus of bacteria that is found in the intestines of animals and humans. This genus consists of 31 species and 13 subspecies[3], of which the best known are *C. jejuni* and *C. coli*, which are mainly responsible for gastroenteritis in humans worldwide[4]. *Campylobacter*is particularly prevalent, with an estimated 400 million cases per year worldwide. While campylobacteriosis cases have often been linked to the consumption of fecal contaminated food and water, the consumption of undercooked meat has also been identified as a source of infection. Above all, humans may be infected by contact with live animals and environments contaminated with animal feces and subsequent incidental ingestion of the pathogens[5].

Human campylobacteriosis symptoms can range from mild diarrhea to bloody diarrhea, and *Campylobacter*infections can lead to long-term detrimental neurological consequences in the form of postinfection Guillain–Barré syndrome[6], Miller Fisher syndrome (MFS), and functional bowel diseases, such as irritable bowel syndrome[7]. In developing countries such as Ethiopia, it is one of the most common bacteria isolated from the stools of children under five years old with diarrhea, largely as a result of contaminated food or water. However, despite its extremely high worldwide incidence, it is underdiagnosed and underreported[8].

The majority of *Campylobacter* bacteria are highly resistant to beta-lactam drugs, including ampicillin, amoxicillin, and cefotaxime. *Campylobacter* species particularly *C. jejuni* and *C. coli*has shown an intrinsic resistance to the penicillin, majority of the cephalosporins, rifampicin, sulfamethoxazole/trimethoprim, and to vancomycin[9]. The most effective medications for treating campylobacteriosis are believed to be macrolides and fluoroquinolones, although some strains of this bacterium are becoming resistant to these drugs[6]. *The* resistance of *Campylobacter*to common antibiotics used to treat infections is a rising problem worldwide and may limit the selection of available therapies[10]. Therefore, the emergence of drug-resistant *Campylobacter*strains underscores the need for robust surveillance systems to monitor the prevalence and distribution of antibiotic resistance. Additionally, there is a need for more prudent use of antibiotics in both human and veterinary medicine to reduce selective pressure and minimize the development and spread of antibiotic resistance[11].

A few recently reported studies of *Campylobacter*species from apparently healthy food animals and humans in Ethiopia showed isolation levels ranging from 5 to 16.7%[12,13]. This persistent occurrence of *Campylobacter* highlights its relevance as a public health concern and demands proper control. In addition, many countries, including Ethiopia, have reported a rapid increase in *Campylobacter* strains resistant to antimicrobial agents, particularly fluoroquinolones and macrolides. Nonetheless, there is a scarcity of data on the prevalence of antimicrobial resistance and the various risk factors that contribute to the occurrence of *Campylobacter* in Ethiopia. Despite the scarcity of data, few fragmented and limited studies have been conducted on *Campylobacter*species in the eastern parts of the country, where camel meat is one of the main sources of protein. For instance, Tegegne et al.[14] studied the microbiological safety and hygienic quality of camel meat at abattoirs and retail houses in Jigjiga city and reported an overall 5% prevalence of *Campylobacter*. In this study, only Jigjiga was targeted, and antimicrobial susceptibility tests were not performed. The authors identified *Campylobacter* at the genus level only with culture-based techniques. The lack of well-documented information regarding the epidemiological status and antimicrobial susceptibility pattern of *Campylobacter* species in camels in eastern Ethiopia makes it difficult to quantify the role of camels in the dissemination of the pathogen and design appropriate control and prevention measures. Therefore, the objective of this study was to investigate and assess the associated risk factors and determine the antimicrobial susceptibility profiles of *Campylobacter* species from camels slaughtered at municipal abattoirs in the towns of Harar, Babile, Jigjiga and Dire Dawa in eastern Ethiopia.

Materials and methods

Description of the study area

The study was conducted at the Harar, Babile, Jigjiga and Dire Dawa municipal abattoirs. All the municipal abattoirs in these towns provide slaughter services for camels. The animals used for slaughter were mainly from the surrounding districts of the east Hararge zone, the Somali regional state, and other nearby areas.

Harar town is geographically located between 9.11° and 9.24° north of latitude and 42.03 and 42.16° east of longitude and is located 526 km east of Addis Ababa and 31 km west of the Babile district[15]. The Dire Dawa city administration is geographically located in the eastern part of Ethiopia at 9°36′ N and 41°52′ E and is located 515 km away from Addis Ababa. The area is situated 1200 m above sea level and has a mean annual rainfall and humidity of 594 mm and 41.82%, respectively. The mean annual maximum and minimum temperatures of the town are 31.4 °C and 18.41 °C, respectively[16]. Babile town is located in the eastern corner of the eastern Hararge zone of the Oromia Regional State, bordering the Gursum, Fedis, Harari and Somali Regional States. It is located at 9°08'N latitude, 42°21'E longitude, and 557 km away from Addis Ababa. The town has an altitude that ranges from 950 to 2000 m above sea level. The mean annual minimum and maximum temperatures range from 18 to 28 °C, while the mean annual rainfall and humidity range from 700 to 900 mm and 33–38%, respectively. The town has a total area of 3169.06 km^2. The two prevailing agricultural production systems are pastoral and agro-pastoral[16]. Jigjigatownis the administrative capital of the Ethiopian Somali Regional State. Geographically, it is located approximately 628 km east of Addis Ababa, 74 km east of the Babile district and 60 km west of the border with the Republic of Somali-land. The town has an altitude of 1609 m above sea level, a latitude and longitude of 9°21'N and 42°48`E, and a mean annual rainfall and humidity of 712 mm and 57.1%, respectively. The mean annual maximum and minimum temperatures of the town are 27.49 °C and 12.3 °C, respectively[16] (Fig. 1).

Study design and sample size determination

A cross-sectional study was conducted from June 2022 to August 2023 to investigate the occurrence of *Campylobacter*species in camel carcasses, fecal samples, and environmental swab samples. The sample size was determined using the formula given by Thrusfield[17], with a 95% confidence interval at 5% precision, based on the 5% expected incidence reported in a previous study by Tegegne et al.[14].

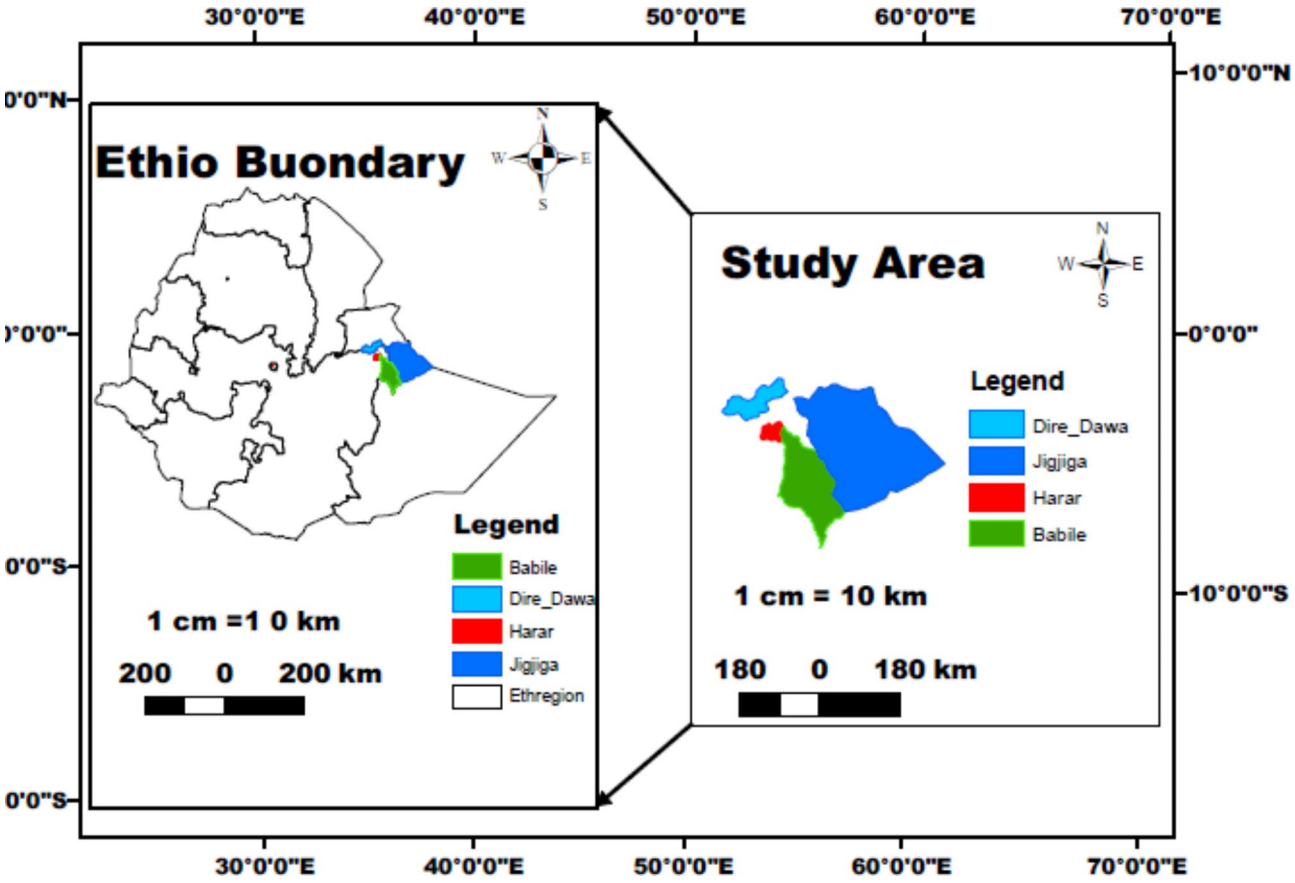

Fig. 1. Map of the study area (Dire Dawa city, Harar, Babile and Jigjiga).

Study sites	Sample Type			Total
	Carcass swab	Fecal	Environmental	
Dire Dawa	39	39	8	86
Harar	24	24	8	56
Babile	32	32	8	72
Jigjiga	51	51	8	110
Total	146	146	32	324

Table 1. Distributions of samples with respect to study sites and sample type.

$$N = \frac{Z^2 * Pexp(1\text{-}Pexp)}{d^2}$$

Accordingly, 73 samples were calculated, and this number was doubled to 146 to increase the precision of the estimate. The estimated number of camels slaughtered at each abattoir was obtained from abattoir records. Two separate pairs of samples (146 fecal and 146 carcass samples) were collected, for a total of 292 samples. Additionally, 32 environmental swab samples were collected. Therefore, 324 overall carcass, fecal and environmental swab samples were collected (Table 1).

Sampling technique

A total of 146 fresh fecal, 146 carcass and 32 environmental swab samples were collected from each systematically and purposively selected camel for laboratory analysis. Swab samples were collected by the use of commercially available transport tubes containing buffered peptone water that protects *Campylobacter*species from drying and the toxic effects of oxygen, as recommended by OIE[18]. The selected carcasses were swabbed using sterile cotton-tipped swabs (2 × 3 cm) fitted with a shaft on specific sites on the carcass, abdomen (flank), thorax (lateral), and breast (lateral), which are the sites with the highest rates of contamination. The sterile cotton at each site was first soaked in 10 ml of buffered peptone water (BPW), which was first rubbed horizontally and then vertically several times on the carcasses. On completion of the rubbing process, the swab was placed into the transport

media (BPW) and the wooden shaft of the it was broken leaving the cotton swab inside of the test tube. Swab samples from four sites on the right and left sides of an animal were taken as a pool. Fecal samples (approximately 10 gm) were collected directly from the rectum immediately after slaughter. The fecal samples were subsequently placed in a sterile screw-capped container containing 10 ml of BPW[18]. Environmental samples (10 × 10 cm) were taken from the surfaces of the walls, floors, personnel hands, knives, hooks, and aprons with sterile cotton tipped swabs on each sampling day as a pooled sample in screw-capped test tubes containing 10 ml of BPW. Finally, the samples were immediately transported to Haramaya University Central Laboratory, Food Microbiology and Toxicology Lab. in an ice box with ice packs for microbiological analysis and molecular detection of the pathogen.

Survey data collection

A semi-structured interview questionnaire was presented for 60 abattoir workers (8, 15, 18, and 19 respondents, based on their consent from Babile, Harar, Dire Dawa and Jigjiga, respectively) with the intent of determining carcass contamination. The information collected included the sociodemographic characteristics of the abattoir workers, their knowledge and practices and their observational assessments of the abattoirs during each sampling day.

Isolation and identification of *Campylobacter* species

Isolation and identification of *Campylobacter*species was done following the protocol described by Rahimi et al.[19]. Selective solid media for the isolation of *Campylobacter* species were prepared using chromogenic agar media (CHROMagar™ *Campylobacter* base) (George Sand – La Plaine Saint-Denis, France). A selective supplement (CHROMagar™ *Campylobacter* CP572) (George Sand – La Plaine Saint-Denis, France) was filter sterilized through a 0.45 µm pore size cellulose acetate filter and added to the CHROM agar according to the manufacturer's instructions (Paris, France). Briefly, the samples were processed immediately and one gram of the collected fecal samples were suspended in 9 mL of the selective enrichment broth (CHROMagar™ *Campylobacter*CP572) and incubated at 42 °C for 48 h under microaerophilic condition using sachets (CampyGen Compact)[20]. Subsequently, 0.1 mL of the enrichment broth was plated onto *Campylobacter* selective agar (CHROMagar™ *Campylobacter* base) for selective isolation of *Campylobacter* species and incubated under microaerophilic conditions using sachets at 42°C for 48 h. Swab samples from transport medium were also plated to CHROM agar and incubated in same manner mentioned above.

Suspected colonies on CHROM agar (small colonies with a brick-red color) on the selective media were sub-cultured and incubated under microaerophilic conditions. For this test, presumptive colonies were subjected to subculturing on selective agar and incubated aerobically at 41.5 ± 1 °C for 22 ± 1 h under microaerophilic conditions. Presumptive colonies were subjected to further identification based on standard microbiological and biochemical procedures, including Gram reactions, motility tests, production of catalase and oxidase, hippurate hydrolysis tests, and susceptibility to cephalothin and nalidixic acid disks. Hippurate-positive isolates were identified as *C. jejuni* and nalidixic acid susceptible, and hypurate-negative isolates were considered *C. coli*[21]. Then, pure colonies of the identified *Campylobacter* species were picked up with a sterile loop, immersed in 0.5 ml of brain-heart infusion broth medium and preserved at -20 °C.

Antimicrobial susceptibility test

*An in vitro*antimicrobial susceptibility test was applied to the isolates obtained from the collected samples using Kirby–Bauer disc diffusion technique using Mueller–Hinton agar with 5% defibrinated sheep blood according to the Clinical Laboratory Standards Institute[22]. The following antimicrobial agents were tested for *Campylobacter* species: ampicillin (AMP) (10 µg), amoxicillin with clavulanic acid (AMC) (30 µg), chloramphenicol (C) (30 µg), ceftriaxone (CRO) (10 µg), sulfamethoxazole-trimethoprim (STX) (25 µg), erythromycin (E) (15 µg), ciprofloxacin (CIP) (30 µg), and nalidixic acid (NA) (5 µg).

Molecular detection of *Campylobacter* by polymerase chain reaction (PCR)

DNA extraction

From the culture broth, DNA was extracted using a Genomic DNA Purification Kit and a QIAamp PowerFecal Pro DNA Kit (Qiagen, CA, USA) following the manufacturer's protocol. Briefly, 0.25 ml of the culture sample was subjected to genomic DNA extraction according to the manufacturer's instructions, after which the sample was suspended in 100 ml of nuclease-free water. DNA quality and quantity were assessed by a UV5 Nano spectrophotometer, and the DNA was stored at -20 °C until further use.

Confirmation of *Campylobacter* isolates using TaqMan real-time PCR

Campylobacter was detected from culture samples using TaqMan real-time PCR. The primers used in PCRs targeting *Campylobacter*16 S rRNA were as follows (forward: GATGACACTTTTCGGAGCGTAA and reverse: GCTTGCACCCTCCGTATTA using a probe, CGTGCCAGCAGCC-MGB) based on Platts-Mills et al.[23]. PCR was carried out in a total final volume of 25 µl containing 0.1 nM of each primer, 12.5 mL of PrimeTime gene expression master mix (Integrated DNA Technology, USA), 0.05 nM of the probe, 50 ng of normalized DNA, and nuclease-free water. QuantStudio 5 was used to run the real-time PCR. A positive control containing template genomic DNA from *C. jejuni* (ATCC 81–176) and *C. upsaliensis* (ATCC 49816) was used. As a negative control, nuclease-free water was used. The reaction thermocycler conditions were optimized with initial denaturation at 95 °C for 10 min and 1 cycle of 45 cycles of denaturation at 95 °C for 15 s, annealing at 55 °C for 1 min and extension at 72 °C for 1 min. Finally, an additional extension was achieved for 7 min at 72 °C, after which the samples were stored at 4 °C. A cutoff C_T value of 35 was used for the detection of *Campylobacter* in each sample: average $C_T$for nuclease-free water − 2.5 × standard deviation[24].

Approval of ethics

During the study, all the experimental protocols were approved by the Haramaya University Research Grant Review Committee (HURGRC) after reviewing the proposal as per the guidelines and regulations of the Haramaya University Research and Community Engagement Office. All the methods and protocols used in this study were conducted in accordance with the regulations and guidelines of the university. We obtained verbal consent from abattoir workers who were interviewed in accordance with their knowledge and practices and public health awareness assessments. The participants were informed about the entire purpose of the study in accordance with their level of understanding to provide relevant information.

Data management and analysis

All the data were stored and prepared in the Microsoft Excel sheet, and the analysis was performed using the STATA 12 statistical package software. Descriptive statistics, chi-square tests and univariate and multivariate logistic regression analyses were conducted to assess the associations among the independent variables and the outcome variable; variables found to be significant at a P value < 0.2 were used to construct a multivariate model. Odds ratios (ORs) were calculated with 95% confidence intervals (CIs) to determine the strength of the associations, and differences were considered significant at $p < 0.05$.

Results

The overall prevalence of *Campylobacter* species

The overall prevalence of *Campylobacter* species was 7.7% (25/324). The most prevalent *Campylobacter* species was *C. jejuni* (5.5%) followed by *C. coli* (2.2%). There were no significant differences among the study sites. However, the highest prevalence of *Campylobacter* was recorded in Babile town (40%), followed by Jigjiga (24%). The samples from Babile town had the highest *C. jejuni* occurrence among the study sites ($P = 0.037$). The proportion of *C. coli* in young camels was significantly greater than that in adult camels ($P = 0.003$). Similarly, there were significantly more *Campylobacter* species in the environmental samples than in the other sample types ($P = 0.001$) (Table 2).

Multivariate logistic regression analysis of *C. coli* and *C. jejuni*

Multivariate logistic regression analysis for the occurrence of *C. jejuni* revealed a significant association among the study sites ($P < 0.05$). The odds of occurrence of *C. jejuni* in Babile municipal abattoir was 4.55 times greater than those in Dire Dawa and the rest of the municipal abattoirs ($p = 0.041$; AOR = 4.549; 95% CI = 1.065–19.43). Multivariate logistic regression analysis of the occurrence of *C. jejuni* isolates from different sample types revealed a significant association ($P < 0.05$). The odds of occurrence of *C. jejuni* in samples collected from

Variables	Categories	No. examined	No positive (%)	No. (%) of samples positive	
				C. jejuni	*C. coli*
Study site	Dire Dawa	86	5 (5.8)	3 (3.5)	2 (2.3)
	Harar	56	4 (7.1)	2 (3.6)	2 (3.6)
	Babile	72	10 (13.9)	9 (12.5)	1 (1.4)
	Jigjiga	110	6 (5.5)	4 (3.6)	2 (1.8)
	Total	324	25 (7.7)	18 (5.5)	7 (2.2)
	χ2 (p value)		5.1057 (0.164)	8.51 (0.037)*	0.802 (0.849)
Sex	Male	263	13 (5)	7 (2.67)	6 (2.3)
	Female	29	2 (6.9)	2 (6.9)	0
	Total	292	15 (5.1)	9 (3)	6 (2)
	χ^2 (p *value*)		0.2046 (0.651)	1.568 (0.21)	0.676 (0.411)
Age	Young	79	7 (8.9)	2 (2.53)	5 (6.3)
	Adult	213	8 (3.75)	7 (3.3)	1 (0.47)
	Total	292	15 (5.1)	9 (3)	6 (2)
	χ2 (p value)		2.586 (0.108)	0.18 (0.675)	9.078(0.003)*
Body condition	Medium	104	5 (4.8)	2 (2)	3 (2.9)
	Good	188	10 (5.3)	7 (3.7)	3 (1.6)
	Total	292	15 (5.1)	9 (3)	6 (2)
	χ2 (p value)		0.0359 (0.850)	0.7265(0.394)	0.553 (0.457)
Sample type	Carcass	146	10 (6.8)	8 (5.5)	2 (1.4)
	Fecal	146	5 (3.4)	1 (0.7)	4 (2.7)
	Environment	32	10 (31.25)	9 (28)	1 (3.1)
	Total	324	25 (7.7)	18 (5.56)	7 (2.2)
	χ2 (*p value*)		28.819 (0.001)*	37.67(0.001)*	0.8043(0.669)

Table 2. *Campylobacter* prevalence and species distribution according to different risk factors.

abattoir environments was 7.52 times greater than those in carcass and fecal samples ($P=0.001$; AOR = 7.5217; 95% CI = 2.4745–22.864) (Table 3).

Prevalence of *Campylobacter* species in different sample types among sites

There was a statistically significant difference among the different sample types in terms of the occurrence of *C. jejuni* ($p=0.001$). A high prevalence of *Campylobacter* species was detected in the carcass swab samples collected from Babile (7.7%), followed by those collected from Jigjiga (5.9%). Examination of 146 camel fecal samples for intestinal carriage revealed that 5 (3.42%) were *Campylobacter* species positive (Table 3). The numbers and percentages of *Campylobacter* species isolated from fecal samples were 1 and 4 for *C. jejuni* and *C. coli*, respectively. *C. jejuni* and *C. coli* accounted for 9 and 1%, respectively, of the *Campylobacter* species isolated from the environmental samples (Table 4).

PCR confirmation of *Campylobacter* isolates

Molecular detection of *Campylobacter* from culture samples was determined based on the threshold cycle values ($_{CTs}$) obtained for each sample against the no-DNA controls (nuclease-free water controls), which provided background noise estimates (i.e., fluorescence signals that were obtained through nonspecific amplification via PCR). Thus, it was used to examine *Campylobacter*-positive and Campylobacter-negative samples. For the detection of *Campylobacter* in the culture samples, a cutoff C_T value of 35 was used for each sample (average C_T value for nuclease-free water − 2.5 × standard deviation). With this PCR test of 24 culture samples examined, 13 (54.2%) were found to be positive for *Campylobacter* (Table 5; Fig. 2).

Antimicrobial susceptibility profile of *Campylobacter* isolates

Among the 20 isolates tested, all (100%) were resistant to one or more antimicrobial agents, whereas two (1 *C. jejuni* and 1 *C. coli*) were susceptible to the 5 antimicrobial agents tested. Three isolates (15%) were resistant to a single antimicrobial agent, and 5 isolates (25%) were resistant to 2 antimicrobial agents. The highest levels of *Campylobacter* resistance were recorded for chloramphenicol (70%) and amoxicillin-clavulanic acid (65%), while the least common antimicrobial agents for this specific test were ceftriaxone (5%), followed by ciprofloxacin and nalidixic acid (10%) (Table 6) (Fig. 3).

Multidrug resistance was observed in 12 (60%) *Campylobacter* isolates. Among these MDR isolates, 9 (75%) were *C. jejuni* and 3 (25%) were *C. coli.* Of these, 5 (41.7%) were from carcasses, 3 (25%) were from feces, and 4 (33.3%) were recovered from abattoir environment samples. The MDR for the maximum number of antimicrobial disks (five antimicrobial agents) observed was registered for *C. jejuni* strains (Table 7).

Results of the questionnaire survey

Sociodemographic characteristics of the respondents

Of the 60 respondents interviewed, 55 (91.7%) were male, while the remaining 5 (8.3%) were female. The majority of the respondents were aged between 30 and 41 years, and nearly half (45%) of them could not read or write. Forty-three (71.7%) of them had abattoir work experience of 1 to 3 years (Table 8).

Knowledge and practices of the respondents

Among the 60 respondents, none (100%) had taken any course related to abattoir work. However, 23 (38.3%) of them responded that they had received lessons related to their work. Most of the respondents (68.3%) washed their hands using water only (Table 9).

General observational assessment of abattoirs

According to the observation survey, 36.7% of abattoir workers did not wear protective cloths/aprons, and 40% of the workers did not use detergents or disinfectants for cleaning abattoirs. Most of the time (68.3%), there was demarcation between the dirty and clean areas in the abattoir. However, the present study showed that 73.3% of the time, carcasses and offal come into contact with floors, walls or soiling during dressing and evisceration (Table 10).

Variables	Categories	No. examined	No. (%) of C. jejuni isolates	AOR (95% CI)	*p* value
Study site	Dire Dawa	86	3 (3.5)	1	
	Harar	56	2 (3.6)	0.7884 (0.1167–5.327)	0.807
	Babile	72	9 (12.5)	4.549 (1.065–19.43)	0.041*
	Jigjiga	110	4 (3.6)	1.189 (0.24–5.889)	0.83
Sample type	Carcass	146	8 (5.5)	1	
	Feces	146	1 (0.7)	0.1153 (0.01411-0.9425)	0.044*
	Environment	32	9 (28)	7.5217(2.4745–22.864)	0.001*

Table 3. Multivariable logistic regression analysis for the occurrence of *C. Jejuni* isolates from camel meat samples in selected towns in eastern Ethiopia.

Variables	Total Ex'd	Dire Dawa			Harar			Babile			Jigjiga		
		No. Ex'd	No. positive		No. Ex'd	No. positive		No. Ex'd	No. positive		No. Ex'd	No. positive	
			C. jej	*C. col*		*C. jej*	*C. col*		*C. jej*	*C. col*		*C. jej*	*C. col*
Carcass swab	***146***	***39***	2(***5.1***)	1(***2.56***)	***24***	-	***1***(***4.2***)	***32***	3(***7.7***)	-	***51***	3(***5.9***)	-
Fecal sample	146	***39***	-	1(***2.56***)	***24***	-	1(***4.2***)	***32***	1(***3.1)***	1(***3.1***)	***51***	-	1(***1.97***)
Environment	32	***8***	1(***12.5***)	-	***8***	2(6.3)	-	***8***	5(***62.5***)	-	***8***	***1***(12.5)	1(***12.5***)
Total	**324**	**86**	**3(3.5)**	**2(2.3)**	**56**	**2(3.6)**	**2(3.6)**	**72**	**9(12.5)**	**1(1.4)**	**110**	**4(3.6)**	**2(1.8)**

Table 4. Prevalence of *Campylobacter* species isolated from different samples across study sites.

Well Position	Sample Code	Target Name	C_T Value	Remark
A1	B3E2	Target 1	38.080	Negative
A2	B6F4	Target 1	40.086	Negative
A3	AC6	Target 1	22.353	Positive
A4	B6F1	Target 1	25.534	Positive
A5	B3E6	Target 1	23.985	Positive
A6	H6C7	Target 1	22.572	Positive
A7	A3C6	Target 1	33.124	Positive
A8	B2H1	Target 1	35.366	Negative
B1	A7E5	Target 1	37.209	Negative
B2	J1A1	Target 1	39.697	Negative
B3	A7C7	Target 1	37.078	Negative
B4	A2C5	Target 1	32.522	Positive
B5	B6E1	Target 1	23.970	Positive
B6	B6C1	Target 1	31.870	Positive
B7	H5C2	Target 1	Undetermined	Negative
B8	B6FA	Target 1	21.909	Positive
C1	H4C4	Target 1	38.128	Negative
C2	H2C5	Target 1	25.195	Positive
C3	B1C1	Target 1	40.162	Negative
C4	J3E1	Target 1	32.604	Positive
C5	D3C4	Target 1	33.673	Positive
C6	D2C1	Target 1	37.774	Negative
C7	D2F1	Target 1	33.560	Positive
C8	D4C5	Target 1	37.153	Negative
D1	PC1	Target 1	12.900	Positive
D2	PC2	Target 1	13.714	Positive
D3	NC	Target 1	38.926	Negative
D4	BC	Target 1	36.801	Negative

Table 5. Details of PCR *Campylobacter* detection with C_T values in 28 samples, including 2 positive and 2 negative control samples.

Discussion

In this study, the total prevalence of *Campylobacter*species was relatively in agreement with that reported by Tegegne et al.[14], who reported a 5% prevalence of *Campylobacter*species in camel meat samples from Jigjiga town. Berhanu et al.[12] and Debelo et al.[25] from the Jimma municipal abattoir also reported overall prevalence rates of 5.6% and 7.9%, respectively, which are in agreement with the findings of the present study. In contrast, Chala et al.[13] from Addis Ababa and Hagos et al.[26] from Mekele reported relatively more *Campylobacter* isolates from different sample sources, with a prevalence of 18.5% and 16.67%, respectively. The differences could be a result of the different sampling techniques employed (meat sample, carcass swab, or carcass rinse fluid sample) and/or laboratory methodologies employed in different studies (bacteriological and biochemical testing against polymerase chain reaction assays).

The prevalences of *C. jejuni* (72%) and *C. coli* (28%) in this study are in agreement with those of Berhanu et al.[12], who reported 78.6% *C. jejuni* and 21.4% *C. coli*. Similarly, Hagos et al.[26] reported *C. jejuni* and *C. coli*incidences of 81.25% and 18.75%, respectively, which is consistent with the findings of the present study. However, Seble[27] reported lower incidences of 25.4% and 9.0% for *C. jejuni and C. coli*, respectively. In the present study, a significantly high proportion of *C. coli* isolates was noted among the different age groups of camels. Significant differences were also recorded between sample types ($P=0.001$), which may be due to the nonhygienic slaughtering process and cross contamination and may be related to abattoir environmental conditions that favor bacterial persistence. Multivariate analysis revealed that the odds of occurrence of *C. jejuni* in Babile municipal abattoirs was 4.55 times greater than that in Dire Dawa and the other municipal abattoirs. This indicates that the municipal abattoirs at the study sites need to implement hygienic slaughtering practices.

In the present study, 6.8% of *Campylobacter*species were detected in camel carcass swab samples, similar to the findings of a study conducted by Tegegne et al.[14], who reported a 5% overall prevalence of *Campylobacter*species in camel meat samples from Jigjiga municipal abattoir and retail houses. In contrast, some studies outside Ethiopia, such as Gwida et al.[2], reported a higher (33%) prevalence of *Campylobacter* species in raw camel meat from Egypt. This difference in prevalence may be attributed to differences in sample size, laboratory identification test employed and agro-ecological conditions of the study sites. The proportions of *Campylobacter* species isolated from camel carcass swabs for *C. jejuni* (80%) and *C. coli*(20%) are in agreement with the findings of Sabzmeydani et al.[28] from Iran, who reported 84.24% *C. jejuni* and 15.76% *C. coli*. This percentage is greater

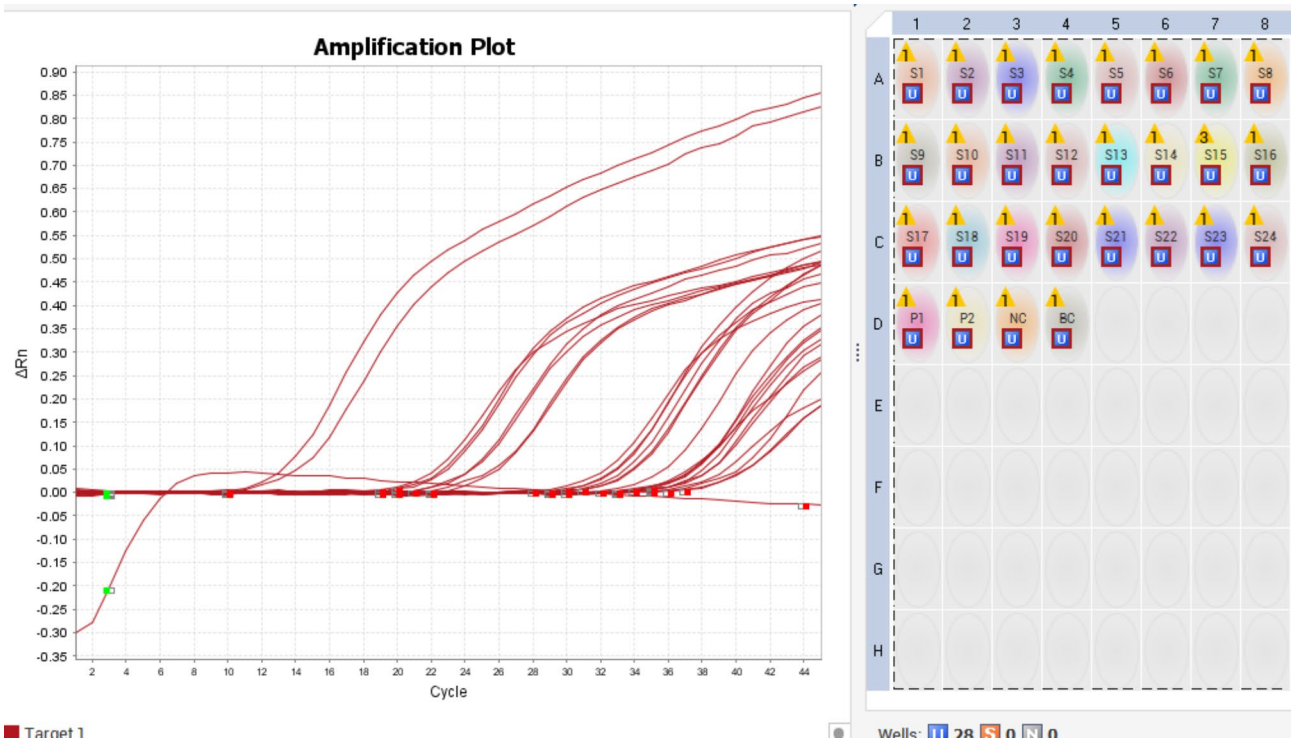

Fig. 2. PCR amplification plot. The red lines indicate the C_T value of each sample. Samples within wells are shown on the left.

Drugs	Drug potency	*C. jejuni* (*n* = 14)			*C. coli* (*n* = 6)		
		S	I	R	S	I	R
		N (%)	*N* (%)	*N* (%)	*N* (%)	*N* (%)	*N* (%)
AMC	30 µg	2 (14.2)	2 (14.2)	10(71.4)	2 (33.3)	1 (16.7)	3 (50)
C	30 µg	1 (7.1)	2 (14.2)	11 (78.6)	2 (33.3)	1 (16.7)	3 (50)
CIP	30 µg	11 (78.6)	2 (14.2)	1 (7.1)	4 (66.7)	1 (16.7)	1 (16.7)
CRO	10 µg	13 (93)	-	1 (7.1)	5 (83.3)	1 (16.7)	-
E	15 µg	6 (43)	3 (21.4)	5 (35.7)	3 (50)	1 (16.7)	2 (33.3)
SAM	10 µg	4 (28.6)	4 (28.6)	6 (42.8)	4 (66.7)	-	2 (33.3)
STX	25 µg	2 14.2)	3 (21.4)	9 (64.3)	2 (33.3)	2 (33.3)	2 (33.3)
NA	5 µg	10 (71.4)	3 (21.4)	1 (7.1)	4 (66.7)	1 (16.7)	1 (16.7)

Table 6. Antibiotic resistance profiles of *Campylobacter* species isolated from camel carcasses, feces and environmental samples in selected areas of eastern Ethiopia. *AMC: amoxicillin-clavunated*, *C: chloramphenicol*, *CIP: ciprofloxacin*, *CRO: ceftriaxone*, *erythromycin*, *AMP: ampicillin*, *STX: sulfamethoxazole-trimethoprim*, *NA: nalidixic acid*, *S: susceptible*, *I: intermediate R: resistant*.

than that reported by Shafiei et al.[29] from India, who reported 57.8% *C. jejuni* and 42.1% *C. coli*. Hence, our findings demonstrated that *C. jejuni*is the most commonly identified species. This finding was in contrast with the findings of Gwida et al.[2]. The presence of *Campylobacter* in the intestinal tract of animals is a potential risk factor for carcass contamination, as determined by shedding patterns and hygienic slaughtering practices. The occurrence of *Campylobacter*species in carcasses might be related to cross-contamination during manual skinning, evisceration, and processing in the slaughterhouse[30].

The proportions of *Campylobacter* species isolated from fecal samples that were *C. jejuni* (20%) and *C. coli*(80%) were in agreement with those in a previous report by Gwida et al.[2], who described 10% and 90% of *Campylobacter* species from camel feces as *C. jejuni* and *C. coli*, respectively. However, the present study differs from a report by Shafiei et al.[29], who reported 62.5% and 37.5% for *C. jejuni* and *C. coli*, respectively. In this study, a considerably greater proportion of *Campylobacter* species was observed in the carcass swabs (6.85%) and environmental samples (31%), possibly due to poor hygienic conditions during the slaughtering process. The high prevalence of *Campylobacter* in environmental samples may be attributed to fecal contamination and

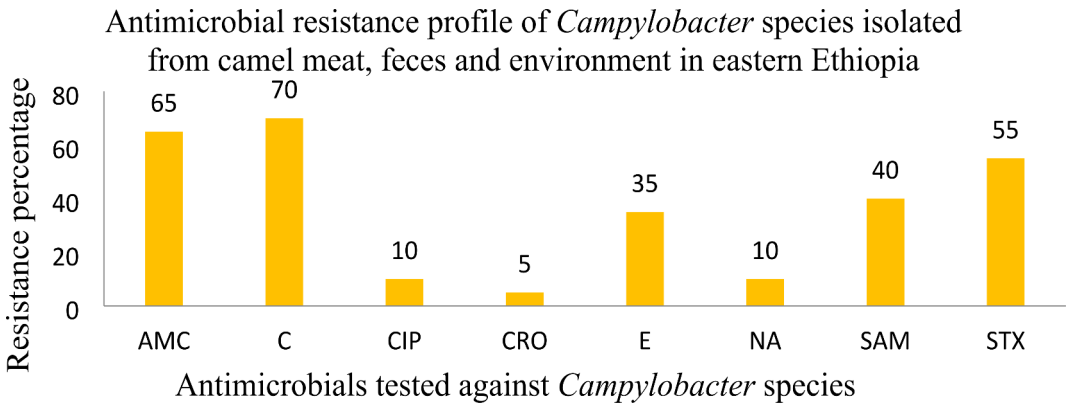

Fig. 3. Antimicrobial resistance profiles of *Campylobacter* species isolated from camel meat, feces and environmental samples.

Number	Resistant profile	Nu. of resistant isolates (%)	
		C. jejuni (*n* = 14)	*C. coli* (*n* = 6)
One drug	STX	1 (7.1)	1 (16.7)
Two drugs	NA	-	1 (16.7)
	AMC, C	2 (14.3)	1 (16.7)
	SAM, STX	1 (7.1)	-
	AMC, NA	1 (7.1)	-
Three & more drugs	AMC, C,E, SAM, STX, CIP, AMC, CRO	9 (75)	3 (25)
Total		**14 (78)**	**6 (86)**

Table 7. Multidrug resistance profile of *Campylobacter* isolates from camel meat.

Variables	Response	Frequency	Percentage
Address	Dire Dawa	18	30
	Harar	15	25
	Babile	8	13.3
	Jigjiga	19	31.7
Sex	Male	55	91.7
	Female	5	8.3
Age	18–29	20	33.3
	30–41	26	43.3
	42–53	14	23.3
Educational status	Cannot read and write	27	45
	Elementary	26	43.3
	Secondary	7	11.7
Abattoir work experience (years)	1–3 years	43	71.7
	4–6	12	20
	7–10	5	8.3

Table 8. Sociodemographic characteristics of abattoir workers at the study sites.

persistence of the microorganism in the environment since cracks and crevices in the abattoir floor and wall coupled with poor cleaning and drainage systems favor environmental persistence of the bacteria.

The highest level of resistance recorded to chloramphenicol (70%) and amoxicillin-clavulanic acid (65%) was in line with the findings of Berhanu et al.[12], who reported the highest level of resistance of *Campylobacter*isolates to ampicillin (10 µg) (100%) and amoxicillin (30 µg) (78.57%). However, Berhanu et al.[12] reported that chloramphenicol and amoxicillin were the least effective drugs, which is in contrast with the findings of the present study. The extensive use of these drugs in medical and veterinary practices might be the reason for

Variables	Responses	Frequency	Percentage
Have you attended a course related to your work?	Yes	-	-
	No	60	100
Have you received any lesson in personal hygiene?	Yes	23	38.3
	No	37	61.7
Washing hands with	Soup & water	19	31.7
	Water only	41	68.3
Do you wash your hands and knives after skinning and evisceration?	Yes	55	91.7
	No	5	8.3
Do you spray wash the carcass prior to inspection?	Yes	45	75
	No	15	25
Is there enough water available in abattoir	Yes	21	35
	No	39	65

Table 9. Knowledge and handling practices of abattoir workers in the study towns.

Variables	Responses	Frequency	Percentage
Do abattoir workers wear protective cloth/apron?	Yes	38	63.3
	No	22	36.7
Do workers use detergent/disinfectants for cleaning?	Yes	24	60
	No	36	40
Is there daily cleanliness of abattoir?	Yes	46	76.7
	No	14	23.3
Is there demarcation between the dirty and clean areas in the abattoir?	Yes	41	68.3
	No	19	31.7
Do the carcasses and offal come into contact with floors, walls or soiling?	Yes	44	73.3
	No	16	26.7

Table 10. General observational assessment of abattoirs in the selected towns in eastern Ethiopia.

such high resistance. In recent years, an increased prevalence of macrolide-resistant *Campylobacter*has been detected in certain regions of the world[31], and the findings of the present study are in agreement with this trend. For instance, our current study revealed 35% resistance to erythromycin, which is considered the drug of choice for the clinical treatment of campylobacteriosis, and resistance to this drug is a public health concern, as options for the treatment of *Campylobacter*infections are currently limited[32]. Nowadays macrolides are also choice antimicrobials that has been used as growth promoting in animal farming in the study areas. These trends can be considered as the main factor in the selection pressure of *Campylobacter*resisting to erythromycin. Kassa et al.[33] in Ethiopia reported 0.7% *C. jejuni* and 3.9% *C. coli* resistance strains to the drug erythromycin from 186 *Campylobacter* strains that were isolated from food animals.

Various investigations from different parts of the world have strongly indicated the emergence of multidrug-resistant *Campylobacter* strains. Since raw meat is widely consumed in Ethiopia, the occurrence of *Campylobacter* in meat increases the likelihood of pathogen transmission to humans. In this study, 48% of the *Campylobacter*isolates exhibited resistance to three or more antimicrobial agents. The increase in MDR to antimicrobial agents could be associated with the extensive use of antimicrobial agents not only as therapeutic agents for human infections but also for prophylaxis and growth promotion in animal husbandry. Similar MDR patterns have been observed in a previous study conducted in Ethiopia for these antimicrobial agents[33]. Thus, there is convincing evidence that MDR resistance has emerged and increased among food animals because of the use of antimicrobial agents in animal production, after which MDR strains spread to the food chain and cause infection in humans[34]. Mechanical hoists were absent at the study sites, and sufficient manual hoists were not present at some of the study sites. A lack of cleaning facilities, poor drainage systems, and insufficient water availability appeared to be the major constraints on the daily cleanliness of abattoirs. The absence of chlorinated and hot water baths and the inability to use detergents on clean floors and equipment might further increase the probability of carcass contamination.

This study revealed that nearly half (45%) of abattoir workers are illiterate. Personnel and other workers at the abattoir were also not adequately trained. Hence, most of these methods do not follow hygienic standards, which invariably contributes to microbial contamination. For instance, these workers dress carcasses on a bare floor in which the slaughter floor is smeared with blood, rumen contents and other waste from previously dressed animals, increasing the risk of contamination of subsequent carcasses. For example, unrestrained movement, putting knives in the rectal openings, not taking care to wash hands or knives frequently, slaughtering, skinning, eviscerating animals on the ground, absence of clear demarcation between the carcass and offal, absence

of adequate water, and hot and/or chlorinated water for cleaning are identified as risk factors that facilitate persistence of pathogens and transfer of microbes onto sterile carcass surfaces.

Conclusion

A considerable proportion of C*ampylobacter* (7.7%) was detected in camel meat, feces, and environmental samples from the towns of interest. In comparison to others, Babile town had a significantly greater incidence of *Campylobacter* species (13.9%), and there was a greater occurrence of C*ampylobacter* species in camel carcass swabs and environmental samples than in fecal samples. This indicates possible carcass cross-contamination by *Campylobacter* species during the slaughtering process, which could have been prevented by applying good hygienic practices at abattoirs. The study revealed that more than one-third of the tested *Campylobacter* isolates exhibited considerably high resistance to erythromycin, and almost half of the isolates were multidrug resistant and may pose a threat to humans. A lack of awareness of abattoir workers and the absence of abattoir hygienic standard operating procedures could be important factors associated with the prevalence of *Campylobacter* contamination of carcasses at abattoirs. Therefore, further epidemiological studies on the magnitude of zoonotic enteric campylobacteriosis along the food chain and molecular characterization of *Campylobacter* species to identify genes responsible for drug resistance should be conducted. Regular coordinated actions should be implemented on the basis of the rational use of veterinary and medical drugs together with training and awareness of good hygienic practices.

Data availability

All the datasets used during the study are available from the corresponding author of the manuscript on reasonable request.

Received: 10 May 2024; Accepted: 17 October 2024
Published online: 01 November 2024

References

1. Faye, B. Role, distribution and perspective of camel breeding in the third millennium economies. *Emirates J. Food Agric.* **27**(4) 318–327 (2015).
2. Gwida, M., Amira, Z., Heba, E. S., Rasha, E. & Mona, E. Prevalence of *Campylobacter*, *Enterococcus* and *Staphylococcus aureus* in slaughtered camels. *Vet. Med.* **64** (12), 521–530 (2019).
3. Parte, A. C., Sardà Carbasse, J., Meier-Kolthoff, J. P., Reimer, L. C. & Göker, M. List of prokaryotic names with standing in nomenclature (LPSN) moves to the DSMZ. *Int. J. Syste Evol. Microbiol.* **70**, 5607–5612 (2020).
4. Acke, E. *Campylobacteriosis* in dogs and cats: a review. *N. Z. Vet. J.* **66**, 221–228 (2018).
5. Thomas, K. M. et al. Prevalence of *Campylobacter* and *Salmonella* in African food animals and meat: a systematic review and meta-analysis. *Int. J. Food Microbiol.* **315**, 108382 (2020).
6. Kaakoush, N. O., Castaño-Rodríguez, N., Mitchell, H. M. & Man, S. M. Global epidemiology of *Campylobacter* infection. *Clin. Microbiol. Rev.* **28**, 687–620 (2015).
7. Mughal, M. H. *Campylobacteriosis*: A GthreatThreat. *Biomedical J. Sci. Tech. Res.* **11** (5), 8804–8808 (2018).
8. Diriba, K., Awulachew, E. & Anja, A. Prevalence and associated factor of *Campylobacter* species among less than 5-year-old children in Ethiopia: a systematic review and meta-analysis. *Eur. J. Med. Res.* **26** (1), 1–10 (2021).
9. Fitzgerald, C., Whichard, J. & Nachamkin, I. Diagnosis and Antimicrobial susceptibility of *Campylobacter* species. In: Nachamkin C, C Szymanski C.M, Blaser, M., editors. *Campylobacter*, 3rd edition. USA: ASM press. pp. 227–245 (2008).
10. European Food Safety Authority (EFSA). The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2017. *Eur. Food Saf. Auth. J.* **17**, 5598 (2019).
11. Nisar, M. et al. Occurrence of *Campylobacter* in retail meat in Lahore, Pakistan. *Acta Trop.* **185**, 42–45 (2018).
12. Leykun, B. et al. Occurrence, Risk Factors, and Antimicrobial Susceptibility Test of Thermophilic *Campylobacter* Species of Bovine Carcass at Municipal Abattoir and Butcher Shops of Jimma Town, Southwest Ethiopia. *Infection and Drug Resistance*, **14**, 3753–3762. (2021).
13. Chala, G., Eguale, T., Abunna, F., Asrat, D. & Stringer, A. Identification and characterization of *Campylobacter* species in livestock, humans, and water in livestock owning households of peri-urban Addis Ababa, Ethiopia: a one health approach. *Front. Public. Health*. **9** (1), 750551 (2021).
14. Tegegne, H. A. et al. Microbiological safety and hygienic quality of camel meat at abattoir and retail houses in Jigjiga city, Ethiopia. *J. Infect. Dev. Ctries.* **13**(3), 188–194 (2019).
15. Salih, M. D., Junaidu, A. U., Abubakar, M. B., Magaji, A. A. & Mohammed, L. G. Isolation and characterization of *Campylobacter* spp. from Camel (*Camelusdramedarius*) in Sokoto State, Northwestern, Nigeria. *Int. J. Anim. Veterinary Adv.* **1**, 25–27 (2009).
16. Central Statistical Agency (CSA). Federal Democratic Republic of Ethiopia, Central Statistical Agency, Addis Ababa, Ethiopia. Population projection of Ethiopia for the year 2014. 4–38. (2013).
17. Thrusfield, M. *Veterinary Epidemiology* (Wiley, 2018).
18. World Organization for Animal Health (OIE). *Campylobacter jejuni* and *Campylobacter coli*. 1185–1189 in Manual of Diagnostic Tests and Vaccines for Terrestrial Animals. 6th ed., Vol. 2. OIE, Paris, France. (2008).
19. Rahimi, E., Amroabadi, M. A. & Khamesipour, F. Investigation of prevalence of thermotolerant Campylobacter spp. in livestock feces. *Can. J. Anim. Sci.* **97**, 207–213 (2017).
20. Forbes, B. A., Sahm, D. F. & Weissfeld, A. S. Diagnostic microbiology St Louis: Mosby, 288–302. (2007).
21. Hariharan, H., Sharma, S., Chikweto, A., Matthew, V. & DeAllie, C. Antimicrobial drug resistance as determined by the E-test in *Campylobacter jejuni*, *C. coli*, and *C. lari* isolates from the ceca of broiler and layer chickens in Grenada. *Comparative immunology, microbiology and infectious diseases*, 32(1): 21–28. (2009).
22. Clinical and Laboratory Standards Institute (CLSI). M100-ED29: 2019 Performance Standards for Antimicrobial Susceptibility Testing, 29th edn, Wayne, PA. (2019).
23. Platts-Mills, J. A. et al. Detection of Campylobacter in stool and determination of significance by culture, enzyme immunoassay, and PCR in developing countries. *J. Clin. Microbiol.* **52**, 1074–1080 (2014).
24. Deblais, L. et al. *Prevalence and Load of the Campylobacter Genus in Infants and Associated Household Contacts in Rural Eastern Ethiopia: A Longitudinal Study from the Campylobacter Genomics and Environmental Enteric Dysfunction (CAGED) Project*891–16 (Public and Environmental Health Microbiology, 2023). 7.
25. Debelo, M., Mohammed, N., Tiruneh, A. & Tolosa, T. Isolation, identification and antibiotic resistance profile of thermophilic *Campylobacter* species from Bovine, knives and personnel at Jimma Town Abattoir, Ethiopia. *Plos One*. **17** (10), 1217 (2022).

26. Hagos, Y. et al. Isolation, identification, and antimicrobial susceptibility pattern of *Campylobacter jejuni* and *Campylobacter coli* from cattle, goat, and chicken meats in Mekelle, Ethiopia. *PloS One*. **16** (2), 246 (2021).
27. Seble, H. Prevalence, associated risk factors and antimicrobial susceptibility pattern of thermophilic *Campylobacter* spp. of ovine carcass at Addis Ababa abattoir enterprise, Ethiopia. Addis Ababa university, college of agriculture and veterinary medicine department of microbiology, immunology and veterinary public health, pp 1–36. (2014).
28. Sabzmeydani Ali, Rahimi, E. & Amir Shakerian Incidence and Antibiotic Resistance Properties of *Campylobacter* species isolated from Poultry Meat. *Int. J. Enteric Pathogen*. **8** (2), 60–65 (2020).
29. Shafiei, A., Rahimi, E. & Shakerian, A. Prevalence, virulence, and Antimicrobial Resistance of *Campylobacter* species isolated from carcasses of camels slaughtered in slaughterhouses of Chaharmahal and Bakhtiari Province. *Epidemiol. Health Syst. J.* **8** (3), 115–121 (2021).
30. Wagenaar, J. A., French, N. P. & Havelaar, A. H. Preventing *Campylobacter* at the source: why is it so difficult? *Clin. Infect. Disease*. **57** (11), 1600–1606 (2013).
31. Shakir, Z., Alhatami, A. O., Ismail, K. Y. & Muhsen, A. H. Antibiotic Resistance Profile and multiple antibiotic resistance index of *Campylobacter* species isolated from Poultry. *Arch. Razi Inst.* **76** (6), 1707–1716 (2021).
32. Wilkinson, D. A. et al. Updating the genomic taxonomy and epidemiology of *Campylobacter hyointestinalis*. *Sci. Rep.* **8** (1), 2393 (2018).
33. Kassa, T., Gebre-Selassie, S. & Asrat, D. Antimicrobial susceptibility patterns of thermotolerant *Campylobacter* strains isolated from food animals in Ethiopia. *Vet. Microbiol.* **17** (1), 82–87 (2007).
34. Dadi, L. & Asrat, D. Prevalence and antimicrobial susceptibility profiles of thermotolerant *Campylobacter* strains in retail raw meat products in Ethiopia. *Ethiop. J. Health Dev.* **22** (2), 1–7 (2009).

Acknowledgements

We would like to acknowledge Haramaya University for the financial support we provided and for providing the material for this research. We are grateful to the Haramaya University central lab for giving permission to perform the lab work. We would like to thank Ms. Amanda Ojeda from University of Florida for bringing us lab consumables for Campylobacter isolation. We greatly acknowledge all abattoir workers who participated in this study.

Author contributions

MY proposed and designed the research idea. MY, JK, TW, and YT outlined the research and designed the methodology. MB and JK carried out the sample collection, performed the laboratory work, and analyzed and interpreted the data. JK prepared the first draft of the manuscript for publication. MY, JK, and TW reviewed the final version of the manuscript. YT was involved in providing laboratory consumables. All the authors read and approved the final version of the manuscript.

Funding

The work was funded by the Haramaya University Office of Research and Community Engagement under a regular research grant with the grant code HURG-2020-01-01-52.

Declarations

Competing interests

The authors declare no competing interests.

Additional information

Correspondence and requests for materials should be addressed to J.K.