Occurrence and Antimicrobial Resistance Profiles of Campylobacter jejuni, Campylobacter coli, and Campylobacter upsaliensis in Beef Cattle on Cow–Calf Operations in South Africa

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Abstract

This study investigated occurrence and antimicrobial resistance profiles of *Campylobacter* spp. isolates in beef cattle on five cow–calf operations in South Africa. A total of 537 fecal samples from adult beef cattle ($n = 435$) and rectal swabs from calves ($n = 102$) were screened for *Campylobacter jejuni*, *Campylobacter coli*, and *Campylobacter upsaliensis* by culture and polymerase chain reaction. Furthermore, 86 *Campylobacter* spp. isolates including 46 *C. jejuni*, 2 4 *C. coli*, and 16 *C. upsaliensis* were tested for antimicrobial resistance against a panel of 9 antimicrobials. Overall, *Campylobacter* spp. was detected in 29.7% of cattle. Among the 158 *Campylobacter* spp.-positive cattle, 61.8% carried *C. jejuni*, 25% carried *C. coli*, and 10% carried *C. upsaliensis*. Five animals (3.1%) had mixed infections: three cows carried *C. jejuni* and *C. coli* concurrently, one cow had both *C. jejuni* and *C. upsaliensis*, and one cow harbored *C. coli* and *C. upsaliensis*. Antimicrobial resistance profiling among 86 *Campylobacter* spp. isolates revealed that 52.3% of the isolates were resistant to one or more antimicrobials. Antimicrobial resistance was observed in 46.7% of *C. jejuni* isolates, 35.6% of *C. coli*, and 17.8% of *C. upsaliensis*. Thirty-six percent of isolates were resistant to clindamycin, 19.7% to nalidixic acid, 18.6% to tetracycline, and 17.4% to erythromycin. Lower resistance rates were recorded for azithromycin (8.1%), florfenicol (3.4%), gentamicin (4.8%), and telithromycin and ciprofloxacin (5.8%). Multidrug resistance (MDR) was observed in 32.5% of isolates. Significantly higher levels of MDR were detected among *C. jejuni* (36.9%) and *C. coli* (33.3%) isolates in comparison to *C. upsaliensis* (18.7%). Two main multiresistance patterns were detected: nalidixic acid/clindamycin (17.8%) and tetracycline/clindamycin (14.2%). To the best of our knowledge, this is the first study which has shown that beef cattle on cow–calf operations in South Africa constitute an important reservoir and a potential source of clinically relevant and antimicrobial resistant *Campylobacter* spp. strains.

Keywords: *Campylobacter* spp., beef cattle, antimicrobial resistance, South Africa

Introduction

Campylobacter spp. is the leading cause of foodborne bacterial gastroenteritis globally (World Health Organization, 2012; EFSA, 2018). *Campylobacter jejuni* and *Campylobacter coli* are the most common species of public health or clinical importance (Man, 2011). In addition, *Campylobacter upsaliensis* has also emerged in humans but to a lesser extent (Lynch *et al.*, 2011; Couturier *et al.*, 2012).

Cattle are an important reservoir and cattle products are a potential source of *Campylobacter* spp. for humans (Stanley and Jones, 2003; Inglis *et al.*, 2004; Thépault *et al.*, 2018). Human foodborne *Campylobacter* spp. has been associated with transmission from cattle to consumption of food or water contaminated with animal feces and/or contact with infected animals (Fernández and Hitschfeld, 2009; Wieczorek *et al.*, 2013; El-Zamkan and Hameed, 2016). In Africa, a few reports have detected *Campylobacter* spp. in raw cow milk and other dairy products (El-Zamkan and Hameed, 2016; Kashoma *et al.*, 2016).

Campylobacter gastroenteritis is usually self-limiting in humans while severe cases and other extraintestinal complications including bacteremia and septic arthritis may need treatment with antimicrobials. However, the misuse and abuse of antimicrobials in clinical medicine and animal husbandry exert selective pressure on pathogenic bacteria including *Campylobacter* spp. Antimicrobial selective pressure facilitates survival and emergence of antimicrobial resistant *Campylobacter* spp. (Chang *et al.*, 2015). Consequently, antimicrobial resistant *Campylobacter* spp. strains have emerged worldwide and this can lead to treatment failure in humans and animals. Particularly, resistance to macrolides (erythromycin) and fluoroquinolones (ciprofloxacin), which are considered antimicrobials of choice in the treatment of human Campylobacteriosis, has emerged among animal and human *Campylobacter* spp. isolates (González-Hein *et al.*, 2013; Webb *et al.*, 2018).

Although *Campylobacter* is a recognized zoonotic foodborne pathogen in industrialized countries, in developing countries including South Africa, current studies on the prevalence and antimicrobial resistance patterns of *Campylobacter* spp. from cattle remain scanty (Platts-Mills and Kosek, 2014). This study investigated occurrence and antimicrobial resistance profiles of *C. jejuni*, *C. coli*, and *C. upsaliensis* in beef cattle on five cow–calf operations in South Africa.

Materials and Methods

Sample source

This study was conducted on five cow–calf operations in the Gauteng and North West provinces of South Africa. The cow–calf operations supply calves to feedlots and are routinely serviced by the Onderstepoort Veterinary Animal Hospital. Only cow–calf operations consisting of more than 20 cows/heifers on which animals were maintained on grazing pasture throughout the year were considered for the study.

Sample collection

A total of 537 fresh fecal samples including 453 from adult cows and 102 from calves were collected. Fresh rectal fecal samples were obtained from adult cows and heifers during routine pregnancy diagnosis checks using a new plastic examination glove for each animal. Rectal swabs were used to collect fecal samples from calves. Fecal samples were placed in sterile specimen bottles, transported on ice to the laboratory, stored at 4°C, and processed in the next 24 h. Each herd was visited once. Cattle herds were designated using alphabetical letters: farm A ($n = 65$), farm B ($n = 102$ calves), farm C ($n = 76$), farm D ($n = 181$), and farm E ($n = 113$) from Gauteng and North West provinces in South Africa. Farms A, B, and C were located in Gauteng and farms C and D in North West province.

Campylobacter *spp. isolation and identification*

Campylobacter spp. were cultured, isolated, and identified according to Karama *et al.* (2019). Briefly, fecal swabs were spread on Campy CVA agar (Becton Dickinson and Company) plates and incubated in a microaerophilic atmosphere at 37°C for 48–72 h. Bacterial colony sweeps were harvested from Campy CVA agar plates showing growth. DNA was extracted from colony sweeps by the boiling method (Karama *et al.*, 2019). Multiplex polymerase chain reaction (PCR) was used to screen DNA for *C. jejuni*, *C. coli* (Forbes and Horne, 2009), and *C. upsaliensis* (Klena *et al.*, 2004). PCR primers are described in Table 1. *C. jejuni* ATCC 33560, *C. coli* ATCC 33559, and an in-house *C. upsaliensis* dog isolate (Karama *et al.*, 2019) were used as positive controls in PCRs. Campy CVA agar plates that were positive for *C. jejuni*, *C. coli*, and/or *C. upsaliensis* on initial PCR screening were streaked on horse blood agar plates and incubated at 37°C for 48–72 h to obtain single colonies. At least, three suspect *Campylobacter* spp. colonies were obtained from each horse blood agar plate and multiplied separately on horse blood agar for purification. Once again, DNA was extracted from purified single colony bacterial sweeps by the boiling method and screened for *C. jejuni*, *C. coli* (Forbes and Horne, 2009), and *C. upsaliensis* (Klena *et al.*, 2004) by multiplex PCR. Confirmed *C. jejuni*, *C. coli*, and *C. upsaliensis* isolates were stored at −80°C until further processing.

Table 1. Oligonucleotide Primers Used in This Study

Primers	*Sequence (5′–3′)*	*References*
lpxAC.*jejuni* (forward)	ACAACTTGGTGACGATGTTGTA	Klena *et al.* (2004)
lpxAC.*coli* (forward)	GATAGTAGACAAATAAGAGAGAATMAG	Forbes and Horne (2009)
lpxAC.*upsaliensis* (forward)	AAGTCGTATATTTTCYTACGCTTGTGTG	Klena *et al.* (2004)
lpxAR1 (reverse)	CAATCATGTGCGATATGACAATAYGCCAT	Forbes and Horne (2009)
lpxAR2 (reverse)	CAATCATGAGCAATATGACAATAAGCCAT	Forbes and Horne (2009)
lpxARKK2m (reverse)	CAATCATGDGCDATATGASAATAHGCCAT	Klena *et al.* (2004)

Antimicrobial susceptibility testing by the broth microdilution method

A total of 86 *Campylobacter* spp. isolates (1 isolate per animal) including 46 *C. jejuni*, 24 *C. coli*, and 16 *C. upsaliensis* were tested for resistance against a panel of 9 antimicrobials including ciprofloxacin, nalidixic acid, azithromycin, erythromycin, tetracycline, florfenicol, telithromycin, clindamycin, and gentamicin by the broth microdilution method (CLSI, 2015). Sensititre™ *Campylobacter* minimum inhibitory concentration (MIC) plates (Sensititre; TREK Diagnostic Systems Ltd.) were used for antimicrobial resistance testing according to the manufacturer's instructions. *C. jejuni* ATCC 33560 and *C. coli* ATCC 33559 were used as control strains. MICs were read visually using a VetMIC-Reading Mirror (Statens Serum Institute). MIC breakpoints for azithromycin, ciprofloxacin, erythromycin, gentamicin, tetracycline, and nalidixic acid were evaluated according to the Clinical and Laboratory Standards Institute (CLSI, 2015) interpretive criteria. However, florfenicol, telithromycin, and clindamycin MIC breakpoints were interpreted using the National Antimicrobial Resistance Monitoring System (NARMS, 2006) interpretive criteria for enteric bacteria. Initially, each isolate was assigned to the susceptible (S), intermediate, or resistant category. However, in the final interpretation of antimicrobial susceptibility results, intermediate readings were assigned to the resistant (R) category. Multidrug resistance (MDR) was defined as resistance to two or more classes of antimicrobials.

Statistical analysis

Data were summarized and described using percentages in Microsoft Excel spreadsheets. The Fisher's exact test was used to determine statistical differences between the prevalence rates of *Campylobacter* spp. in the two provinces surveyed. The chi-square test was used to determine whether there were statistical differences among the prevalence rates of *C. jejuni*, *C. coli*, and *C. upsaliensis*. A p value ≤ 0.05 was considered statistically significant. The sample size for this study was calculated based on convenient sampling approach. Fecal samples were collected from all cattle that were screened for pregnancy diagnosis. However, to adjust for the clustering effect (intra-cluster) in the cattle herds surveyed, the 95% confidence interval was calculated by taking into account the cluster size and assuming an intra-class correlation coefficient of 0.1 using the formulas by Dohoo *et al.* (2003). Statistical analysis was performed using R software (R Foundation for Statistical Computing, 2017, Vienna, Austria; http://www.R-project.org/).

Results

Occurrence of Campylobacter *spp. in beef cattle*

Of the 537 cattle fecal samples tested, PCR revealed that 29.4% (158/537; 95% confidence interval: 16.23–42.57%) of cattle carried *Campylobacter* spp., of which 62.6% (99/158) were identified as *C. jejuni* subsp. *jejuni*, 25.3% (40/158) as *C. coli*, and 10.1% (16/158) as *C. upsaliensis* (Fig. 1). Mixed infections were observed in 3.1% (5/158) of cattle, including three cows that carried both *C. jejuni* and *C. coli*, one cow was *C. jejuni* and *C. upsaliensis* positive, and one cow had *C. coli* and *C. upsaliensis* (Fig. 1). The difference between the prevalence of *C. jejuni*, *C. coli*, and *C. upsaliensis* was statistically significant ($p < 2.2 \times 10^{-16}$). Furthermore, significant differences were detected between the prevalence of *C. jejuni–C. coli* ($p = 4.92 \times 10^{-11}$), *C. jejuni–C. upsaliensis* ($p < 2.2 \times 10^{-16}$), and that of *C. coli–C. upsaliensis* ($p = 7.031 \times 10^{-4}$).

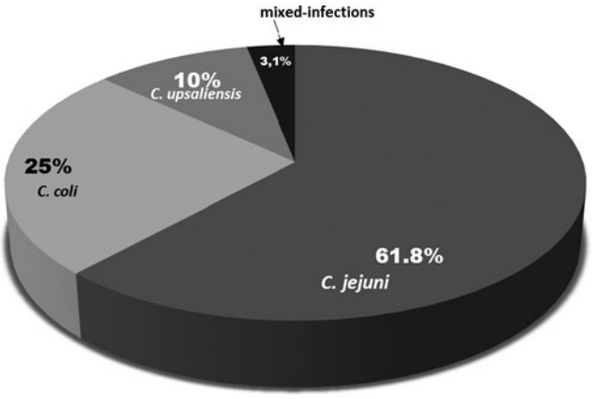

FIG. 1. Distribution of different *Campylobacter* spp. in cattle.

Distribution of Campylobacter *spp. in cattle and calves on different farms*

Of the 435 adult cows, 33.8% (147/435) harbored *Campylobacter* spp. Among the 147 *Campylobacter* spp.-positive animals, 61.2% (90/147) carried *C. jejuni*, 27.2% (40/147) *C. coli*, and 9.5% (14/147) *C. upsaliensis*. Of the 102 calves tested, 10.8% (11/102) carried *Campylobacter* spp., including 81.8% (9/11) which had *C. jejuni* and 18.1% (2/11) which carried *C. upsaliensis*. *C. coli* was not detected in calves. The overall prevalence of *Campylobacter* spp. on farm A was 32.3% (21/65). On farms B and C, *Campylobacter* spp. was detected in 10.8% (11/102) of calves and 53.9% (41/76) of cattle. On farms D and E, 53.9% (41/76) and 19.5% (22/113) of cattle were contaminated with *Campylobacter* spp., respectively. The distribution of different species of *Campylobacter* by farm is depicted in Table 2.

Antimicrobial resistance profiles of Campylobacter *isolates*

Broth microdilution was carried out to determine the antimicrobial resistance profiles of 86 confirmed *Campylobacter* isolates including 46 *C. jejuni* subsp. *jejuni*, 24 *C. coli*, and 16 *C. upsaliensis*. Overall, 52.3% (45/86) of the tested *Campylobacter* spp. isolates were resistant to one or more antimicrobials (Table 3). Among the 45 antimicrobial resistant isolates, 46.7% (21/45) were *C. jejuni*, 35.6% (16/45) as *C. coli*, and 17.8% (8/45) as *C. upsaliensis*.

Of the 46 *C. jejuni* isolates, 32.6% (15/46) were resistant to clindamycin, 19.5% (9/46) to nalidixic acid, 17.3% (8/46) to tetracycline, and 15.2% (7/46) to erythromycin. Three *C. jejuni* isolates (6.5%) were resistant to azithromycin and ciprofloxacin, whereas two *C. jejuni* isolates (4.3%) showed resistance to telithromycin. Two *C. jejuni* isolates were each resistant to gentamicin and florfenicol, respectively (Table 3). Among the 24 *C. coli* antimicrobial resistant isolates, which were resistant to one or more antimicrobial

Table 2. Prevalence of *Campylobacter* spp. in Cattle on Cow–Calf Operations in Gauteng and North West Provinces

		Distribution of Campylobacter *spp. among 537 cattle*				
Provinces	*Cow–calf operations*	*Positive cattle (%)*	Campylobacter jejuni *(%)*	Campylobacter coli *(%)*	Campylobacter upsaliensis *(%)*	*Co-infections (%)*
Gauteng	Farm A: $n=65$	21 (32.3)	11 (52.3)	3 (14.3)	4 (19.0)	3 (14.3)
	Farm B: $n=102$ (calves)	11 (10.8)	9 (81.8)	0 (0)	2 (18.1)	0 (0)
	Farm C: $n=76$	41 (53.9)	21 (51.2)	16 (39.0)	4 (9.7)	0 (0)
North West	Farm D: $n=181$	65 (35.9)	46 (70.7)	17 (26.1)	1 (1.5)	1 (1.5)
	Farm E: $n=113$	22 (19.5)	12 (54.5)	4 (18.1)	5 (22.7)	1 (4.5)
Total	$N=537$	160 (29.7)	99/160 (61.8)	40 (25)	16 (10)	5 (3.1)

classes, 50% (12/24) were resistant to clindamycin, 25% (6/24) to nalidixic acid and tetracycline, 20.8% (5/24) to erythromycin, and 12.5% (3/24) to azithromycin and gentamicin. Resistance to ciprofloxacin, florfenicol, and telithromycin was low among the *C. coli* isolates (two isolates for each antimicrobial) (Table 3). Among the 16 antimicrobial resistant *C. upsaliensis* isolates tested, 25% (4/16) were resistant to clindamycin, 18.7% (3/16) to erythromycin, and 12.5% (2/16) to tetracycline and nalidixic acid. Lower resistance levels were observed against azithromycin and telithromycin (one isolate per antimicrobial). None of the *C. upsaliensis* isolates was resistant to ciprofloxacin, gentamicin, and florfenicol (Table 3).

MDR (resistance to two or more antimicrobials classes) was recorded in 32.5% (28/86) of isolates and was more frequent among *C. jejuni*, which showed multiresistance to erythromycin, tetracycline, nalidixic acid, and clindamycin mainly. Of the 46 *C. jejuni* isolates tested, 36.9% (17/46) were multiresistant (resistant to 2 or more antimicrobials classes): 19.5% (9/46) were resistant to 3 antimicrobials, 13.0% (6/46) were resistant to 4 antimicrobials. One *C. jejuni* isolate, 2.1% (1/46) was resistant to five antimicrobials and another isolate showed resistance to six antimicrobials including azithromycin, erythromycin, tetracycline, nalidixic acid, telithromycin, and clindamycin. Among *C. coli* isolates, 33.3% (8/24) were multiresistant, 12.5% (5/24) were resistant to two antimicrobials, one was resistant to four antimicrobials, and two isolates (8.3%) were resistant to all nine antimicrobials tested. *C. coli* isolates (50%; 4/8) were mainly multiresistant against clindamycin+tetracycline+nalidixic acid. Among *C. upsaliensis* isolates, only three isolates (3/16; 18.7%) displayed MDR to three antimicrobial agents each.

Discussion

Campylobacter spp. occurrence rates in healthy cattle are variable and can range from 5.3% to 78.5% in different countries (Rahimi and Tajbakhsh, 2008; Ramonaitė *et al.*, 2013; Wieczorek *et al.*, 2013; Smith *et al.*, 2018). Overall, the prevalence of *Campylobacter* spp. in the beef fecal samples tested in this study was 29.7%, consistent with rates that have been reported in beef cattle in Malaysia (33%) (Premarathne *et al.*, 2017), Chile (35.9%) (Fernández and Hitschfeld, 2009), and Finland (31.1%) (Hakkinen *et al.*, 2007). However, much lower rates of *Campylobacter* spp. have been reported in Ghana (13.2%) (Karikari *et al.*, 2017), Cambodia (5.3%) (Osbjer *et al.*, 2016), and Iran (5.3%) (Rahimi and Tajbakhsh, 2008).

C. jejuni was the most frequent (62.6%) species in beef cattle, followed by *C. coli* (25.3%) and *C. upsaliensis* (10.1%). The predominance of *C. jejuni* over *C. coli* and *C. upsaliensis* in cattle is in agreement with previous reports from South Africa (Uaboi-Egbenni *et al.*, 2012), United States (Cha *et al.*, 2017), Canada (Webb *et al.*, 2018), France (Thépault *et al.*, 2018), and Finland (Hakkinen, 2010). However, some reports from the United States (Sanad *et al.*, 2012; Smith *et al.*, 2018) and Ghana (Karikari *et al.*, 2017) showed that *C. coli* was the most frequent species in cattle samples.

C. upsaliensis was detected in 10.1% of beef cattle. The occurrence of *C. upsaliensis* in 10.1% of beef cattle was of particular interest, as this emerging and clinically important *Campylobacter* spp. is not commonly detected in cattle but mainly found in dogs (Acke, 2018). Similar studies that have searched for *C. upsaliensis* in Ghana and Lithuania did not detect *C. upsaliensis* in cattle (Ramonaitė *et al.*, 2013;

Table 3. Antimicrobial Resistance in *Campylobacter jejuni*, *Campylobacter coli*, and *Campylobacter upsaliensis*

Antimicrobials	Campylobacter jejuni, n=*46 (%)*	Campylobacter coli, n=*24 (%)*	C. upsaliensis, n=*16 (%)*	*Total* Campylobacter *spp.,* N=*86 (%)*
Azithromycin	3 (6.5)	3 (12.5)	1 (6.2)	7 (8.1)
Ciprofloxacin	3 (6.5)	2 (8.3)	0 (0)	5 (5.8)
Erythromycin	7 (15.2)	5 (20.8)	3 (18.7)	15 (17.4)
Gentamicin	1 (2.1)	3 (12.5)	0 (0)	4 (4.6)
Tetracycline	8 (17.3)	6 (25)	2 (12.5)	16 (18.6)
Florfenicol	1 (2.1)	2 (8.3)	0 (0)	3 (3.4)
Nalidixic acid	9 (19.5)	6 (25)	2 (12.5)	17 (19.7)
Telithromycin	2 (4.3)	2 (8.3)	1 (6.2)	5 (5.8)
Clindamycin	15 (32.6)	12 (50)	4 (25)	31 (36.0)

Karikari *et al.*, 2017). In addition to mild gastroenteritis, *C. upsaliensis* has been incriminated in bloody diarrhea and extraintestinal infections including bacteremia in debilitated and immunocompromised patients, spontaneous abortion, hemolytic uremic syndrome, and Guillain–Barre syndrome in humans (Bourke *et al.*, 1998; Couturier *et al.*, 2012). The occurrence of *C. upsaliensis* in the cattle may point toward the presence of a dog reservoir, which may be acting as a source of *Campylobacter* spp. for cattle on the farms, which were surveyed. However, further investigations will be needed to evaluate to what extent cattle constitute a reservoir of less common but clinically relevant *Campylobacter* spp. such as *C. upsaliensis*.

The prevalence of *Campylobacter* spp. in calves was low (6.9%), in contrast to studies that have reported higher rates of *Campylobacter* spp. in calves in France (99.4%) and Lithuania (86.5%) (Ramonaitė *et al.*, 2013; Thépault *et al.*, 2018). The low rate of *Campylobacter* spp. in calves in this study is in agreement with similar reports from Austria (14.9%) and Algeria (14.0%) (Klein *et al.*, 2013; Guessoum *et al.*, 2016). However, it should be noted that calves were tested on one farm only, and the number of samples tested was not representative to conclusively explain differences between the proportions of *Campylobacter* spp. found in calves in this study and the aforementioned reports from other countries. The expectation is that calves should have higher *Campylobacter* spp. rates, as they are more susceptible to *Campylobacter* spp. colonization because of a weak immune system (Klein *et al.*, 2013). However, the low prevalence of *Campylobacter* spp. in calves in this study shows that *Campylobacter* spp. carriage levels in calves may not only be dependent on a weak immune system but also on other factors that still remain to be identified.

Antimicrobial resistance profiling revealed that 52.3% of *Campylobacter* isolates were resistant to one or more antimicrobial agents. Low rates of antimicrobial resistance were detected in this study in comparison to *Campylobacter* spp. resistance levels that have been reported in beef cattle in the United States (83.7%), France (64.6%), and Poland (65.4%) (Chatre *et al.*, 2010; Wieczorek *et al.*, 2013; Cha *et al.*, 2017). The low antimicrobial resistance rates observed in this study may be ascribed to the fact that the cattle herds which were surveyed were fed on grazing pasture all year round with no exposure to antimicrobials that exert selective pressure on bacteria and facilitate the survival of resistant *Campylobacter* spp.

Among the nine antimicrobials tested, the highest resistance rate was recorded for clindamycin (36%). Resistance to clindamycin was mostly observed among *C. coli* (50%), followed by *C. jejuni* (32.6%) and *C. upsaliensis* (25%). High resistance to clindamycin was in contrast to reports from Canada and the United States, which have documented much lower proportions of *Campylobacter* spp. isolates that were resistant to clindamycin (Cha *et al.*, 2017; Tang *et al.*, 2017; Webb *et al.*, 2018).

Lower resistance levels were recorded for nalidixic acid (19.7%), tetracycline (18.6%), and erythromycin (17.4%) in *C. coli* isolates mainly, consistent with previous reports from the United States, Malaysia, Iran, and Japan (Rahimi and Tajbakhsh, 2008; Haruna *et al.*, 2013; Cha *et al.*, 2017; Premarathne *et al.*, 2017; Tang *et al.*, 2017). However, much higher resistance rates to nalidixic acid (70.4%), tetracycline (51.4%), and erythromycin (up to 97%) have been previously recorded in France, Poland, and Ghana, respectively, mainly among *C. coli* isolates (Chatre *et al.*, 2010; Wieczorek *et al.*, 2013; Karikari *et al.*, 2017). Resistance to nalidixic acid, tetracycline, and erythromycin is intriguing as these antimicrobials are supposed to be minimally used on cow–calf operations and for therapeutic purposes only.

Very low resistance rates were recorded for azithromycin (8.1%), florfenicol (3.4%), gentamicin (4.8%), and telithromycin and ciprofloxacin (5.8%). Resistance to ciprofloxacin in this study was comparable to that reported in beef cattle isolates in Canada (Webb *et al.*, 2018). However, higher *Campylobacter* resistance rates to ciprofloxacin have been reported previously in *C. jejuni* (33.3%) and *C. coli* (56.3%), which were recovered from dairy cattle in South Africa (Uaboi-Egbenni, 2012).

Resistance against erythromycin and ciprofloxacin is of clinical significance because these antimicrobials are used to treat *Campylobacter*-associated gastroenteritis. A number of surveys have shown that for *C. jejuni* and *C. coli*, there is generally agreement between nalidixic acid and ciprofloxacin, and similarly between erythromycin and azithromycin resistance rates (Englen *et al.*, 2007; Chatre *et al.*, 2010; Rahimi *et al.*, 2010; Wieczorek *et al.*, 2013). However, in this study, no agreement was observed between nalidixic acid and ciprofloxacin, or erythromycin and azithromycin antimicrobial resistance rates, consistent with a few of studies, which have reported similar results (Gormley *et al.*, 2010; Kashoma *et al.*, 2015, 2016). Furthermore, Webb *et al.* (2018) observed that upon arrival at cow feeding operations, there was no agreement between ciprofloxacin and nalidixic acid resistance rates among *C. jejuni* cattle isolates. However, ciprofloxacin and nalidixic acid resistance rates become similar or marginally different only as animals are progressively fed rations supplemented with antimicrobial growth promoters. The absence of selective pressure due to lack of antimicrobial promoters in the diet of the cattle population studied may have precluded the parallel development of resistance against ciprofloxacin and nalidixic acid and perhaps erythromycin and azithromycin among the *Campylobacter* spp. isolates tested.

This study revealed that 35.2% (28/86) of cattle *Campylobacter* isolates were multiresistant. Similar proportions of multiresistant isolates were previously observed among *Campylobacter* spp. isolates, which were recovered from cattle fecal samples (Noormohamed and Fakhr, 2014; Cha *et al.*, 2017; Premarathne *et al.*, 2017; Tang *et al.*, 2017). MDR to nalidixic acid+clindamycin (17.8%) and tetracycline+clindamycin (14.3%) was the most common resistance profile. Multidrug was mostly (60.7%) observed among *C. jejuni* isolates in contrast to other studies that have recorded much higher levels in *C. coli* isolates from cattle (Wieczorek *et al.*, 2013; Okunlade *et al.*, 2015).

Conclusions

To the best of our knowledge, this is the first study that has investigated the occurrence of *Campylobacter* spp. of public health significance in beef cattle in South Africa. The cattle surveyed represent an important reservoir and a potential source of clinically relevant and antimicrobial resistant *Campylobacter* spp. for humans. Data from this study will be

useful for understanding the epidemiology of *Campylobacter* and formulating policies aimed at mitigating human zoonotic foodborne campylobacteriosis.

Disclosure Statement

No competing financial interests exist.

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