

## Risk Factors Associated with Occurrence of Thermophilic *Campylobacter* in Cattle Herds Raised on Integrated Small-Scale Farms in Kajiado County, Kenya

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### ABSTRACT

Integrated farms are small-holder farms that rear a mixture of different food animals in close proximity. Subsequently, a survey was carried out to establish two aspects: (1) occurrence rate of thermophilic *Campylobacter* in cattle in 55 integrated small-scale farms within Kajiado County; a total of 265 cattle rectal swabs were randomly collected for bacterial isolation, and (2) factors associated with *Campylobacter* occurrence; these included administration of pre-tested questionnaires, to collect data on respective farm characteristics and management practices, and isolation of *Campylobacter* from respective water and chicken cloacal swabs (as possible sources of infection). The collected rectal/cloacal swabs and water samples were specifically processed for *Campylobacter* isolation, followed by confirmation using a singleplex polymerase chain reaction (PCR) assay, while the questionnaire data was analyzed using logistic regression models. *Campylobacter* in cattle were detected in 72.7% (95% confidence interval (95% CI) =60.9-84.5) of the surveyed farms. The farm/herd level *Campylobacter* positivity ranged from 12.5% to 100%; 27.3% (95% CI=15.5-39.1) of the surveyed farms were *Campylobacter* negative. Of the *Campylobacter* positive farms, the mean prevalence was 48.14%, with a median of 50%. Farm stocking dairy breeds [adjusted odds ratio (AOR)=12.7, 95% CI: 3.2-60], presence of companion animals in farms that did not co-graze cattle with other ruminants (AOR=10, 95% CI=1.2-95.9), *Campylobacter* positivity in chicken (AOR=5.8, 95% CI=2.2-16.2), presence of donkey (AOR=5.0, 95% CI=1.1-27.4), presence of pigs (AOR=4.9, 95% CI=1.2-23.5), and minimal hygiene of the housing unit (AOR=3.3, 95% CI=0.9-12.6) were associated with *Campylobacter* carriage in cattle. Keeping chicken and other birds irrespective of their *Campylobacter* status appeared to have a “protective” effect (AOR=0.2, 95% CI=0.03-0.6), against *Campylobacter* positivity in cattle. This suggests a complex web of transmission pathways of campylobacters in cattle and the environment. Interventions targeting these factors coupled with stringent biosecurity and sanitary measures are recommended so as to minimize the risk of *Campylobacter* transmission and/or occurrence in cattle environment.

**Key words:** Thermophilic *Campylobacter*, Risk Factors, Management Practices, Biosecurity.

### INTRODUCTION

Global livestock production has drastically changed in the last decade, from subsistence farming to intensive

system. Kajiado County is dominated by pastoralists who were traditionally known to keep mainly herds of cattle in large numbers, among other ruminants. Over the years, these pastoralists have had to encounter a number of

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livelihoods threatening challenges including; climate change, changes in land tenancy and use, population increase, rapid urbanization, globalization, intensification and communal conflicts (Said et al. 2019). Consequently, majority of these farmers are slowly adopting diversified or integrated farming; where they raise manageable herds of cattle alongside other livestock species including poultry alongside numerous farm produce (i.e. integrated crop–livestock farming). More-over, most countries are advocating for diversification of farming systems as a substitute for intensive agriculture, affirming readiness to change to eco-friendly agriculture, in agreement with the United Nations Sustainable Development Goal number 12 (Patterson et al. 2022). Even with diversification, each farm is a unique combination of numerous environmental characteristics that could set baseline conditions for the presence of pathogenic bacteria (Strawn et al. 2019). In addition, farms stocking several species of animals may have different biosecurity barriers in place than those farms that only keep one type of animal species (Ellis-Iversen et al. 2009a). It is also a common practice in some farms to apply raw manure on grazing fields or on fodder crops such as napier grass to improve soil fertility. Application of raw manure can introduce faecal enteropathogens (including *Campylobacter* spp.) thereby contaminating pasture.

Thermotolerant campylobacters are important points of reference for animal and human health research, owing to their zoonotic potential, wide variety of reservoir hosts, and environmental perseverance (for instance survival in water) (Hannon et al. 2009). Natural reservoirs for *Campylobacter* include chicken and other domestic poultry, wild birds, swine, pets, donkey, ruminants, among others (Conrad et al. 2018). Overall, poultry remains the most important reservoir owing to: the high body temperature of chicken of 42°C, which makes their gut ideal niche for optimum growth of campylobacters; and the free-roaming nature of chicken more so under free-range system; this may spread *Campylobacter* through fecal contamination of the environment, pasture, and surface water. More-over, studies have demonstrated that poultry and wild birds are the most important contributors to surface water contamination with campylobacters, followed by ruminants and swine (Mughini-Gras et al. 2016). However, campylobacters survival outside the host body and/or in the environments is generally thought to be poor; with some studies suggesting that the ability to survive may vary with strain (Mustafa 2003; Mulder et al. 2020). Subsequently, surface-water may act as a vehicle of transmission for *Campylobacter* among domestic animals including cattle. This justifies research on myriad potential sources, reservoirs and/or transmission pathways that might be involved in cattle.

Cattle are considered asymptomatic gastro-intestinal carriers (persistent or intermittent) of *Campylobacter* spp, with the carriage ranging from 4% to 89.4% according to a number of studies (Harvey et al. 2004; Häkkinen et al. 2007; Kwan et al. 2008; Fernández and Hirschfeld 2009; Chatre et al. 2010; Wanja et al. 2022). Campylobacters have been reported as primary or secondary causes of clinical gastroenteritis and/or diarrhea in calves (Acha et al. 2004; Klein et al. 2013), septicemic abortion in cows (Bae et al. 2005) and bovine mastitis (Modi et al. 2015).

Apparently healthy bovine may harbour one or more *Campylobacter* species including: *Campylobacter jejuni*, *C. lari*, *C. coli*, *C. hyointestinalis* and *C. fetus* (Salihu et al. 2009). This suggests that both apparently healthy and *Campylobacter*-infected cattle may excrete the organisms in faeces; thereby predisposing other farm animals or humans to infections. Of the human *Campylobacter* infections, *C. jejuni* has been implicated for 90% of cases worldwide (Gillespie et al. 2002). Zoonotic contagion of campylobacters from cows occurs through consumption of unpasteurized milk or beef or direct contact with feces of infected cows. A probable role of cattle in epidemiology of human campylobacteriosis is further asserted by a number of source-attribution studies, where up to 36% of human *C. jejuni* cases are attributed to cattle-derived *C. jejuni* genotypes (Wilson et al. 2008; Mullner et al. 2009; Sheppard et al. 2009). Furthermore, bovine-associated campylobacters also pose an extra indirect human health hazard (Vandeplas et al. 2008). For instance, slurry run-off from cattle facilities may contaminate surface water (river) and ground water (shallow unprotected boreholes) (Sanad et al. 2011). This necessitates need to document on-farm risk factors associated with transmission/occurrence of *Campylobacter* spp. in cattle herds so as to frame suitable and operative control programs in the low-resource settings.

Farm management practices and environment influence occurrence and persistence of campylobacter, which may be crucial for cattle re-infection, and for human infections (An et al. 2018). Even though, farm management and animal health practices have received more attention as risk factors influencing transmission of livestock diseases; there has been relatively less extensive research on risk factors associated with occurrence of campylobacteriosis in livestock, particularly, in developing countries (Uddin et al. 2021). In Kenya especially in Kajiado County, the epidemiology of campylobacters in cattle and the likely transmission dynamics (i.e. the likely sources of contamination and transmission mechanisms) is lacking or not fully understood. Owing to the potential role of cattle in the epidemiology of human campylobacteriosis; there is need to gather epidemiological information in regard to transmission web of campylobacters in cattle. Therefore, this study was undertaken to assess farm characteristics and/or management practices and climatic factors as potential risk factors associated with *Campylobacter* positivity in integrated smallholder cattle herds in Kajiado County. The findings of this study will form a reference point for designing practical solutions.

## MATERIALS AND METHODS

### Ethical Consideration

The study was approved by Biosafety, Animal use and Ethics committee, Faculty of Veterinary Medicine, University of Nairobi (FVM BAUEC/2020/274). Verbal consent was sought from farmers prior to interviewing; where the objectives of the study and their privileges were elaborated in local languages (Maa, Kikuyu and Swahili).

### Study Area and Design

A seasonal based cross-sectional study was carried out between November 2020 and December 2021 among

integrated cattle farms in Kajiado County; particularly in areas of Ongata Rongai, Ngong, Kiserian, Kitengela, Isinya and Mashuru (Fig. 1). The County borders Nairobi, spreads to Tanzania border further South. The study involved fecal (from cattle and chicken) and water sampling; administration of semi-structured questionnaires (to collect potential risk factors), and assessment of hygiene status of cattle environment. Climatic variables were also retrieved from local weather stations and included in the model as environmental factors.

### Inclusion Criteria for Study Farms

There were no official records of farms available to guide the enrolment of farms to be studied in Kajiado County. As such, the study relied on the staff from the county's veterinary department to come up with a list of farms in their area of jurisdiction. Enrolment of integrated small-scale farms was based on: (1) farms primarily rearing  $\geq 200$  heads of cattle, (2) farms rearing multiple species of livestock including poultry. This resulted in an overall sample size of 55 integrated small-scale farms.

### Collection of Cattle Rectal Swabs, Chicken Cloacal Swabs and Water Samples

On each farm visit, cattle rectal, chicken cloacal swabs and water samples (from cattle trough and/or other designated cattle watering points like dam or river) were collected from each of the participating farm. A total of 265 cattle rectal swabs and 142 chicken cloacal specimens were collected from 55 and 38 of the integrated smallholder farms, respectively.

Additionally, a 250mL water sample was collected from cattle troughs (and/or other designated cattle watering points like dam or river). A pooled water sample was collected in case where there were more than one cattle pen with separate water troughs. A total of 50 water samples (42 water samples from privately owned cattle's water troughs in 42 farms, and, 8 water samples from

communal animal watering points being used by 13 farms) was collected.

Individual fecal swabs was aseptically placed in a cap screwed bijou bottle containing Stuart's transport media, labelled accordingly and stored in cool box with ice packs (water samples in sampling bottle were also placed in separate cool box) in the field and stored at 4°C, until testing at the bacteriology laboratory in the Department of Veterinary Pathology, Microbiology and Parasitology.

### Isolation and Identification of Thermophilic *Campylobacter*

Cattle rectal swabs, and chicken cloacal swabs were specifically processed for *Campylobacter* isolation (Hitchins et al. 1998). Individual samples were enriched using 5mL of Bolton broth and incubated for 24 hours at 42°C under aerobic conditions; the bijou bottle containing the broth inoculum was filled leaving minimal air space. For water samples, 100mL volume were filtered through a 0.45µm filter membrane; the filter was then placed in a universal bottle containing 20mL of Bolton enrichment broth for *Campylobacter* without antibiotics. After 3 hours of incubation at 42°C, 0.2mL of a selective supplement (SR 0167E, Oxoid) was added and incubated further.

After 24 hours of incubation, a loopful from the cultured broths was then streaked onto modified charcoal cefoperazone desoxycholate agar (mCCDA) plates with selective supplement added, and incubated at 42°C, under microaerobic conditions. After 48 hours, the inoculated mCCDA plates were visually examined and colony morphology characteristics. Plates that showed no bacterial growth were re-incubated for a further 24 hours under the same conditions; if no growth was seen thereafter, it was indicated negative for thermophilic *Campylobacter*.

Putative *Campylobacter* colonies appeared as: small to medium sized, flat with entire margin, glistening grey to off-white/creamy pigmentation, spreading and sticky appearance. These were further subjected to further tests. The isolates were; Gram negative comma-shaped rods to coccobacilli, oxidase positive and variable catalase activity. Putative *Campylobacter* isolates were confirmed by singleplex PCR using 859bp 16S rRNA primers following standard protocol (Han et al. 2016). Using the enrolled integrated farms as sampling units, a site with at least one PCR-positive cattle/chicken swab isolate and water samples isolate were classified as positive for *Campylobacter*.

### Questionnaire Administration and Assessment of Environmental Hygiene

A pretested semi-structured questionnaire was administered through face-to-face interviews during farm visit; it was themed to collect information on farm characteristics (herd size, breed type, other animals in the farm); management practices (housing, water supply, feeding regime and manure disposal), biosecurity measures in place. The dampness and cleanliness of cattle environment were scored (1=dry and clean, 2=wet and dirty) (Hughes 2001).



**Fig. 1:** A map of Kajiado County showing its location in Kenya and sites where sampling and interviews were conducted.

### Documentation of Climatic Variables

Climatic data [rainfall, daily ambient temperature and relative humidity for the sampling period) was retrieved from Ngong and Wilson Airport weather stations (nearest weather station with similar microclimate as other parts of Kajiado County). Also, FAO's country pasture and forage resource zoning which is based on average annual rainfall, was included as a proxy for the microclimates in Kajiado County (FAO 2006). Only two zones were used to classify the surveyed farms: zone III/semi-humid (800-1400mm) and V/semi-arid (450-900mm).

### Statistical Data Analysis and Model Building

Collected data was entered, validated, and stored in Microsoft Excel spreadsheet. Descriptive and inferential statistics were performed using R software version 4.1. The proportions of categorical-independent variables were stratified into a dichotomous table of *Campylobacter* positivity and negativity groups in cattle herd. Chi-square ( $\chi^2$ ) test of independence was applied to assess for association between independent variables and outcome/dependent variable (*Campylobacter* status in cattle).

All variables with  $P < 0.2$  in the Chi-square tests were used to develop the univariate and multivariate binary logistic regressions. A stepwise regression was applied in the saturated logistic model and two-way interaction of terms tested. The final model was compared to saturated model using likelihood ratio test (LRT) and a  $P < 0.05$  signifying improved performance of model. Akaike Information Criterion (AIC) values for the two models were compared and final model chose only when the value was lower than that of saturated model. Correlated variables were individually added to the model and picked if the overall model performance was enhanced, as measured using the AIC value. In terms of levels within each categorical risk factor, for comparison purposes, the risk factor associated with the least *Campylobacter* spp. positivity was used as a reference. Adjusted OR that considered all cofounder variables were calculated, and confidence intervals (CIs). Odds ratio significance was computed using the Wald's test. A 5% level of significance was used.

## RESULTS

### Characteristics of Farms Surveyed

Fifty-five small-scale farms were enrolled in this study and were located in six regions of Kajiado County: Kitengela (n=4), Isinya (n=4), Kiserian (n=7), Ongata Rongai (n=9), Mashuru (n=13) and Ngong (n=18). Sixteen farms practiced beef keeping (mainly Borana, Sahiwal and their crosses) under settled outdoor grazing or transhumant pastoral systems. The rest practiced dairy farming (mainly Friesian and their crosses, some Ayrshire and Jersey) under zero grazing unit. Forty-two percent of the farmers kept between 1 and 10 heads, whereas the rest owned more than 10 heads of cattle. Free range and backyard chicken farming was a common practice in most of the farms surveyed. Seventeen of the 55 farms (30.9%, 95%CI=18.7-43.1) raised cattle and small ruminants only, while the rest raised a combination of poultry and livestock (mainly cattle co-reared with either goats or sheep). The main sources of cattle drinking water were

untreated borehole water at 81.8% (95%CI=71.6-92.0), followed by treated tap water at 10.9% (95%CI=2.7-19.1), dams and/or groundwater and seasonal river water were used at 5.5% (95%CI=-0.5-11.5) and 1.8% (95%CI=-1.7-5.3) respectively. Thirty-four-point five percent (95%CI=21.9-47.1) of the farms shared the source water with animals from other farms (Fig. 2).

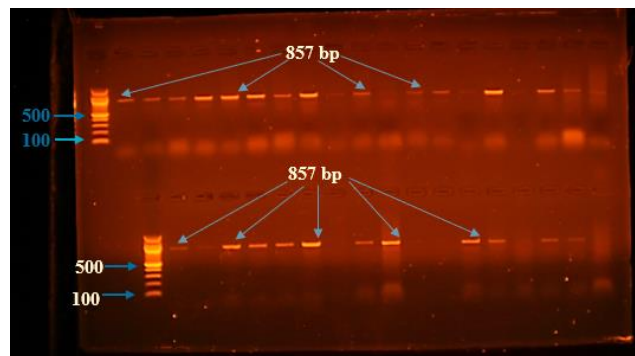
### Thermophilic *Campylobacter* Status in Cattle Herds

Putative *Campylobacter* isolates presented a specific amplification of 857bp primer via a genus-specific (16S rRNA gene) polymerase chain reaction (PCR) (Fig. 3).

Farm- and/or herd-level prevalence of *Campylobacter* spp. was 72.7% (95%CI=60.9-84.5) representing 72.2% (95%CI=51.5-92.9) and 73% (95%CI=58.7-87.3) in the agroecological zone III (Ngong region) and agroecological zone V (Mashuru, Kitengela, Rongai, Isinya and Kiserian), respectively. However, there was no significant difference in the farm/herd-level positivity of *Campylobacter* among the zones ( $P > 0.05$ ). The proportion of positive samples within each surveyed farm ranged between 12.5% and 100%. However, samples from 27.27% (95%CI=15.5-39.1) of the surveyed farms were *Campylobacter* negative. The 72.73% *Campylobacter* positive farms had a mean prevalence was 48.14% and a median of 50%.



**Fig. 2:** A communal (shared) animal watering point “oltinka” with cattle co-grazing with other animals. Note some animals are drinking ground water



**Fig. 3:** Agarose gel electrophoresis visualization of amplification of 857bp 16S rRNA gene for genus *Campylobacter* identification. M: DNA ladder, where each band represents 100bp.

### Thermophilic *Campylobacter* Status in Chickens and Water Sample

Among the 38 farms that kept chicken, 28 were found to be positive with *Campylobacter* spp. overall via PCR. Therefore, a flock-/farm-level prevalence was confirmed as 73.7% (95% CI=59.7–87.7%). Of the 28-*Campylobacter* positive farms, the prevalence ranged between 20% and 100%; with a mean and median of 61% and 55% respectively. On the other hand, *Campylobacter* was detected in 17 water samples, which represented 87.5% (95%CI=64.5-110.4) and 23.8% (95%CI=10.9-36.7) in the communal watering points and privately-owned cattle's water trough, respectively. There was a significant variation observed in the water-level *Campylobacter* spp (P=0.000). Water samples from borehole had the highest level of *Campylobacter* positivity at 36.4% (95%CI=22.2-50.6), followed by treated tap water at 50% (95%CI=-19.3-119.3). Water samples obtained from both dams and/or groundwater and seasonal river were *Campylobacter* negative.

### Climatic Variables Assessed for the Participating Farms

The mean and range of selected continuous variables assessed for the participating farms over the sampling period were as shown in Table 1. The mean of daily maximum temperature, daily minimum temperature, humidity and amount of rainfall were statistically indifferent across the seasons and agro-ecological zones i.e. there was minimal variations in terms of seasonal and agro-ecological zones.

### Questionnaire Data (independent variables) and Association with *Campylobacter* Positivity in Cattle Herds

Farm characteristics and management practices, and *Campylobacter* status of chicken and water samples for the given farm were then included in the model as potential risk factors (independent variables). From the data of the questionnaire and the results of statistical analysis, 17 of the 23 factors tested showed significant associations with *Campylobacter* positivity in cattle in the surveyed farms (Chi-square; P<0.05) (Table 2).

### Univariate and Multivariate Logistic Regression Models

A number of risk factor covariates were considered in both unadjusted/crude (univariate logistic) and adjusted (multivariate logistic) models as tabulated in Table 3.

Several risk factors were found to have significant association with *Campylobacter* positivity in cattle in the unadjusted or univariate logistic regression model. These included: cattle breeds [crude odds ratio (COR)=3.8, 95%CI=2.1–7.1]; *Campylobacter* positivity in chicken (presence of chicken harboring *Campylobacter* spp.) (COR=3.0, 95%CI=1.8–5.3); *Campylobacter* positivity in water (cattle drinking water contaminated with *Campylobacter* spp.) (COR=0.6, 95%CI=0.3–1.0); brought new stock without isolation (COR=3.9, 95%CI=1.5–11.0); keeping small ruminants in the farm (COR=0.5, 95%CI=0.3–0.9); presence of donkeys (COR=0.4, 95%CI=0.2–0.8), presence of pigs (COR=3.2, 95%CI=1.4–7.1); keeping chicken and other birds irrespective of their *Campylobacter* status (COR=2.5, 95%CI=1.4–4.6); co-grazing cattle with other ruminants (COR=0.4, 95%CI=0.2–0.7); housing unit (feed store and feed trough) accessible to rodents and wild birds (COR=2.6, 95%CI=1.5–4.9); condition and hygiene status of the enclosure (COR=3.2, 95%CI=1.8–5.6); histories of diarrhea, abortion and mastitis in the last 6 months (COR=1.9, 95%CI=1.1–3.4); and feeding cattle on poultry litter and/or leftovers (COR=2.2, 95%CI=1.0–4.6).

In the adjusted (multivariate logistic) model, *Campylobacter* positivity in chicken (presence chicken harboring *Campylobacter* spp.) increased the odds of *Campylobacter* positivity in cattle by 5.8 times (95%CI=2.2–16.2). Keeping chicken and other birds irrespective of their *Campylobacter* status offered 80% protective effect to *Campylobacter* positivity in cattle [adjusted odds ratio (AOR)=0.2, 95%CI=0.03–0.6]. Presence of multiple animals in the farm seemed to increase the odds of *Campylobacter* positivity in cattle, with the highest exposure seen in farms stocking dairy cattle breeds (AOR=12.7; 95%CI=3.2–60.0). The presence of donkeys (AOR=5, 95%CI=1.1–27.4) and pigs (AOR=4.9, 95%CI=1.2–23.5) were also individually associated with increased odds of acquiring *Campylobacter* by 5 times, as compared to farms that neither kept donkeys nor pigs. The condition and hygiene status of the enclosure recorded a significant association at 10% level of significance; with 3.3 odds of exposure of outcome in the wet and dry category compared to the moderately dry category (95%CI=0.9–12.6).

There was a significant interaction between farms that kept companion animals and did not co-graze cattle with other ruminants, modifying the odds of acquisition of *Campylobacter* in cattle by 10 times (95%CI=1.2–95.9). The wide confidence intervals can be attributed to the low sample size in this category.

**Table 1:** Range and mean±SEM of selected climatic variables assessed for model building and retrieved from local weather stations on in Kajiado County

Zone	Climatic variables	Warm-dry season		Wet-rainy season	
		Range	Mean±SEM	Range	Mean±SEM
ACZ	Rainfall (mm)	1.83–53.60	17.10±4.71	18.7–305.4	122.20±19.28
III	Daily maximum temperature (°C)	19.39–27.57	22.54±0.82	21.35–25.20	23.39 ± 0.27
	Daily minimum temperature (°C)	10.94–14.46	12.08±0.34	12.88–14.83	13.73 ± 0.15
	Relative humidity (%)	47.68–65.00	55.86±2.22	42.30–69.57	54.51 ± 2.20
ACZ V	Rainfall (mm)	0.03–4.18	1.97±0.64	1.11–13.38	7.88 ± 1.48
	Daily minimum temperature (°C)	21.71–27.16	24.63±0.80	24.03–27.36	25.94 ± 0.36
	Daily maximum temperature (°C)	13.32–15.42	14.27±0.30	15.74–16.73	16.23 ± 0.11
	Relative humidity (%)	M	M	M	M

<sup>a</sup>FAO's agroecological zones (ACZ) were used to categorize participating farms: ACZ III or semi-humid region (800-1400mm annual rainfall) and ACZ V or semi-arid (450-900mm annual rainfall); M=Missing data.

**Table 2:** Dichotomous analysis for selected categorical variables stratified by thermophilic *Campylobacter* status of 265 rectal swabs collected from cattle in 55 small-scale farms in Kajiado County

Variable	Modality	Thermophilic <i>Campylobacter</i> positivity (%)	Thermophilic <i>Campylobacter</i> negativity (%)	95% CI		P Value	Chi-square value (df=1)
				Lower	Upper		
Geographical location of the farm in Kajiado County based on FAO's climate zones <sup>a</sup>	ACZ III	29 (39.2)	45 (60.8)	0.338	1.060	0.078	3.20
	ACZ IV	53 (27.7)	138 (72.3)				
Sampling season	Wet rainy season	49 (40.8)	71 (59.2)	1.138	3.99	0.002 <sup>b</sup>	10.04
	Dry-warm season	33 (22.8)	112 (77.2)				
Farm herd size	≤ 10 animals	62 (32.1)	131 (67.9)	0.677	2.237	0.496	0.47
	≥ 10	20 (27.8)	52 (72.2)				
Cattle breed	Dairy	64 (42.1)	88 (57.9)	2.111	6.980	0.000 <sup>b</sup>	21.87
	Beef	18 (15.9)	95 (84.1)				
Cattle grazing system	Indoor/confined (zero grazing)	62 (44.3)	78 (55.7)	0.134	0.429	0.000 <sup>b</sup>	25.72
	Free-roaming grazing system	20 (16.0)	105 (84.0)				
Cattle housing and/or enclosure type	Mixed housing	50 (28.6)	125 (71.4)	0.422	1.246	0.245	1.34
	Group housing	32 (35.6)	58 (64.4)				
Farm Biosecurity e.g. a footbath	Yes	8 (36.4)	14 (63.6)	0.525	3.244	0.566	0.32
	No	74 (30.5)	169 (69.5)				
Kept and co-graze cattle with other ruminants (shoats)	Yes	36 (23.1)	120 (76.9)	0.241	0.699	0.001 <sup>b</sup>	10.90
	No	46 (42.2)	63 (57.8)				
Presence of companion animals in the farm	Yes	14 (32.6)	29 (67.4)	0.543	2.199	0.802	0.063
	No	68 (30.6)	154 (69.4)				
Kept chicken that were <i>Campylobacter</i> positive	Yes	50 (44.6)	62 (55.4)	1.78	5.23	0.000 <sup>b</sup>	16.98
	No	32 (20.9)	121 (79.1)				
Kept pigs in the farm	Yes	16 (55.2)	13 (44.8)	1.445	6.951	0.004 <sup>b</sup>	8.27
	No	66 (28.0)	170 (72.0)				
Keeping chicken and other birds irrespective of their <i>Campylobacter</i> status	Yes	61 (38.4)	98 (61.6)	1.418	4.476	0.002 <sup>b</sup>	10.62
	No	21 (19.8)	85 (80.2)				
Kept donkeys in the farm	Yes	18 (20.0)	72 (80.0)	0.238	0.791	0.006 <sup>b</sup>	7.99
	No	64 (36.6)	111 (63.4)				
Brought new cattle stock in the last 6 months	Yes	11 (61.1)	7 (38.9)	1.452	10.451	0.007 <sup>b</sup>	7.50
	No	71 (28.7)	176 (71.3)				
Source drinking water for cattle	Untreated borehole water	75 (30.2)	173 (69.8)	0.227	1.689	0.349	0.85
	Treated tap water	7 (41.2)	10 (58.8)				
Cattle drinking water shared with animals from other farms	Shared	21 (17.5)	99 (82.5)	0.164	0.519	0.000 <sup>b</sup>	19.24
	Individual	61 (42.1)	84 (57.9)				
Cattle drinking contaminated with <i>Campylobacter</i>	Yes	32 (25)	96 (75.0)	0.341	0.986	0.044 <sup>b</sup>	4.12
	No	50 (36.5)	87 (63.5)				
Enclosure condition and hygiene	Wet and dirty	59 (41.8)	82 (58.2)	1.799	5.548	0.000 <sup>b</sup>	17.24
	Moderately dry and clean	23 (18.5)	101 (81.5)				
Housing unit (feed store and feed trough) accessible to rodents and wild birds	Yes	64 (37.9)	105 (62.1)	1.450	4.809	0.001 <sup>b</sup>	10.99
	No	18 (18.8)	78 (81.3)				
Feeding practice	Floor	20 (16.4)	102 (83.6)	2.181	6.988	0.000 <sup>b</sup>	23.32
	Built-in trough	62 (43.4)	81 (56.6)				
Fed cattle on hay and napier grass	Yes	65 (41.9)	90 (58.1)	2.117	7.147	0.000 <sup>b</sup>	21.74
	No	17 (15.5)	93 (84.5)				
Fed cattle on chicken feed leftover and/or litter	Yes	15 (46.9)	17 (53.1)	1.032	4.628	0.041 <sup>b</sup>	4.07
	No	67 (28.8)	166 (71.2)				
Histories of diarrhoea, abortion and/or mastitis in the last 6 months	Yes	55 (36.9)	94 (63.1)	1.119	3.323	0.018 <sup>b</sup>	5.77
	No	27 (23.3)	89 (76.7)				

<sup>b</sup>Denotes independent variables considered significant (P<0.05) at 95% confidence interval. <sup>a</sup>FAO's agroecological zones (ACZ) were used to categorize participating farms: ACZ III or semi-humid region (800-1400mm annual rainfall) and ACZ V or semi-arid (450-900mm annual rainfall)

**Table 3:** Univariate and multivariate logistic regression analysis of potential risk factors covariates for thermophilic *Campylobacter* positivity (PCR positive) of 265 rectal swabs collected from cattle in 55 small-scale farms in Kajiado County

Risk factor	Modality	COR	95%CI (COR)	P-value	AOR	95%CI (AOR)	P-value
Geographical location of the farm in Kajiado County based on FAO's climate zones <sup>a</sup>	AEZ III (reference) (n=45)	–	–	–	–	–	–
	AEZ V (n=138)	0.6	0.3-1.1	0.0721	1.2	0.5-3.1	0.7092
Thermophilic <i>Campylobacter</i> positivity in chicken (keeping chicken harboring <i>Campylobacter</i> spp.)	No (ref) (n=121)	–	–	–	–	–	–
	Yes (n=62)	3.0	1.8-5.3	<0.0001 <sup>b</sup>	5.8	2.2-16.2	0.0005 <sup>b</sup>
Thermophilic <i>Campylobacter</i> positivity in water (cattle drinking water contaminated with <i>Campylobacter</i> spp.)	No (ref) (n=86)	–	–	–	–	–	–
	Yes (n=97)	0.6	0.3-1.0	0.0362 <sup>b</sup>	1.9	0.7-4.9	0.1959
Cattle breeds	Beef (ref) (n=95)	–	–	–	–	–	–
	Dairy (n=88)	3.8	2.1-7.1	<0.0001 <sup>b</sup>	12.7	3.2-60.0	0.0006 <sup>b</sup>
Brought new cattle stock in the last 6 months	No (ref) (n=176)	–	–	–	–	–	–
	Yes (n=7)	3.9	1.5-11.0	0.0069 <sup>b</sup>	0.9	0.2-3.3	0.8122
Presence of small ruminants in the farm	No (ref) (n=40)	–	–	–	–	–	–
	Yes (n=143)	0.5	0.3-0.9	0.0216 <sup>b</sup>	0.5	0.1-1.6	0.233
Presence of companion animals in the farm	No (ref) (n=154)	–	–	–	–	–	–
	Yes (n=29)	1.1	0.5-2.2	0.8024	0.3	0.1-1.2	0.107
Presence of donkeys in the farm	No (ref) (n=111)	–	–	–	–	–	–
	Yes (n=72)	0.4	0.2-0.8	0.0064 <sup>b</sup>	5.0	1.1-27.4	0.0498 <sup>b</sup>
Presence of pigs in the farm	No (ref) (n=170)	–	–	–	–	–	–
	Yes (n=13)	3.2	1.4-7.1	0.0039 <sup>b</sup>	4.9	1.2-23.5	0.0373 <sup>b</sup>
Keeping chicken and other birds irrespective of their <i>Campylobacter</i> status	No (ref) (n=85)	–	–	–	–	–	–
	Yes (n=98)	2.5	1.4-4.6	0.0016 <sup>b</sup>	0.2	0.03-0.6	0.0114 <sup>b</sup>
Co-grazing cattle with other ruminants	No (ref) (n=63)	–	–	–	–	–	–
	Yes (n=120)	0.4	0.2-0.7	0.0011 <sup>b</sup>	0.9	0.3-3.2	0.8709
Feeding cattle on poultry litter and/or leftovers	No (ref) (n=166)	–	–	–	–	–	–
	Yes (n=17)	2.2	1.0-4.6	0.0409 <sup>b</sup>	1.6	0.6-4.5	0.3779
Housing unit (feed store and feed trough) accessible to rodents and wild birds	No (ref) (n=78)	–	–	–	–	–	–
	Yes (n=105)	2.6	1.5-4.9	0.0015 <sup>b</sup>	0.5	0.1-2.5	0.3767
Condition and hygiene status of the enclosure	Moderately clean and dry (ref) (n=101)	–	–	–	–	–	–
	Wet and dirty (n=82)	3.2	1.8-5.6	<0.0001 <sup>b</sup>	3.3	0.9-12.6	0.0638 <sup>c</sup>
Histories of diarrhea, abortion and mastitis in the last 6 months	No (ref) (n=89)	–	–	–	–	–	–
	Yes (94)	1.9	1.1-3.4	0.0180 <sup>b</sup>	1.7	0.5-5.2	0.3867
Presence of companion animals in farms that did not co-graze cattle with other ruminants	No (ref) (241)	–	–	–	–	–	–
	Yes (24)	–	–	–	10.0	1.2-95.9	0.0379 <sup>b</sup>

<sup>b</sup>Independent variables considered significant (P<0.05) at 95% confidence interval; <sup>a</sup>FAO's agroecological zones (ACZ) were used to categorize participating farms: ACZ III or semi-humid region (800-1400mm annual rainfall) and ACZ V or semi-arid (450-900mm annual rainfall); ref=Reference group; N=265; COR= Crude odds ratio(ratio of the sides); 95% CI (COR)= Confidence interval for crude odds ratio to 95%; AOR= Adjusted odds ratio (ratio of the sides); 95% CI (AOR): Confidence interval for adjusted odds ratio to 95%.

## DISCUSSION

This study describes the unique characteristics of small-scale farms in Kajiado County while ascertaining significant associations between risk factors and *Campylobacter* positivity in cattle. This study detected *Campylobacter* species in over 72.7% of the participating small-scale farms. However other studies in different geographical regions have reported high or low farm and/or herd level prevalence (Ellis-Iversen et al. 2009b;

Klein et al. 2013; Ocejo et al. 2019; Hoque et al. 2021). Animal husbandry practices among other predisposing factors might increase the likelihood of *Campylobacter* shedding by either enhancing the risk of introduction or maintaining the existing *Campylobacter*. Maintenance of *Campylobacter* within a herd and/or a flock can be achieved by: lowered host's immunity, close contact to a contaminated source; increased fecal shedding or by heightened environmental endurance (Ellis-Iversen et al. 2009b).

Although thermotolerant *Campylobacter* prevalence in livestock particularly poultry has been investigated frequently in previous studies, documentation on assessment of *Campylobacter* positivity and associated risk factors in integrated smallholder farms is scanty. Risk factors for the transmission and/or occurrence of campylobacter pathogens on smallholder farms may be diverse, especially if they only rear one livestock type, unlike in integrated farms with a diversity of species. This study investigated potential risk factors which might influence transmission pathways; without elaborating the precise biological mechanisms of *Campylobacter* involvement in cattle. As such, the explanations given thereafter are hypothetical and require further investigation. But even then, an understanding of probable risk factors enhancing occurrence and/or transmission of thermophilic campylobacters in farms, can be instrumental in designing practical control measures.

Cattle are also common reservoirs of campylobacters. The odds of thermophilic *Campylobacter* positivity were 12.7 times higher with farms which kept dairy cattle over those that kept beef cattle. This finding is consistent with other studies conducted elsewhere (Ellis-Iversen et al. 2009b; Thépault et al. 2018). The variation in thermophilic *Campylobacter* carriage in beef and dairy cattle observed in this study may, however, reflect the husbandry practices and/or conditions of the animals rather than the type of breed. Nearly all the dairy cattle sampled were under zero-grazing (confinement) systems. An interaction between breed and sub-optimal housing conditions (dirty conditions) may increase fecal shedding of *Campylobacter*.

The final multivariable model also included presence of (or rather coming into contact /co-graze with) other farm animals including: keeping chicken harboring *Campylobacter* spp. (AOR=5.8, 95%CI=2.2-16.2, P=0.0005); presence of donkeys (AOR=5.0, 95%CI=1.1-27.4, P=0.0498); presence of pigs (AOR=4.9, 95%CI=1.2-23.5, P=0.0373) were significantly associated with occurrence of thermophilic *Campylobacter* spp. in cattle. This agrees with other studies conducted elsewhere (Ellis-Iversen et al. 2009b; Pires et al. 2019; Hoque et al. 2021; Patterson et al. 2022). Domestic animals including pigs, chicken and donkey are known reservoirs of thermophilic campylobacters (Nguyen et al. 2016; Carron et al. 2018; Conrad et al. 2018). *Campylobacter* shed in feces from all the carriers/reservoirs may end up contaminating large farm environment including pasture, soil and water sources. Consequently, this facilitates the introduction of *Campylobacter* into the farm. The effect of companion animals (dogs and cats) on *Campylobacter* positivity in cattle was amplified/modified by failure to co-graze cattle with small ruminants; increasing the AOR from 0.3, (95%CI=0.1-1.2, P=0.107) to 10 (95%CI=1.2-95.9, P=0.0379). Thermotolerant *Campylobacter* has been isolated from the gastrointestinal tracts of both healthy and diseased dogs and cats (Conrad et al. 2018; Karama et al. 2018; Thépault et al. 2020; Mbindyo et al. 2021). Companion animals and particularly dogs may scavenge offals of already infected mammalian species; thereby introducing the organisms to the farm.

Ironically, there was inverse association between keeping chicken and other birds irrespective of their

*Campylobacter* status and *Campylobacter* positivity in cattle (AOR=0.2, 95%CI=0.03-0.6, P=0.0114); i.e. seemed to be protective against thermophilic *Campylobacter* positivity in cattle. The protective effect of keeping chicken and other birds may suggest organism's ecological niche; *Campylobacter* thrives optimally at 42°C, similar to the normal body temperature of poultry and therefore, more likely ('preference') to colonize/inhabit the gut of birds over other animals including cattle. The protective effect could also suggest protective immunity due to constant or frequent exposure. Nonetheless, there is need to investigate this biological 'protective' effect plausibly.

Farms where cattle were housed in a persistently wet and dirty environmental conditions appeared to have a higher probability (AOR=3.3, 95%CI=0.9-12.6, P=0.0638) to being positive for thermophilic *Campylobacter* colonization. Paradoxically, the association between the two was found to be insignificant (P>0.05). This finding is supported by Hoque et al. (2021), who also reported that floor wetness would potentially increase the likelihood (AOR=2.0, 95%CI=0.1-56.3, P=0.67) of thermophilic *Campylobacter* positivity in cattle. However, the finding was not intuitively easy to construe. A probable hypothesis is that this being a cross-sectional study, the observation (hygiene and condition of the establishment) reported was probably a one-time case and not a long-term. As such, a much-controlled experimental study design or longitudinal studies are recommended.

In the current study, some of the potential risk factors were found to be insignificant (P>0.05) for farm-level thermophilic *Campylobacter* positivity in cattle in the multivariable logistic regression model. These included: geographical location of the participating farms; thermophilic *Campylobacter* positivity in cattle drinking water; histories of diarrhea, abortion and mastitis in the last 6 months; accessibility of housing unit (feed store and feed trough) by rodents and wild birds; co-grazing cattle with other ruminants and/or presence of small ruminants in the farm, and bringing new cattle stock in the last 6 months without temporary isolation. The disparity in seasonal means of daily ambient temperatures, humidity and rainfall in different agro-ecological zones in Kajiado County were minimal; which possibly lead to the insignificance of geographical distribution effect on the variation of thermophilic *Campylobacter* positivity in cattle herds. Presence of *Campylobacter* organisms in cattle drinking water from the respective farm is not an indication of colonization but rather a case of fecal contamination. Subsequently, the question would be: "how long the organisms can persist in water under the given environmental conditions to cause re-infection". Furthermore, if water troughs are cleaned on daily basis and source is potable; then trough water cannot be considered as a consistent reservoir. Therefore, water positivity status reflects the general level of cleanliness and contamination at sampling. Subsequently other transmission pathways in cattle are probably involved. Even though, *Campylobacter* spp. are one of etiological agents for diarrhea, abortion and mastitis in cattle; the latter could be due to other causes which need to be investigated. Rodents and wild birds are known



*Campylobacter* carriers (Sanad et al. 2013; Battersby 2015; Hald et al. 2015), and therefore carry the risk of contaminating cattle-environment as they scavenge for feed-leftovers. Presence of potentially pathogenic bacteria is one of hazards associated with feeding poultry litter to cattle.

### Conclusion

The findings of this study suggest that some farm characteristics, livestock husbandry practices and geo-environmental factors may be associated with occurrence and/or transmission of campylobacters. *Campylobacter* organisms were detected in the surveyed farms, evoking that cattle are reservoir for this organism, which may be spread to or may have been acquired from other animals. A number of independent variables were identified as potential risk factors including stocking dairy breeds, presence of companion animals including cats and dogs, *Campylobacter* positivity status in chicken (keeping chicken harboring campylobacters), presence of donkey, pigs, and companion animals and low levels of hygiene in the farm. These factors need to be eliminated or minimized while designing on-farm mitigation strategy to minimize fecal shedding of *Campylobacter* in cattle. More-over, the study recommends more research need to be carried-out on the disease so as to help further understand these its transmission dynamics and biological interactions.

### Author's Contributions

DWW, PGM, LCB and GOA designed the study, DWW collected data, DWW performed the experiments, closely supervised by PGM, LCB and GOA. DWW, DWM and RO analyzed the data, all the authors were involved in the drafting of the manuscript and approved the final submitted manuscript.

### REFERENCES

- Acha SJ, Kühn I, Jonsson P, Mbazima G, Katouli M and Möllby R 2004. Studies on calf diarrhoea in Mozambique: prevalence of bacterial pathogens. *Acta Veterinaria Scandinavica* 45: 1. <https://doi.org/10.1186/1751-0147-45-27>
- An JU, Ho H, Kim J, Kim WH, Kim J, Lee S, Mun SH, Guk JH, Hong S and Cho S, 2018. Dairy cattle, a potential reservoir of human campylobacteriosis: epidemiological and molecular characterization of *Campylobacter jejuni* from cattle farms. *Frontiers in Microbiology* 9: 3136. <https://doi.org/10.3389/fmicb.2018.03136>
- Bae W, Kaya KN, Hancock DD, Call DR, Park YH and Besser TE, 2005. Prevalence and antimicrobial resistance of thermophilic *Campylobacter* spp. from cattle farms in Washington State. *Applied and Environmental Microbiology* 71(1): 169-174. <https://doi.org/10.1128/AEM.71.1.169-174.2005>
- Battersby SA, 2015. Rodents as carriers of disease. *Rodent pests and their control* 81-100.
- Carron M, Chang YM, Momanyi K, Akoko J, Kiiru J, Bettridge J, Chaloner G, Rushton J, O'Brien S, Williams N and Fevre EM, 2018. *Campylobacter*, a zoonotic pathogen of global importance: Prevalence and risk factors in the fast-evolving chicken meat system of Nairobi, Kenya. *PLoS Neglected Tropical Diseases* 12: 8. <https://doi.org/10.1371/journal.pntd.0006658>
- Chatre P, Haenni M, Meunier D, Botrel MA, Calavas D and Madec JY, 2010. Prevalence and antimicrobial resistance of *Campylobacter jejuni* and *Campylobacter coli* isolated from cattle between 2002 and 2006 in France. *Journal of Food Protection* 73: 5. <https://doi.org/10.4315/0362-028X-73.5.825>
- Conrad CC, Stanford K, Narvaez-Bravo C, Neumann NF, Munns K, Tymensen L, Jokinen C and McAllister TA, 2018. Zoonotic fecal pathogens and antimicrobial resistance in Canadian petting zoos. *Microorganisms* 6: 3. <https://doi.org/10.3390/microorganisms6030070>
- Ellis-Iversen J, Cook AJ, Smith RP, Pritchard GC and Nielsen M, 2009a. Temporal patterns and risk factors for *Escherichia coli* O157 and *Campylobacter* spp. in young cattle. *Journal of Food Protection* 72: 3. <https://doi.org/10.4315/0362-028X-72.3.490>
- Ellis-Iversen J, Pritchard GC, Wooldridge M and Nielsen M, 2009b. Risk factors for *Campylobacter jejuni* and *Campylobacter coli* in young cattle on English and Welsh farms. *Preventive Veterinary Medicine* 88: 42-48. <https://doi.org/10.1016/j.prevetmed.2008.07.002>
- FAO, 2006. Country Pasture/Forage Resource Profile for Kenya. <https://pdfs.semanticscholar.org/1d7b/3d82527bce586638645a32e68f9df501b759.pdf>
- Fernández H and Hitschfeld M, 2009. Occurrence of *Campylobacter jejuni* and *Campylobacter coli* and their biotypes in beef and dairy cattle from the south of Chile. *Brazilian Journal of Microbiology* 40: 3. <https://doi.org/10.1590/S1517-83822009000300005>
- Gillespie IA, O'Brien SJ, Frost JA, Adak GK, Horby P, Swan AV, Painter MJ, Neal KR and *Campylobacter Sentinel Surveillance System Collaborators* 2002. A case-case comparison of *Campylobacter coli* and *Campylobacter jejuni* infection: a tool for generating hypotheses. *Emerging Infectious Diseases* 8: 9. <https://doi.org/10.3201/eid0809.10.3201/eid0809.010187>
- Häkkinen M, Heiska H and Hänninen ML 2007. Prevalence of *Campylobacter* spp. in cattle in Finland and antimicrobial susceptibilities of bovine *Campylobacter jejuni* strains. *Applied and environmental microbiology* 73: 10. <https://doi.org/10.1128/AEM.02579-06>
- Hald B, Skov MN, Nielsen EM, Rahbek C, Madsen JJ, Wainø M, Chriél M, Nordentoft S, Baggesen DL and Madsen M 2015. *Campylobacter jejuni* and *Campylobacter coli* in wild birds on Danish livestock farms. *Acta Veterinaria Scandinavica* 58: 1. <https://doi.org/10.1186/s13028-016-0192-9>
- Han X, Zhu D, Lai H, Zeng H, Zhou K, Zou L, Wu C, Han G and Liu S, 2016. Prevalence, antimicrobial resistance profiling and genetic diversity of *Campylobacter jejuni* and *Campylobacter coli* isolated from broilers at slaughter in China. *Food Control* 69: 160-170. <https://doi.org/10.1016/j.foodcont.2016.04.051>
- Hannon SJ, Allan B, Waldner C, Russell ML, Potter A, Babiuk LA and Townsend HG, 2009. Prevalence and risk factor investigation of *Campylobacter* species in beef cattle feces from seven large commercial feedlots in Alberta, Canada. *Canadian Journal of Veterinary Research* 73: 4.
- Harvey RB, Droleskey RE, Sheffield CL, Edrington TS, Callaway TR, Anderson RC, Drinnon DL, Ziprin RL, Scott HM and Nisbet DJ, 2004. *Campylobacter* prevalence in lactating dairy cows in the United States. *Journal of Food Protection* 67: 7. <https://doi.org/10.4315/0362-028X-67.7.1476>
- Hitchins AD, Feng P, Watkins WD, Rippey SR and Chandler LA 1998. *Bacteriological analytical manual*. Food and Drug Administration, Washington, DC.

- Hoque N, Islam SK, Uddin M, Arif M, Haque AKM, Neogi SB, Hossain MM, Yamasaki S and Kabir SM 2021. Prevalence, risk factors, and molecular detection of *Campylobacter* in farmed cattle of selected districts in Bangladesh. *Pathogens* 10: 3. <https://doi.org/10.3390/pathogens10030313>
- Hughes J, 2001. A system for assessing cow cleanliness. In *Practice* 23: 9. <https://doi.org/10.1136/inpract.23.9.517>
- Karama M, Etter E, McCrindle C, El-Ashram S, Prosperi A, Ombui JN, Kalake A and Cenci-Goga BT, 2019. Prevalence and risk factors associated with *Campylobacter* spp. occurrence in healthy dogs visiting four rural community veterinary clinics in South Africa. *Onderstepoort Journal of Veterinary Research* 86: 1. <https://doi.org/10.4102/ojvr.v86i1.1673>
- Klein D, Alispahic M, Sofka D, Iwersen M, Drillich M and Hilbert F, 2013. Prevalence and risk factors for shedding of thermophilic *Campylobacter* in calves with and without diarrhea in Austrian dairy herds. *Journal of Dairy Science* 96: 2. <https://doi.org/10.3168/jds.2012-5987>
- Kwan PS, Barrigas M, Bolton FJ, French NP, Gowland P, Kemp R, Leatherbarrow H, Upton M and Fox AJ, 2008. Molecular epidemiology of *Campylobacter jejuni* populations in dairy cattle, wildlife, and the environment in a farmland area. *Applied and Environmental Microbiology* 74: 16. <https://doi.org/10.1128/AEM.02198-07>
- Mbindyo SN, Kitaa JMA, Aboge GO, Abuom TO and Mulei CM, 2021. A review of *Campylobacter* infections in dogs. *International Journal of Veterinary Science* 10(4): 259-266. <https://doi.org/10.47278/journal.ijvs/2021.057>
- Modi S, Brahmabhatt MN, Chatur YA and Nayak JB, 2015. Prevalence of *Campylobacter* species in milk and milk products, their virulence gene profile and anti-biogram. *Veterinary World* 8: 1. <https://doi.org/10.14202/vetworld.2015.1-8>
- Mughini-Gras L, Penny C, Ragimbeau C, Schets FM, Blaak H, Duim B, Wagenaar JA, de-Boer A, Cauchie HM, Mossong J and Van Pelt W, 2016. Quantifying potential sources of surface water contamination with *Campylobacter jejuni* and *Campylobacter coli*. *Water Research* 101: 36-45. <https://doi.org/10.1016/j.watres.2016.05.069>
- Mulder AC, Franz E, de-Rijk S, Versluis MA, Coipan C, Buij R, Müskens G, Koene M, Pijnacker R, Duim B and Mughini-Gras L, 2020. Tracing the animal sources of surface water contamination with *Campylobacter jejuni* and *Campylobacter coli*. *Water Research* 187. <https://doi.org/10.1016/j.watres.2020.116421>
- Mullner P, Spencer SE, Wilson DJ, Jones G, Noble AD, Midwinter AC, Collins-Emerson, JM, Carter P, Hathaway S and French NP, 2009. Assigning the source of human campylobacteriosis in New Zealand: a comparative genetic and epidemiological approach. *Infection, Genetics and Evolution* 9: 6. <https://doi.org/10.1016/j.meegid.2009.09.003>
- Mustafa KH, 2016. Survival of *Campylobacter jejuni* in the Environment. Doctor in Philosophy Thesis, The University of Liverpool (United Kingdom). [https://livrepository.liverpool.ac.uk/3000171/1/MustafaKas\\_Mar2016.pdf](https://livrepository.liverpool.ac.uk/3000171/1/MustafaKas_Mar2016.pdf)
- Nguyen TNM, Hotzel H, Njeru J, Mwituria J, El-Adawy H, Tomaso H, Neubauer H and Hafez HM, 2016. Antimicrobial resistance of *Campylobacter* isolates from small scale and backyard chicken in Kenya. *Gut Pathogens* 8: 39. <https://doi.org/10.1186/s13099-016-0121-5>
- Ocejo M, Oporto B and Hurtado A, 2019. Occurrence of *Campylobacter jejuni* and *Campylobacter coli* in cattle and sheep in northern Spain and changes in antimicrobial resistance in two studies 10-years apart. *Pathogens* 8: 3. <https://doi.org/10.3390/pathogens8030098>
- Patterson L, Navarro-Gonzalez N, Jay-Russell MT, Aminabadi P and Pires AF, 2022. Risk factors of Shiga toxin-producing *Escherichia coli* in livestock raised on diversified small-scale farms in California. *Epidemiology and Infection* 150: E125. <https://doi.org/10.1017/S0950268822001005>
- Pires AFA, Patterson L, Kukielka EA, Aminabadi P, Navarro-Gonzalez N and Jay-Russell MT, 2019. Prevalence and risk factors associated with *Campylobacter* spp. and *Salmonella enterica* in livestock raised on diversified small-scale farms in California. *Epidemiology and Infection* 147: e321. <https://doi.org/10.1017/S095026881900205X>
- Said MY, Bedelian C, Moiko S, Muhwanga J, Atela J and Abuya R, 2019. Projected climate change and its potential impact on cattle in Kajiado county: PRISE Research Brief. Nairobi: Kenya Markets Trust. <https://www.kenyamarkets.org/wp-content/uploads/2020/06/Research-Brief-Projected-climate-change-and-its-potential-impact-on-cattle-in-Kajiado-County.pdf>
- Salihu MD, Abdulkadir JU, Oboegbulem SI, Egwu GO, Magaji AA, Lawal M and Hassan Y, 2009. Isolation and prevalence of *Campylobacter* species in cattle from Sokoto state, Nigeria. *Veterinaria Italiana* 45: 4.
- Sanad YM, Closs Jr G, Kumar A, LeJeune JT and Rajashekara G, 2013. Molecular epidemiology and public health relevance of *Campylobacter* isolated from dairy cattle and European starlings in Ohio, USA. *Foodborne Pathogens and Disease* 10: 3. <https://doi.org/10.1089/fpd.2012.1293>
- Sanad YM, Kassem II, Abley M, Gebreyes W, LeJeune JT and Rajashekara G, 2011. Genotypic and phenotypic properties of cattle-associated *Campylobacter* and their implications to public health in the USA. *PLoS One* 6: 10. <https://doi.org/10.1371/journal.pone.0025778>
- Sheppard SK, Dallas JF, Strachan NJ, MacRae M, McCarthy ND, Wilson DJ, Gormley FJ, Falush D, Ogen ID, Maiden MC and Forbes KJ, 2009. *Campylobacter* genotyping to determine the source of human infection. *Clinical Infectious Diseases* 48: 8. <https://doi.org/10.1086/597402>
- Strawn LK, Fortes ED, Bihn EA, Nightingale KK, Gröhn YT, Worobo, RW, Wiedmann M and Bergholz PW, 2013. Landscape and meteorological factors affecting prevalence of three food-borne pathogens in fruit and vegetable farms. *Applied and Environmental Microbiology* 79: 2. <https://doi.org/10.1128/AEM.02491-12>
- Thépault A, Poezevara T, Quesne S, Rose V, Chemaly M and Rivoal K, 2018. Prevalence of thermophilic *Campylobacter* in cattle production at slaughterhouse level in France and link between *C. jejuni* bovine strains and campylobacteriosis. *Frontiers in Microbiology* 9: 471. <https://doi.org/10.3389/fmicb.2018.00471>
- Thépault A, Rose V, Queguiner M, Chemaly M and Rivoal K, 2020. Dogs and cats: reservoirs for highly diverse *Campylobacter jejuni* and a potential source of human exposure. *Animals* 10: 5. <https://doi.org/10.3390/ani10050838>
- Uddin M, Neogi SB, Islam SS, Ferdous J, Khan M, Rahman S, Yamasaki S and Kabir SM, 2021. Occurrence and multidrug resistance of *Campylobacter* spp. at duck farms and associated environmental and anthropogenic risk factors in Bangladesh. *BMC Infectious Diseases* 21: 1139. <https://doi.org/10.1186/s12879-021-06834-w>
- Vandeplass S, Marcq C, Dubois Dauphin R, Beckers Y, Thonart P and Théwis A, 2008. Contamination of poultry flocks by the human pathogen *Campylobacter* spp. and strategies to reduce its prevalence at the farm level. *Biotechnologie, Agronomie, Société et Environnement* 12: 3.
- Wanja DW, Mbutia PG, Aboge GO and Bebora LC, 2022. Seasonal prevalence and molecular identification of thermophilic *Campylobacter* from chicken, cattle, and respective drinking water in Kajiado County, Kenya. *International Journal of Microbiology* 2022: 1526641. <https://doi.org/10.1155/2022/1526641>
- Wilson DJ, Gabriel E, Leatherbarrow AJ, Cheesbrough J, Gee S, Bolton E, Fox A, Fearnhead P, Hart CA and Diggle PJ, 2008. Tracing the source of campylobacteriosis. *PLoS Genetics* 4: 9. <https://doi.org/10.1371/journal.pgen.1000203>