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Article

A qualitative risk assessment of *Campylobacter* transmission in dairy cattle in Bangladesh

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Abstract: *Campylobacter*, one of the four key causes of diarrheal diseases of humans, is a zoonotic bacterial pathogen commonly found in cattle, sheep, goats and poultry. As the number of crossbred cattle steadily increases in Bangladesh through intensified livestock production to fulfill the demand of animal-source protein, the risk of pathogenic *Campylobacter* transmission is likely to increase in humans and animals including the farm environment. The objective of this study was to confirm the risk pathways and estimate the likelihood of entry and exposure risks of *Campylobacter* for cattle in the farm holdings. Following OIE risk analysis guidelines and tools, we assessed the risk level of each pathway using secondary and field observation data used in expert opinion elicitation process to formulate and confirm the risk level and their combined risk. The probable risk nodes were combined to obtain the total risk level for each specific transmission pathway using the template adapted by Zepeda-Sein based upon expert opinions. The evaluations revealed that the risk of the entry and exposure of *Campylobacter* is medium with medium levels of uncertainty. Moreover, the consequence pathways showed high risk with low level of uncertainty. Finally, the overall risk for transmission was evaluated as medium with medium level of uncertainty. This study suggests that there is a significant risk of *Campylobacter* transmission which may spread in humans, animals and successfully maintain in the farm environments. Good animal husbandry practices along with personal hygiene and sanitation practices of animal attendants including their family members are needed to minimize the risk of *Campylobacter* transmission from farmed cattle to humans. The findings of this study could be useful for framing functional risk reduction measures at the low-resource settings using One Health approach considering human, animal and environmental health perspectives.

Keywords: exposure; entry; consequence; uncertainty; qualitative risk assessment

1. Introduction

The *Campylobacter* species (spp.), comprised of different types of Gram-negative bacteria, are a leading cause of diarrheal disease in humans worldwide. In 2010, more than 95 million people were confirmed positive for

Campylobacter spp. globally (Kaakoush *et al.*, 2015; Igwaran and Okoh, 2019; Rahman *et al.*, 2021). In the United States, 1.5 million people become infected annually with these bacteria (Ford *et al.*, 2023). Many food-producing animals, including poultry, cattle, sheep and pigs have been demonstrated as the source and reservoir of human campylobacteriosis as zoonosis. Most of the zoonotic *Campylobacter* spp. are well adapted as a commensal in the gastrointestinal tract of these food producing animals (Skarp *et al.*, 2016; Nobi *et al.*, 2024).

Among the *Campylobacter* reservoirs, cattle have been documented as a source of exposure for many bacterial infections to humans. The farm environments play an important role in sustaining *C. jejuni*, and leading to initial exposure and re-infection in farmed cattle, as well as being a source of infection in humans. These commensal pathogens in animals can reach a level of ~3 × 10^4cfu/g in 20% cattle feces (Stein and Katz, 2017; Hoque *et al.*, 2021; Zhang *et al.*, 2024). The most frequently isolated species of *Campylobacter* are *C. jejuni* and *C. coli*, which are associated with human diarrheal disease in developed countries. As a sequel of human enteric disease, *C. jejuni* can result in a severe autoimmune disease called Guillain–Barré syndrome (GBS) (Kaakoush *et al.*, 2015; Rahman *et al.*, 2021). Among the reported cases of human campylobacteriosis, >90% are associated with *C. jejuni* or *C. coli*. Additionally, *C. fetus* is responsible for 2.4% of the total documented cases (Liu *et al.*, 2022).

To meet the ever-growing demand for milk and meat, there has been a significant increase in the use of exotic breeds through genetic improvement over the past several decades, resulting in the development of high-yielding crossbred cattle, which now constitute approximately 15% of the total cattle population (Brito *et al.*, 2021). These crossbred cattle primarily consist of Holstein Friesian, Sindhi, and Sahiwal breeds, with a smaller proportion of Jersey breed, and among them, 52% are milking cows (Sharma *et al.*, 2018). As global demand for animal-origin food, particularly red meat, is expected to double by 2050 in low and middle-income countries (LMICs), the need to enhance livestock productivity becomes even more critical. In response to this increasing demand, the Government has undertaken a variety of initiatives over the past few decades, implementing numerous projects and programs aimed at the development and modernization of the livestock sector to ensure sustainable growth and meet the rising needs of these nations (Henchion *et al.*, 2021; Van Eenennaam, 2024).

In Bangladesh, many people live in close quarters with animals, with some farmers even sharing their living spaces with livestock. While consuming raw milk is not a common practice, it does occur occasionally. These conditions create opportunities for the transmission of zoonotic pathogens between animals and humans (Rahman *et al.*, 2020). It is estimated that around 12% of severe infant diarrhea cases are linked to *Campylobacter jejuni* or *Campylobacter coli*, which are recognized as potential zoonotic threats. However, the exposure of the pathogens from cattle to cattle and cattle to humans through all hypothesized risk pathways in the farm's setting of Bangladesh has not yet been explored using risk assessment techniques including expert opinions elicitations (Kaakoush *et al.*, 2015; Mulu *et al.*, 2024).

In LMICs, the qualitative risk assessment frameworks have proven to be both more useful and appropriate than the quantitative methods since the availability of quantitative data may be constraining (Birgen *et al.*, 2022). Accordingly, qualitative risk assessment is appropriate to inform policy planners in low resource settings, including Bangladesh. Data on cattle *Campylobacter* prevalence and risk factors is inadequate which may lead to high uncertainty levels for risk estimation. Thus, we designed this study to assess the likelihood of entry and exposure of *Campylobacter* spp. from cattle farm holdings of Bangladesh. The specific objectives of this study were to identify risk pathways for *Campylobacter* spp. transmission in the cattle farm holdings (cattle -to -cattle and or human, cattle to farm settings or vice versa), and to evaluate the consequences concerning public health, food safety, and livelihood of the farmers. This study is intended to support the formulation of appropriate evidence-based policymaking processes within the low-resource context of Bangladesh.

2. Materials and Methods

2.1. Ethical approval

The study was approved by the Animal Welfare and Experimentation Ethical Committee (AWEEC) of Bangladesh Agricultural University (AWEEC/BAU/2019(45). Additionally, no animal and human interventions were required in this study. The majority of the data were derived from peer-reviewed published articles along with government reports utilized in the expert opinion elicitation process. However, due to the lack of data in some parameters a stakeholder interview was needed to generate that. For this case, the consent form was recited loudly to the study participants if they were incompetent to read. Later, a signed consent or impression of the left thumb was obtained on the form from the dairy farmers / farm attendants earlier to engagement in the study.

2.2. Study design

The qualitative risk of introduction (entry and exposure) and transmission of *Campylobacter* spp. was done in the cattle farm holdings as per the risk assessment guidelines of the World Organisation for Animal Health (OIE) (Islam *et al.*, 2020b). Risk assessment is an element of the risk analysis process that consists of entry, exposure, and consequence assessment, and finally risk estimation. The overall risk estimation was accomplished using the matrix developed by Zepeda-Sein based upon expert opinions (European Food Safety Authority, 2013). The question for the entry and exposure assessment was characterized as: What are the probabilities of entry and exposure of *Campylobacter* spp. for cattle farm holdings of Bangladesh? The entry and exposure assessment describe the risk pathway(s) required for *Campylobacter* transmission to the susceptible cattle and humans, through a qualitative approach. The entry and exposure of *Campylobacter* could cause adverse impacts for cattle and human or environmental health. However, the consequence assessment can predict the potential impact of a given exposure and its probability of occurring.

2.3. Questionnaire preparation

The questionnaire provided to experts was composed of two sections with 23 broad questions related to entry (n=9); exposure (n=11); and consequence (n= 3) classified according to the risk pathways. The experts answered these questions after evaluating the available data (secondary and primary: field observation data), and using personal skill and experience in their relevant fields. However, the “animal” node of the entry pathway was separated into two distinct nodes (sick and healthy). Moreover, two additional nodes including “rodent and pest” and “natural breeding” were included for this risk pathway based on the unanimous suggestion of the experts.

2.4. Sources of data

The necessary data on risk (release, exposure and consequence) parameters were collected from published (secondary) sources spanning from the 1980s to 2021 within Bangladesh (Figure 1). The sources of secondary data involved peer-reviewed published articles from national and international peer-review journals including grey literature (government documents). Due to the lack of data on some risk parameters, information was collected through field interviews based on a participatory technique from relevant stakeholders. The data from both sources (primary and secondary) assisted the experts to categorize the risk of the individual node targeting the overall risk confirmation process.

Figure 1. Secondary data were gathered from published sources spanning from the 1980s to 2021 in Bangladesh.

2.5. Semi-structured data collection

A questionnaire was formulated to collect the information from relevant stakeholders (farmers/ animal attendants) relating to (1) cleaning and sanitation, (2) farm biosecurity, (3) inappropriate practices of farmers/animal attendants including (3) farm management factors.

2.6. Expert selection

Considering the professional background and expertise, a total of 14 experts from universities (professors of infectious zoonotic diseases), government, national and international agencies (field veterinarians, and veterinarians from animal health, food safety, public health and epidemiology) were recruited. The expert opinion elicitation was carried out using a three-step step process. Initially, they were requested via email two weeks before to join an online workshop enclosing a brief concept note on the objectives and procedures including a clarification of the desired tasks. At the same time, the experts were requested to provide an email reply to join the workshop within five working days of getting the emails. However, a gentle reminder was sent to all experts after four working days of the primary request. Among the 14 communicated experts, 8 (57%) agreed to contribute to the workshop. The background of these experts was bacteriology (n=2), epidemiology (n=2), public health (n=1), animal health (n=1), field veterinarian (n=1) and food safety (n=1). In the next step, who responded, a soft copy of available data and tentative risk pathways were circulated among experts to enable them in the opinion generation process and to disperse the doubts for the risk classification of each node of a particular pathway. A zoom meeting link was forwarded to the participants one day earlier to the workshop commencing. In the third step, the experts contributed in the expert opinion elicitation process based on their current knowledge and experience on *Campylobacter* spp. including transmission dynamics in farmed cattle.

2.7. Expert opinion elicitation workshop

An online-based zoom workshop started with a review of the objectives of the study and the methods employed for expert opinion elicitation. In brief, an outline of the probable risk pathways, nodes along with data requirements were displayed in the workshop. The experts were asked to give their best qualitative probability estimates for each risk pathways (nodes) in the workshop via online google docs. The experts confirmed the risk nodes/parameters of the risk pathway, and conceded to a number grading (the number of scores out of 100) against the corresponding qualitative probabilities (six) described in Table 1. The procedure for expert opinion elicitations was also associated with the experts' experience and knowledge in the relevant field including content analysis of the secondary data that was extrapolated for this procedure. The discussion in the online-based workshop was facilitated by an experienced moderator.

2.8. Risk assessment likelihood categories

Six (6) qualitative probability categories such as negligible, very low, low, moderate/medium, high and very high- levels were utilized in the risk assessment method (Table 1) in accordance with the EFSA report (European Food Safety Authority, 2013). However, a number grading range was defined in the expert elicitation workshop to support clarification of the risk parameters. The detailed description of qualitative probability categories and their corresponding number grading is presented in Table 1.

Table 1. Qualitative probability categories used in *Campylobacter* transmission risk assessment study (adapted from EFSA report) (European Food Safety Authority, 2013).

Qualitative probability	Description	Number grading range (Scores out of 100)
Negligible (N)	Event is so occasional that it is not worth consideration	< 30
Very Low (VL)	Event occurs very rarely, but cannot be ignored	30-45
Low (L)	Event is occasional but does occur	45-60
Moderate/medium (M)	Event occurs often	60-75
High (H)	Event occurs very frequently	75-90
Very High (VH)	Event occurs almost definitely	90-100

2.9. Risk estimation uncertainties

The uncertainty levels were also used in four categories (low, medium, high and unknown) during the risk estimation process adapted from EFSA report shown in Table 2.

Table 2. Level of uncertainties used in this study (adapted from EFSA report) (European Food Safety Authority, 2013).

Uncertainty level	Description
Low (L)	Solid and complete data available with multiple references
Medium (M)	Some data available with a few references
High (H)	Scarce or no data available (no references), data from observations and/or personal communication

2.10. Risk estimation

The combined risk levels of the entry and exposure and the consequence pathways were accomplished by calculating the mean value of all risk parameters of an individual pathway that was given by the experts as numerical grading (Table 1), and then a reciprocal ordinal risk level was established. However, the uncertainty level of risk parameters was reached by consensus among expert opinions on each risk pathway (Table 2). Similarly, in the following step, the likelihood of the introduction of infection was obtained after calculating mean value of entry and exposure risks of parameters. In the succeeding step, the likelihood of combined introduction (entry and exposure) and consequence, the overall transmission risk was obtained as per the matrix described in Table 3.

Table 3. Risk categories combination format applied in this qualitative risk assessment study (Horigan *et al.*, 2023).

		Parameter/node-2[1] /exposure[2]/ (entry X exposure)[3]					
		Negligible (N)	**Very Low (VL)**	**Low (L)**	**Medium (M)**	**High (H)**	**Very High (VH)**
Parameter/ Node-1[1]/entry[2] / consequence [3]	**Negligible (N)**	N	N	N	N	N	N
	Very Low (VL)	N	N	VL	VL	VL	VL
	Low (L)	N	N	VL	VL	L	L
	Medium (M)	N	VL	VL	L	M	M
	High (H)	N	VL	L	M	H	H
	Very High (VH)	N	VL	L	M	H	VH

[1] parameter/node-1 X parameter/node-2

[2] entry X exposure

[3] combination (entry X exposure) X consequence

3. Result

3.1. Entry assessment

In the entry assessment pathway, a total of 9 nodes/risk pathways were finalized. Among the 9 nodes of release pathways, sick animals (diarrhea) and cleaning and disinfection were documented at very high risk with a medium level of uncertainty as all experts agreed together. However, the node animals (healthy) were presented with high risk with medium uncertainty. On the other hand, parameters like manure management, closeness of human habitat to the cattle shed, rodent and pest including udder cleaning before milking were evaluated as medium risk level and the rest of the parameters (rearing several species of animals together or having access by other animals in the farm and washing of cattle regularly) were labeled as low risk. A detail of the risk estimation with their combined probability in risk pathways established through expert opinion elicitation is presented in Figure 2. Thus, we obtained the overall risk of the entry /exposure pathway to be medium with medium level of uncertainty (Table 4).

3.2. Exposure assessment

Initially, ten (10) nodes/ pathways were identified and presented in the expert opinion elicitation meeting, namely, cattle roam outside, stocking density of cattle, feed, water, floor type, use of PPE (mask, gloves, gumboot and apron), taking food/ drink/smoking during working in the cattle farm, contact with animals whilst working, consumption of raw milk and taking a shower immediately after working in dairy farm. However, a new node named “natural breeding/bull sharing” of the exposure pathways was included as suggested by the experts, therefore, 11 total nodes of the exposure pathways were assessed (Figure 3; Table 5).

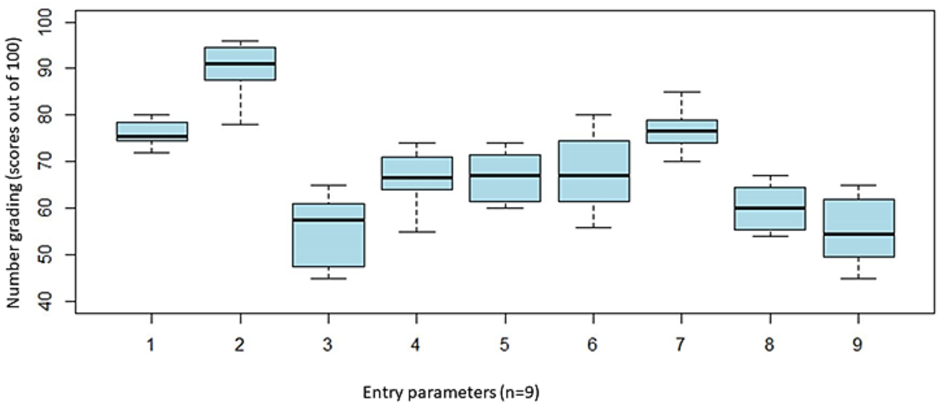

Figure 2. A box-and-whisker plot demonstrates combined probability distributions of *Campylobacter* entry pathways: (1) healthy animals; (2) sick animal (diarrhea); (3) access of other animals in the farm; (4) manure management (biogas plant, manure use purpose); (5) rodent and pest; (6) closeness of human habitat with cattle shed; (7) cleaning and disinfection; (8) udder cleaning and (9) washing of cattle regularly. The box shows the median (solid horizontal line), the lower (25%) and upper quartiles (75%) established through experts' opinion elicitation (n=8).

Table 4. Details of the entry pathways of *Campylobacter* in farmed cattle in Bangladesh.

Entry pathways	**Risk grading (%) (average score of all experts, n=8)**	**Uncertainty level**
Healthy animal	High (76.13)	Low
Sick animal (Diarrhea)	Very High (90.00)	Low
Rearing multiple species together or access of other animals the farm	Low (55.25)	Medium
Manure management, biogas plant/ manure use purpose	Medium (66.50)	Medium
Rodent and pest	Medium (66.75)	Medium
Closeness of human habitat with cattle shed	Medium (67.75)	Medium
Cleaning and disinfection	High (76.75)	Medium
Udder cleaning	Medium (60.13)	Medium
Washing of cattle regularly	Low (55.25)	Medium
Likelihood of entry-of *Campylobacter*	Medium (68.28)	Medium

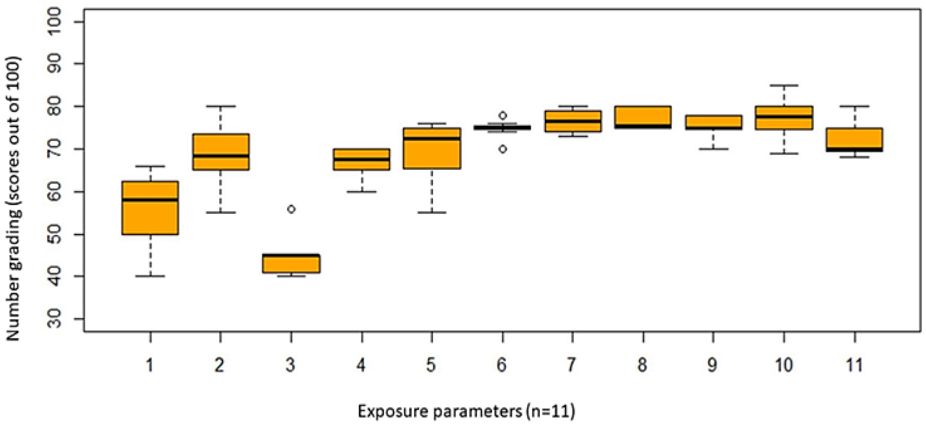

Figure 3. A box-and-whisker plot demonstrates combined probability distributions of *Campylobacter* exposures pathways: (1) cattle roaming outside; (2) stocking density; (3) feed; (4) water source;(5) breeding program/ bull sharing; (6) floor type; (7) use of PPE (mask, gloves, gumboot and apron); (8) taking food/ drink/smoking during working in the cattle farm; (9) contact with animals; (10) consumption of raw milk, and (11) taking a shower immediately after working in dairy farm. The box shows the median (solid horizontal line), the lower (25%) and upper quartiles (75%) established through experts' opinion elicitation (n=8).

Among 11 parameters/nodes of the exposure pathways, use of PPE (mask, gloves, gumboot and apron), taking food/ drink/smoking during working in the cattle farm, frequency of contact with animals, consumption of raw milk were perceived as high risk with medium uncertainty. However, the parameters, like stocking density of cattle, water, natural breeding/ bull sharing, floor, taking a shower immediately after working in a cattle farm were documented at medium risk. The remaining parameters of exposure pathways were captured as low to very low-risk levels. The risk estimation with their combined probability in exposure risk pathways is presented in Figure 3. Hence forward, the overall level of risk was estimated as medium with medium level of uncertainty (Table 5).

Table 5. Details of the exposure pathways of *Campylobacter* in farmed cattle in Bangladesh.

Exposure Pathways	**Risk grading (%) (average score** of **all experts, n=8)**	**Uncertainty level**
Cattle roam outside	Low (55.88)	Medium
Stocking density of cattle	Medium (68.63)	Low
Feed	Very Low (44.75)	Medium
Water	Medium (66.88)	Medium
Natural breeding / bull sharing	Medium (69.63)	High
Floor	Medium (74.75)	High
Use of PPE (mask, gloves, gumboot and apron)	High (76.50)	Medium
Taking food/ drink/smoking during working in the cattle farm	High (77.00)	Low
Contact with animals	High (75.38)	Low
Consumption of raw milk	High (77.25)	Low
Taking shower immediately after working in dairy farm	Medium (72.13)	Medium
Likelihood of exposure of *Campylobacter*	Medium (68.98)	Medium

3.3. Consequence assessment

In consequence assessment, three (3) nodes were defined and subsequently validated by the experts namely, the consequences of exposure among animals, exposure to humans and exposure in and among the farm environments. It was evaluated that *Campylobacter* is likely to cause infection to animals of the farm, animal attendants, or their family members with high risk. However, the probability of circulation of *Campylobacter* in the farm environment (soil and water) was evaluated as the medium (Figure 4; Table 6). Finally, the risk for consequence pathways was evaluated as high with low level of uncertainty.

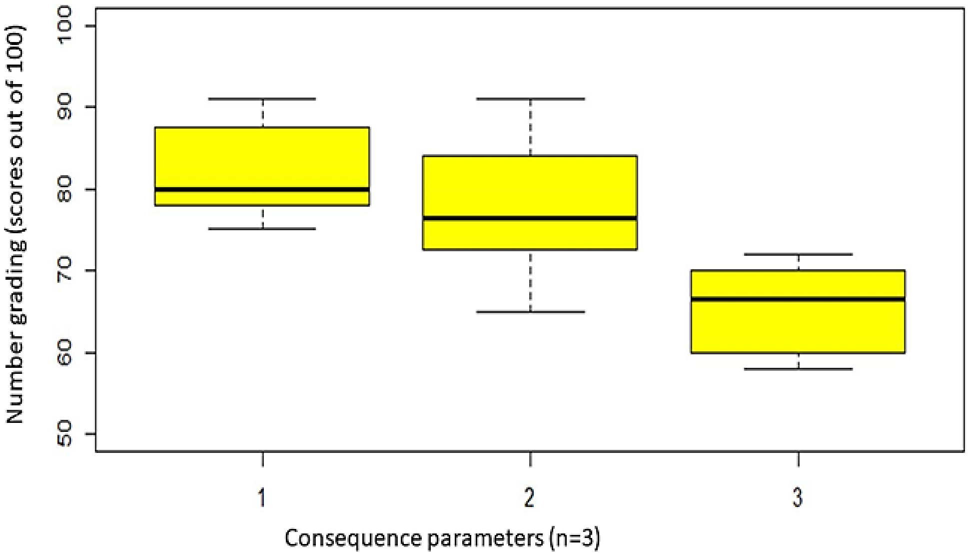

Figure 4. A box-and-whisker plot demonstrates combined probability distributions of *Campylobacter* consequence pathways (1) *Campylobacter* spread among other animals; (2) Transmission in humans; (3) Circulating *Campylobacter* in the cattle farm environment of Bangladesh. The box shows the median (solid horizontal line), the lower (25%) and upper quartiles (75%) established through expert opinion elicitation (n=8).

Table 6. Details of the consequence pathways of *Campylobacter* in farmed cattle in Bangladesh.

Pathways	Risk grading (%)	Uncertainty level
Campylobacter spread among the animals	High (82.13)	Low
Transmission in humans	High (77.75)	Low
Circulating *Campylobacter* in the farm environment	Medium (65.38)	Medium
Likelihood of *Campylobacter* impact for consequence pathway	High(75.08)	Low

3.4. Risk estimation

After joining the aggregated risk of all pathways, the total risk for transmission was medium with a medium level of uncertainty (Table 7; Figure 5).

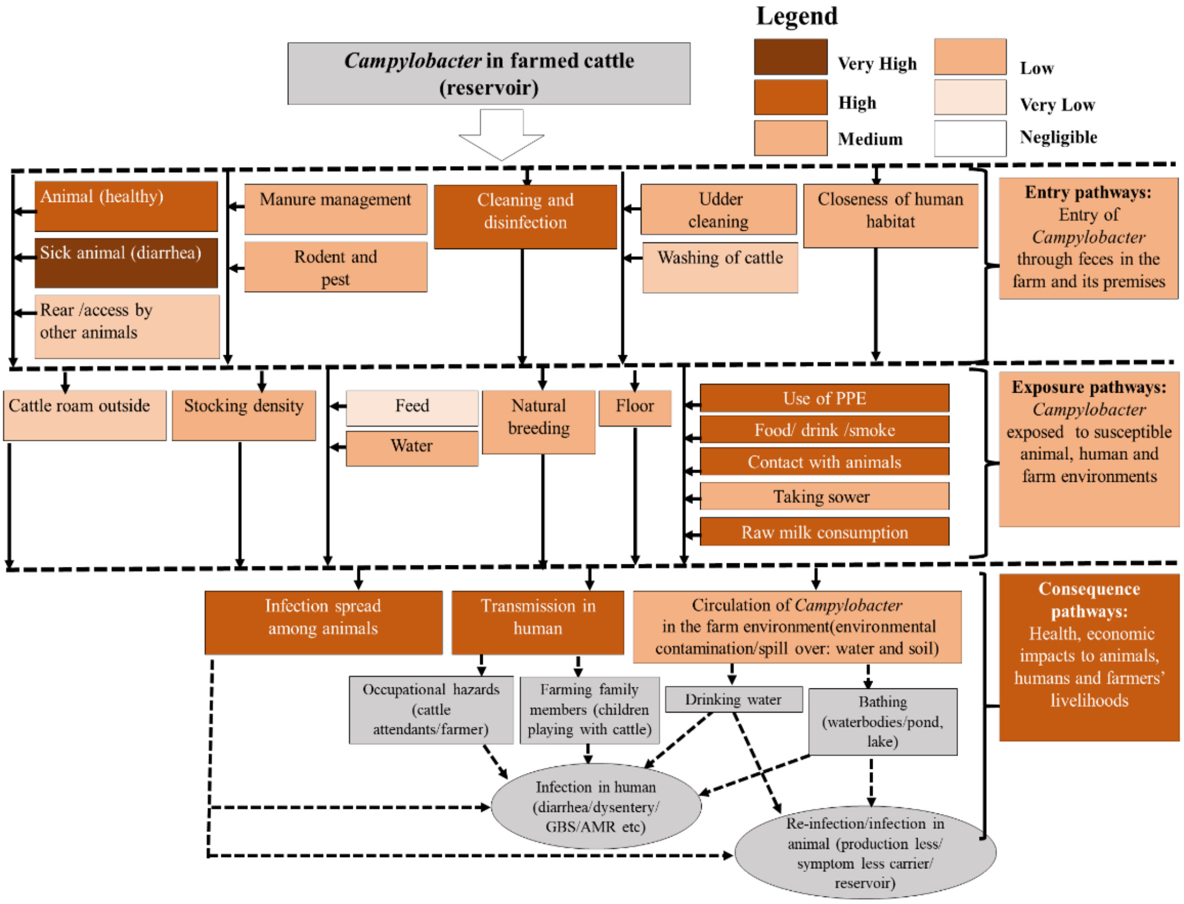

Figure 5. Different risk pathways (entry, exposure and consequence) included for qualitative risk assessment shown with the unique color gradient at an individual risk level.

Table 7. Details of the qualitative risk assessment of the transmission pathways of *Campylobacter* in farmed cattle in Bangladesh.

Pathways	Risk level	Uncertainty level
Entry pathways	Medium	Medium
Exposure pathways	Medium	Medium
Entry and exposure combined	Medium	Medium
Consequence pathways	High	Low
Risk of transmission of *Campylobacter*	Medium	Medium

4. Discussion

We assessed the qualitative risk of *Campylobacter* transmission in the cattle farm settings of Bangladesh. The overall risk for transmission was estimated as medium with a low level of uncertainty. The findings reveal that there is significant risk of *Campylobacter* transmission which may spread in humans, animals and successfully maintain in the farm environment. We recommended good animal husbandry practices (GAHP) along with personal hygiene and sanitation practices of animal attendants including their family members to minimize the risk of *Campylobacter* transmission from farmed cattle to humans.

In the risk assessment of exposure to *Campylobacter* on cattle farms, both sick and healthy animals were categorized as posing very high and high levels of risk for potential exposure or entry of the pathogen. The animal-level prevalence of *Campylobacter* was found to be 30.9% (n=540) and 26.7% (n=60), while the herd-level prevalence was recorded at 53.3%. Additionally, *Campylobacter* spp. showed a higher prevalence in cows (41%, 74/180), followed by calves (28.3%, 51/180), and heifers (23.3%, 42/180) (Kabir *et al.*, 2019; Hoque *et al.*, 2021). *Campylobacter* is an important human bacterial pathogen found in cattle as a reservoir in the gastrointestinal tract of warm-blooded animals as commensal, and excrete through feces with a concentration of ~3×10^4cfu/g (Facciolà *et al.*, 2017; Hoque *et al.*, 2021; Olvera-Ramírez *et al.*, 2023). Therefore, sick (diarrhea) and healthy animals were evaluated to be very high and high risks respectively with low levels of uncertainty.

The parameter like manure management/biogas plant/manure use purpose was documented as medium risk of *Campylobacter* exposures. More than 50% (n=49) farmers use cattle feces in aquaculture, and only 9% of farmers (n=79) utilize cattle manure in the biogas plant which emphasized a medium level of risk of exposure (Islam *et al.*, 2020a; Hoque *et al.*, 2021). The *Campylobacter* is excreted in cattle feces and persists for a longer period in the environment or even in the manure compost pit (Inglis *et al.*, 2010). Closeness of human habitat with the cattle shed was presented as a medium-level of risk. A considerable proportion (83.2% and 57%) of farm attendants/farmers share the same premises with animals that perceived a medium risk level (Hoque *et al.*, 2021; Islam *et al.*, 2021). Cleaning and disinfection practices (floor and utensils: feeder and drinker) was documented as high risk for *Campylobacter* exposure. The likelihood of *Campylobacter* positive status of a farm was documented as 12 and 9 times more in those farms which had no or minimum cleaning and disinfection practices (An *et al.*, 2018; Hoque *et al.*, 2021).

It was reported that 23% and 22% of farmers keep other species together and allow other animals (sheep, goat and poultry) to enter the farm which may facilitate reintroduction of *Campylobacter* in the farm and present a low-level of risk (Islam *et al.*, 2020a; Hoque *et al.*, 2021). About 98.3%(295/300) of the farmers cleaned udder with water before milking and 93% (279/300) of farmers washed cattle regularly. Therefore, these parameters were presented at a low level of risk by expert opinion. The qualitative probability was assessed as a medium in the entry pathway. The uncertainty was perceived as a medium due to insufficient published data in risk pathways that were convinced to collect through stakeholder interviews.

Cattle roaming outside and access to other animals (cattle, sheep and goat) had low risk of exposure as a low proportion of farms 10.67% (32/300) allow cattle to freely roam. Personal hygiene of the cattle attendants like using PPE, taking food and drink or even smoking in the cattle farm, contact with animals and consumption of raw milk demonstrated a high level of exposure risk. Indeed, 97% of farm workers do not use any protective materials, of which 30.9% (N=404) of cattle attendants smoke, drink or eat food whilst working in the cattle farm (Islam *et al.*, 2021). Moreover, the cattle handlers come in contact with animals three times per day and among them, 6% (N=300) consume raw milk, a risky practice for *Campylobacter* exposures in the farm holdings (field observation). However, at present 14 milk processing companies pasteurize and market 1 million liters of raw milk daily for consumers of Bangladesh (Kaakoush *et al.*, 2015; Hoque *et al.*, 2021). Humans can get an infection from animals by direct contactor consumption of raw or unpasteurized milk (Davis *et al.*, 2016). This pasteurization arrangement is not sufficient to cover whole production requirements. The high prevalence of *Campylobacter* at both herd (53.3%), individual animal (30.9%) levels, and in milk samples 20% (n=20) could pose a significant public health threat in Bangladesh (Kabir *et al.*, 2019; Hoque *et al.*, 2021).

The exposure parameters, viz., water, stocking density and breeding program were documented very low to medium levels of risk. Less than half of the (45.6%, N=90) farms provide inadequate space for the cattle (less than 50 sq. ft. /animal) (Hoque *et al.*, 2021). The high stocking density of animals increases the likelihood of *C. jejuni* introduction on farms (Graham *et al.*, 2008; An *et al.*, 2018). Since *Campylobacter* excretes through fecal materials, cattle could contaminate water sources and can cause infection directly to humans or reinfection in cattle (Young *et al.,* 2007). However, it was revealed from field observation that all farms provide good source water (deep tube wells). Bull sharing was captured as medium-level risk because the majority of crossbred cattle were bred through an artificial insemination program with only 14% bred through natural service (field observation). The bulls can act as a reservoir of *C. fetus* and disseminate the pathogens to reproductive cows/heifers through natural breeding (Uddin *et al.,* 2015). This disease is associated with decreased reproductive performance that includes abortion in cows and premature embryonic death (Henker *et al.*, 2020). However, through government and private initiatives the majority of crossbred cattle of the national herd are taken under the artificial insemination program using proven bull semen. Natural breeding is mostly practiced in indigenous cattle in Bangladesh.

In connection with the consequence pathways, the risk parameters of *Campylobacter* transmission to the other animals in cattle farms were measured as high risk with medium uncertainty. A few studies confirmed animal level prevalence of *Campylobacter* as 30.9% and 26.7% in fecal sample of which *C. jejuni* was confirmed as abundant pathogens (70.1%) followed by *C. coli* (28.4%) and *C. fetus* (1.5%) respectively (Kabir *et al.*, 2019; Hoque *et al.*, 2021). The number of crossbred cattle farms was gradually increasing from 37,000 in 2011 to over 500,000 in 2017. The concentration of large ruminants (145 large ruminants/ sq. km) in Bangladesh, and high stocking density in 54.4% farms could enable the transmission in other cattle of the herd. *Campylobacter* spp. were found to be more prevalent in cows (41%, 74/180), than calves (28.3%, 51/180) and heifers 23.3% (42/180) (Hoque *et al.*, 2021).

The likelihood of unexpected impact of *Campylobacter* transmission in health, economic and livelihoods depends upon several factors like a burden in source animal, animal population and husbandry practices, personal hygiene, sanitation among the farmers/animal attendants including community people, and national healthcare and veterinary services. The dimension of impacts and their associated information are required for policy makers for framing prevention and control strategies. *Campylobacter* exposed from cattle farms may activate many sequelae which contribute significantly to the burden of these pathogens in low resource settings, like Bangladesh (Al-Mamun *et al.*, 2023; Islam *et al.*, 2023).

Usually, C. jejuni and occasionally *C. coli* do not cause any clinical signs in mature cattle. However, it may cause diarrhea in calves (Klein *et al.*, 2013; Berhanu *et al.*, 2021). Our field survey confirmed diarrhea in 6.01% (599/9,973) young animals. An overall prevalence of campylobacteriosis was reported be 30.9 % through fecal sample evaluation. The prevalence of diarrhea varies from 20.3- 42.9% in different dairy farms of Bangladesh with crude mortality of 18.9% including other diseases (pneumonia, navel ill, joint ill, septicemic conditions, congenital problems). Thus the loss of calf crop incurs a huge impact on livelihoods by loss of milk production in cows and decreasing availability of replacement stock (Ali *et al.*, 2015). In addition, our field survey confirms that farmers spent BDT 500 (US$ 6) /animal due to diarrheal treatment cost in cattle as a financial burden that has a direct impact on the livelihoods of marginal dairy farmers.

However, *C. fetus* subspecies *venerealis* (*Cfv*) reduces reproductive performance through abortion in cattle and premature embryonic death (Cagnoli *et al.*, 2024). Other species like *C. fetus* subsp. *fetus (Cff),* and *C. jejuni* are also associated with decreased fertility and abortion in cattle (Hoque *et al.*, 2023). *Cfv* causes 20% abortion and 20% reduction of pregnancy/infertility and decreases 7% milk production in infected cattle (Michi *et al.*, 2016). However, due to the lack of data on *C. fetus* we could not substantiate the true burden of this disease in reproductive cattle in Bangladesh. Artificial insemination program is being practiced using proven bull semen mostly in crossbred cattle in Bangladesh. However, this is not sufficient to cover the whole stock. Additionally, the majority of cattle farms are household and small (few cattle) scale farms, therefore, they are not interested to opt out breed upgradation of their cattle through artificial insemination (Souames and Berrama, 2020). Our field survey showed that 14% of farms are still practicing natural breeding. Therefore, these practices would facilitate the transmission of *C. fetus* that has the impact of reproductive health performances by decreasing the production of the annual calf crop. Likewise, the livelihood of marginal livestock rearers would be affected due to these multifaceted production losses. Several studies confirmed approximately 11% repeat breeding, and < 10% abortion in crossbred cows in different locations in Bangladesh that could validate our hypothesis (Asaduzzaman *et al.*, 2017; Hasib *et al.*, 2020; Parvez *et al.*, 2020). In case of reproductive failures (repeat breeding/ abortion) farmers spent around BDT 1300 (US$ 15) per cow. However, our survey confirmed that if a farmer desires to overcome the recurrent loss by purchasing healthy productive female cattle, the restocking cost will be BDT 60,000 (US$ 710) after adjustment of the carcass value of the present stock. These would have a direct influence on the livestock productivity of female cattle resulting in economic and social impact to the dairy industry.

Cattle play a role as a reservoir of *Campylobacter* after getting exposure. Since the proportion of crossbred cattle is rising in Bangladesh that may increase the risk for further exposure of zoonotic pathogens to humans. Therefore, cattle are considered the more likely source of *Campylobacter* and is anticipated to be more risky than the food chain of poultry products, *Campylobacter* is likely to spread in humans due to the risky practices of the cattle handlers (Davis *et al.*, 2013). Additionally, the cattle handlers come in contact with animals three times a day and 6% (n=18) of them consume raw milk (field observation data) which are also responsible for *Campylobacter* exposures among the cattle handlers that will highlight the public health burden. The probability of transmission of *Campylobacter* to the animal attendants or their family members was confirmed as high. Studies conducted in Bangladesh during the 1990s showed that *C. jejuni* was related to watery diarrhea mostly and the prevalence varies from 17 to 26% (Kaakoush *et al.*, 2015; Hoque *et al.*, 2021). Another study confirmed 12.16% prevalence of *Campylobacter* (*C. jenuni* 9.45% and *C. coli* 2.68%) (N=56132) from the stool and rectal swabs spanning from 2005 to 2008 (Ahmed *et al.*, 2012). *C. jejuni* is an important etiological agent of childhood diarrhea in Bangladesh (25.5%, n=102) (Rahman *et al.*, 2021). However, a study in Bangladesh confirmed a higher occurrence of *Campylobacter*-related diseases like AFP/GBS in young children, than developed countries (Islam, 2011). GBS is the primary determinant of acute flaccid paralysis in Bangladesh, with an expected incidence rate 3.25/ 100,000 children below 15 years of age where *Campylobacter* infection seems to be associated with the majority of such cases (Islam, 2011; Islam *et al.*, 2012). In Bangladesh, GBS is usually developed by an enteric infection of *Campylobacter jejuni* and 69% GBS patients were found with the clinical symptom of diarrhea (36%). However, research in Bangladesh confirmed the association among reduced childhood growth and *Campylobacter* infection which was more prevalent between the ages of 12 and 21 months (Islam *et al.*, 2010; Sanchez *et al.*, 2020).

A multisite study confirms several determinants, viz., use of untreated drinking water, poor sanitation including the presence of cattle/ poultry, likely to be associated with *C. jejuni/coli* occurrence. The incidence rate ratio was found to be higher in the Bangladesh site than the other study sites of India, Brazil, Nepal, South Africa Peru and. Pakistan (Kabir *et al.*, 2015; Haque *et al.*, 2019). Therefore, *Campylobacter* has a significant impact on childhood health and safety, nutrition and well-being in Bangladesh. Gastroenteritis, arthralgia, and GBS are important clinical complications of *Campylobacter* infections in humans (Alter *et al.*, 2011). Case-fatality rates in LMICs are assumed to be higher (Sanchez *et al.*, 2020). The estimated average cost for severe diarrheal illness was US$ 27 (2 147 BDT) that constitutes 17% of the average monthly family income. The average cost for non-severe diarrhea was estimated US$ 6.36 (499 BDT) that constitutes 4% of the average monthly family income. Thus, empirically a diarrheal episode has a negative impact on the economic condition of low-income urban people (Sultana *et al.*, 2021). Therefore, a significant burden prevails on children’s and adult health and welfare and livelihoods. Many efforts have been taken to minimize *Campylobacter* infection and its associated GBS risks without considering the source of introduction in the LMICs (Platts-Mills and Kosek, 2014). Moreover, *Campylobacter* infection was reported be associated with functional gastrointestinal disorders and to a lesser extent inflammatory gastrointestinal diseases, celiac disease from the United States and European counties. However, confirmation of such a connection is difficult in low-resource settings like Bangladesh. Data on reactive arthritis associated with *Campylobacter* from the LMICs including is very sparse (Ajene *et al.*, 2013; Porter *et al.*, 2013; Riddle *et al.*, 2013). Our field survey confirmed 5.33% diarrhea and 0.67 % (N=300) GBS like symptoms among the cattle handlers and their family members. About 95% cattle handlers come in contact with the cattle three times in a day without having any protective materials and 30.9% of them take food and drink or even smoke whilst working in the cattle farm and 6% of them consume raw milk (field observation). Additionally, 16.8% (N=404) cattle handlers/ farmers share same premises with the animals (Islam *et al.*, 2021). All these risky practices are connected with infections in humans via cattle, chicken, contaminated milk and water (Membré *et al.*, 2013). A study in the United States confirmed that living or working in a dairy farm had 6.7 times more risk of acquiring *Campylobacter* infection (Davis *et al.*, 2013). Thus cattle rearing scenario may increase the public health risk in Bangladesh. Therefore, better understanding of these drivers of campylobacteriosis, and of ways to prevent it in LMIC are much needed.

In this study, the circulation of *Campylobacter* in the farm environment was measured as a medium risk with a medium uncertainty level. About 99 % (N=300) of the farm had a concrete floor and of these 96.67% were cleaned daily. Approximately 57% of farms preserved semi-liquid feces that may contribute to contamination of water sources with this pathogen for a longer period (field observation) and would create possible spillover risk in humans through the food chains (Mourkas *et al.*, 2020). A study conducted in Bangladesh confirmed the level of environmental contamination of *Campylobacter* to be 15.6% of pooled swabs (n=90) taken from the manure pit (Hoque *et al.*, 2021). *C. jejuni* cannot grow in low temperatures, however, it can survive for a longer period at higher temperatures in harsh-humid environments (Inglis *et al.*, 2010; Membré *et al.*, 2013). This may contribute to human exposure from the cattle farm holdings at the hot humid weather of Bangladesh. Large-scale environmental contamination occurs though cattle faces and sewage effluent (Aktar *et al.*, 2020). In LMICs, campylobacteriosis is normally endemic because of inadequate cleanliness and sanitation practices, and close contact with animals and water sources (tube well and water bodies) (Teschke *et al.*, 2010). Therefore, incessant risk for introduction in humans and animals would signify a severe public burden. Considering environmental determinants appropriate risk reduction measures to be taken to minimize load in a cattle farm setting and to block spillover in the environments.

The livestock *Campylobacter* was progressively showing resistance to clinically available antimicrobial agents which is a major public health concern (Tang *et al.*, 2020). *Campylobacter* isolates showed resistance to ciprofloxacin that varies from 65-88% during 2005 to 2008 due to easy availability of antibiotics from local pharmacies that gives rise to irresponsible use. However, the use of antibiotics in animal production can play an important role in the transfer of resistance traits. There is no study to estimate *Campylobacter*-antimicrobial resistant status in cattle in Bangladesh. About 49% strains of *C. jejuni* and 42% strains *C. coli*, were documented as multidrug-resistant (MDR) against three or more antimicrobial agents, viz., tetracycline, amoxicillin, fluoroquinolones, streptomycin, and macrolides in poultry and corresponding environmental samples (Portes *et al.*, 2023; Poudel *et al.*, 2024).

The intensification of cattle farming and wide global trading dynamics of livestock enhance the transmission of zoonotic pathogens like *Campylobacter*, for instance, the two most common cattle specific genotypes of *C. jejuni* (sequence types: ST-61 and ST-42) are the causative agent of nearly half a million human campylobacteriosis cases in European countries (Mourkas *et al.*, 2020; Zhang *et al.*, 2024). However, the actual burden is likely much higher (Thépault *et al.*, 2017). Additionally, contact with food-producing animals is the primary risk of human campylobacteriosis in developed countries (Davis *et al.*, 2013). The burden of *Campylobacter* among the cattle related people is enormous in Bangladesh, however, never been investigated. Nevertheless, water, sanitation, and hygiene (WaSH) interventions will be required for successful control of this burden in humans in low-resource settings (Ross *et al.*, 2020). In general poultry is considered to be the source of *Campylobacter* infection in humans in Bangladesh. However, a study confirmed that there should be other sources of campylobacteriosis rather than poultry that need to be explored further (Islam *et al.*, 2014). Therefore, cattle might be an important source of human campylobacteriosis in Bangladesh.

The changes of livestock rearing from extensive farming with the indigenous breed to intensive/semi-intensive farming with crossbred cattle is imperative to fulfill the nutritional demands of the human population. This change creates a burden especially in human health and to a lesser extent in animal health. Therefore, such qualitative evaluation will help to formulate and implement a strategy to control *Campylobacter* infection in Bangladesh considering human, animal and environmental perspectives under the One Health platform.

The main limitation of this study is that a substantial proportion of data was generated through stakeholder interviews. However, a lack of multiple references of secondary data utilized in the risk estimation process of the established nodes of the risk pathways was observed. These limitations signify the medium level of uncertainty of overall *Campylobacter* transmission risk at the cattle farm settings in Bangladesh.

5. Conclusions

This study highlights a significant risk of *Campylobacter* transmission among humans, animals, and the farm environment. Implementing good animal husbandry practices (GAHP), such as separating cattle farms from human habitats, isolating sick animals, and maintaining regular cleaning and sanitation, can reduce exposure risks. Proper management of cattle manure and health education for farm workers, focusing on personal hygiene and the use of PPE, are crucial to minimizing transmission. Additionally, improving water treatment, sanitation, and screening breeding bulls for *C. fetus* under artificial insemination programs can further mitigate risks and support the well-being of cattle and farmers.

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Data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Conflict of interest

None to declare.

Authors’ contribution

Sk Shaheenur Islam was involved in design the study, facilitated to conduct expert elicitation workshop, analyzed and interpreted the data, wrote the paper. Nazmul Hoque and Mohammad Arif conducted field survey, facilitated the expert elicitation workshop. David M. Castellan, Nelima Ibrahim, A H M Taslima Akhter and

Sharmin Sultana analyzed the data and wrote manuscript. Mahmudul Hasan Sikder facilitated the expert consultation workshop. A. K. M. Anisur Rahman interpreted the workshop outcome, critically reviewed the manuscript. S. M. Lutful Kabir was involved in fund acquisition, supervision and critically reviewed the manuscript. All authors have read and approved the final manuscript.

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