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RESEARCH ARTICLE

Cattle as reservoirs of zoonotic parasitic neglected tropical diseases: A One Health perspective on schistosomiasis and soil-transmitted helminths in an endemic district in Ghana

Yvonne Ashong[1], Frank T. Aboagye[2], Emmanuel K. Fiankoh[3], Christopher Dorcoo[1], Philomena Jackson[1], Thelma Koo[1], Clement A. Damoah[1], Irene Ayi[1], Charles Quaye[1], and Dziedzom K. de Souza[1]

1. Department of Parasitology, Noguchi Memorial Institute for Medical Research, Accra, Ghana.
2. Biomedical and Public Health Research Unit, Water Research Institute, Council for Scientific and Industrial Research, Accra, Ghana.
3. Department of Animal Experimentation, Noguchi Memorial Institute for Medical Research, Accra, Ghana.

ABSTRACT

Background and Aim: Zoonotic parasitic infections remain a major public health concern in sub-Saharan Africa, especially where humans and livestock share water sources. Cattle may serve as reservoirs for schistosomiasis and soil-transmitted helminths (STHs), thereby undermining control programs that focus solely on humans. This study applied a One Health lens to investigate the parasitic burden in cattle from peri-urban communities near Weija Lake in the Ga South District of Ghana.

Materials and Methods: A cross-sectional study was conducted across 13 cattle kraals (KRLs) from five endemic communities. Fecal samples (n = 131) were collected by certified veterinary officers and analyzed using sedimentation and flotation techniques. Parasites were identified through light microscopy, and prevalence data were analyzed with 95% confidence intervals. Spatial data and KRL-level variables were also recorded to assess environmental risk factors.

Results: Overall, 80.15% (105/131) of cattle were infected with at least one parasite. The most prevalent species was *Fasciola* spp. (58.77%), followed by *Schistosoma* spp. (SCH) (45.03%), hookworm (21.37%), and *Taenia* spp. (14.50%). Mixed infections occurred in 61.90% of cases, with *Fasciola* spp. SCH combinations accounting for 50% of mixed cases. Notably, *Schistosoma mansoni* – a typically human parasite – was detected in 1.53% of cattle. Parasite prevalence varied significantly by location, and proximity to water sources significantly influenced the risk of infection.

Conclusion: The high prevalence of zoonotic parasites, including human-specific *S. mansoni* in cattle, underscores the animals' role in maintaining transmission cycles. These findings support the integration of veterinary interventions with human public health efforts under the One Health framework. Co-targeting cattle in mass deworming campaigns and implementing environmental controls are crucial for the sustainable elimination of neglected tropical diseases.

Keywords: cattle, *Fasciola* spp., Ghana, neglected tropical diseases, One Health, schistosomiasis, soil-transmitted helminths, zoonoses.

INTRODUCTION

Neglected tropical diseases (NTDs) pose a major global health challenge, disproportionately impacting individuals in low- and middle-income countries [1]. Among these, intestinal parasitic infections are some of the most prevalent, affecting over 1 billion people worldwide – particularly in regions such as sub-Saharan Africa, Southeast Asia, and Latin America – where inadequate access to clean water, sanitation, and healthcare worsens their spread [2,3]. Vulnerable groups,

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Corresponding Authors: Charles Quaye, **E-mail:** cquaye@noguchi.ug.edu.gh
Dziedzom K. de Souza, **E-mail:** ddesouza@noguchi.ug.edu.gh

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Co-authors: YA: yashong@noguchi.ug.edu.gh, FTA: frankaboagye71@gmail.com, EKF: emmankay99@gmail.com, CD: cdorcoo@noguchi.ug.edu.gh, PJ: pjackson@noguchi.ug.edu.gh, TK: tkoo@noguchi.ug.edu.gh, CAD: clemdams2000@gmail.com, IA: iayi@noguchi.ug.edu.gh

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including children and economically disadvantaged populations, experience high morbidity, which leads to deteriorated health, reduced productivity, and financial hardship due to NTDs [4].

Schistosomiasis and soil-transmitted helminthiasis (STH) are among the most persistent NTDs in endemic regions, perpetuating poverty and social inequality [3]. Schistosomiasis, a disease caused by trematodes of the genus *Schistosoma*, is the second most common parasitic infection after malaria, placing approximately 240 million people at risk globally [5]. Similarly, STHs such as *Ascaris lumbricoides*, *Trichuris trichiura* (TT), and hookworms (*Necator americanus* and *Ancylostoma* spp.) contribute substantially to the global burden of NTDs and are frequently found in co-infections with schistosomiasis [6].

These parasites are primarily spread through contact with contaminated soil and water, resulting in extensive infection across endemic areas [2, 5]. Their zoonotic potential – defined by the ability to transfer between animals and humans – complicates eradication efforts, as animals, especially livestock, often act as reservoirs. For instance, species such as *Fasciola* spp. and *Schistosoma bovis* are known to have a significant impact on both human and animal health [7]. Cattle, in particular, are known to harbor various zoonotic parasites, including *Schistosoma* species, and may hybridize with human-specific strains, thereby posing added challenges to conventional, human-centered public health strategies [8]. These animal reservoirs maintain parasite life cycles within endemic zones, highlighting the need for innovative, integrated approaches to mitigate zoonotic transmission – especially where human and livestock interactions are frequent [9]. Despite global efforts to eliminate schistosomiasis, regions such as Ghana's Ga South District remain understudied in terms of the disease's zoonotic aspects, particularly regarding the involvement of livestock.

The One Health paradigm has become a crucial strategy for addressing complex zoonotic infections. This interdisciplinary framework recognizes the interdependence of human, animal, and environmental health, promoting cross-sector collaboration [10]. By aligning veterinary practices with human public health programs, the One Health approach provides a sustainable model for managing zoonotic diseases in endemic regions where livestock plays a central role in livelihoods.

In Ghana, schistosomiasis persists as an endemic disease, especially in communities located near freshwater sources that serve as breeding grounds for intermediate snail hosts [11, 12]. In these areas, the close proximity of humans and livestock to infected water sources increases the risk of zoonotic parasite transmission [13]. Although the role of livestock, particularly cattle, in sustaining parasitic infections is recognized, they are often excluded from public health control strategies [4]. This is especially relevant in Ghana, where common livestock practices involve allowing cattle to roam or tethering them near communal water sources for drinking and grazing. In semi-urban settings like the Ga South District, livestock often share water sources with residents for activities such as washing and bathing. Such frequent human–animal interaction at water contact sites elevates the risk of cross-species parasite transmission and sustains local infection cycles.

A limited understanding of these zoonotic transmission patterns continues to impede long-term control and eradication of parasitic diseases in endemic communities. In Ghana, data on the prevalence and types of parasitic infections in livestock remain scarce [14, 15], which reduces the overall effectiveness of current public health interventions.

Despite decades of mass drug administration (MDA) programs targeting schistosomiasis and STHs in human populations, transmission persists in many endemic settings. This ongoing transmission suggests the presence of overlooked reservoirs and environmental factors that facilitate parasite survival and reinfection. In particular, the role of livestock – especially cattle – as reservoirs for zoonotic helminths remains underexplored in Ghana, despite the fact that such interactions are crucial to understanding the persistence of these infections. Most existing studies in the region focus exclusively on human prevalence or environmental risk factors, often neglecting the animal component of transmission cycles. Moreover, although the international literature increasingly documents hybrid schistosome species capable of infecting both humans and animals, there is a paucity of data from West African contexts, such as Ghana, on the zoonotic overlap and co-infection patterns in livestock. In addition, little is known about how geographic and management factors, such as kraal (KRL) proximity to water sources and livestock grazing behaviors, influence the spatial distribution of infections. This lack of integrated epidemiological data across human, animal, and environmental domains limits the development of effective One Health control strategies.

To address these knowledge gaps, the present study aimed to assess the prevalence, diversity, and co-infection patterns of schistosomiasis and STHs in cattle within peri-urban communities of the Ga South District, an endemic region for schistosomiasis in Ghana. By examining fecal samples from cattle across multiple KRLs and communities, this study sought to determine the extent to which livestock harbor zoonotic parasitic infections and potentially sustain transmission cycles. The investigation also evaluated the influence of environmental and management factors, such as distance from water sources and KRL-level practices, on infection prevalence. Ultimately, this study provides foundational data necessary to inform integrated, livestock-inclusive parasite control strategies under the One Health framework, contributing toward the long-term elimination of NTDs in Ghana and similar endemic regions.

MATERIALS AND METHODS

Ethical approval and Informed consent

Ethical clearance was obtained from the Noguchi Memorial Institute for Medical Research Institutional Review Board (NMIMR-IRB CPN 108/23-24). Additional approval for animal studies was obtained from the University of Ghana Institutional Animal Care and Use Committee (UG-IACUC 051/23-24). All procedures involving animals adhered to guidelines from the World Organization for Animal Health and ARRIVE standards. Fecal samples were collected by a certified veterinary officer using non-invasive techniques with minimal animal restraint. Animals were returned to their KRLs immediately after sampling. Prior written informed consent was obtained from all cattle owners, who also received individual feedback and advice on parasite control. No financial incentives were provided.

Study period and location

The study was conducted from July 2024 to December 2024 in five peri-urban communities within the Ga South District, located along the banks of Weija Lake, approximately 17 km west of Accra, Ghana (Figure 1). This district is recognized as an endemic zone for schistosomiasis [16, 17]. The communities' proximity to the lake promotes routine livestock grazing and watering along its banks, creating high potential for parasite transmission between animals and humans. Sample collection occurred during the dry season characterized by low rainfall (<50 mm/month) and average daytime temperatures between 30°C and 35°C. Lower lake water levels during this season increase the frequency of human and livestock contact with the water, intensifying the risk of schistosome transmission.

Study design and sampling strategy

A cross-sectional observational design was used to evaluate the prevalence and diversity of zoonotic parasitic infections in cattle. The study was structured using the PICOS framework: the Population included cattle in Ga South District; no Intervention was administered; no Comparator was required due to the descriptive nature of the study; and the Outcomes measured included the prevalence and types of parasitic infections. Thirteen KRLs were selected based on their proximity to the lake and their interaction with communal water sources. Sampling was conducted over a 2-week period, with approximately 10 cattle sampled per KRL to ensure representative coverage. Although cross-sectional studies do not provide causality or temporal variation, this design allowed for an efficient and cost-effective epidemiological assessment suitable for guiding integrated control strategies under a One Health framework.

Sample size determination

The sample size of cattle was determined using the standard formula for prevalence studies in veterinary epidemiology [18]:

$$n=\frac{z_{1-(a/2)}p(1-p)}{d^2}$$

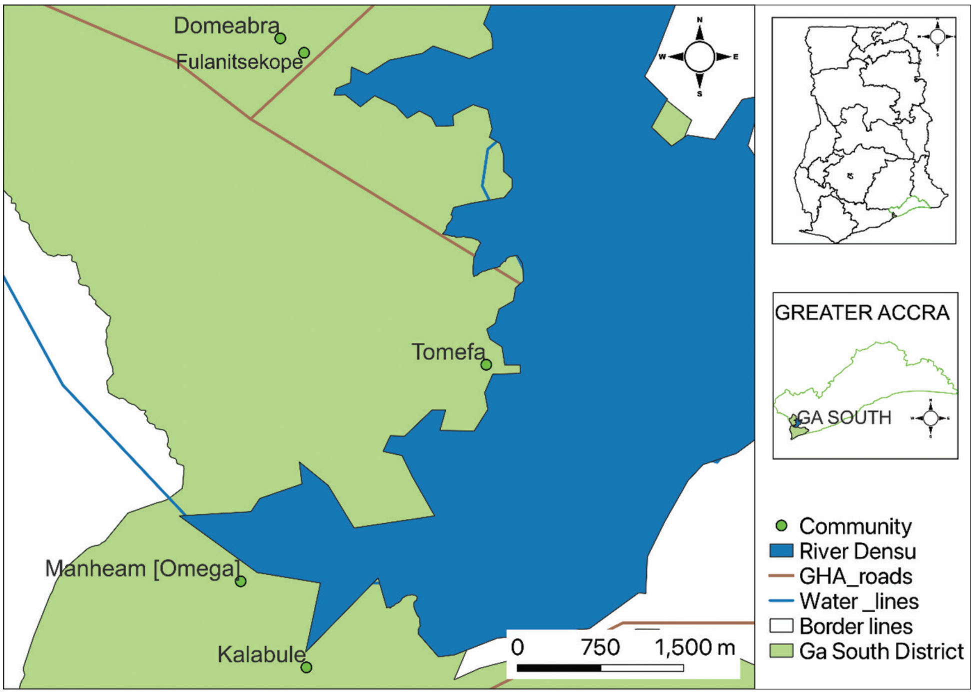

Figure 1: Map of the study area [Source: Map was generated using the geographical coordinates of each kraal, recorded with handheld global positioning system devices, and processed in QGIS v3.28].

Where n is the required sample size, $Z_{1-(a/2)}$ is the standard normal deviate at 95% confidence (1.96), p is the expected prevalence, and d is the desired precision (set at 5%). An expected prevalence of 9.6% (0.096), derived from studies conducted in similar epidemiological settings and based on a prior bovine schistosomiasis study [19], was used to inform the estimate. The sample size was calculated as follows:

$$n = \frac{\left(1.96^2\right) \times 0.096 \times \left(1\text{-}0.096\right)}{(0.05)^2} = 133$$

Thus, the required sample size was approximately 133 cattle. The achieved sample of cattle approximates this requirement and was considered sufficient for the reliable estimation of prevalence within the study population. This sample size enables the detection of infection rates with acceptable precision for public health decision-making and supports the validity of findings within the defined endemic context.

KRL-level and environmental data collection

Structured interviews were conducted with cattle owners or herders using the Open Data Kit platform (ODK Central v2024.2.0, Get ODK Project, San Diego, USA; https://getodk.org), enabling real-time data capture in field settings. Information gathered included animal age, sex, breed, and management practices. Each KRL's geographic coordinates were collected using handheld global positioning system devices and validated using QGIS v3.28 (QGIS Development Team, Beaverton, Oregon, USA; https://qgis.org) for spatial accuracy. These coordinates were also used to calculate each KRL's distance from Weija Lake. Although human and environmental sampling (e.g., water and soil testing) were not included in this phase, future research phases aim to incorporate these components for a more comprehensive zoonotic risk assessment under the One Health framework.

Sample collection and transportation

Fecal samples were collected directly from the rectum of restrained cattle using sterile gloves (changed between animals) by a certified veterinary officer. To minimize cross-contamination, fresh disposable aprons and disinfected footwear were used at each KRL. KRLs were prioritized based on proximity to the lake, intensity of livestock–water interactions, and known history of parasitic infections. Within selected KRLs, cattle were chosen through random sampling. Collected samples were sealed in labeled, airtight containers, placed in ice-packed coolers, and transported to the laboratory. On arrival, they were refrigerated at 4°C and processed within 24 h – aligned with standard parasitological protocols that preserve egg viability [20].

Parasitological examination

Fecal samples were processed using sedimentation techniques following Hansen and Perry [21]. This method was selected for its high recovery efficiency of heavy-shelled eggs, including *Schistosoma* spp. (SCH) and STHs [19, 22, 23]. In brief, 5 g of fecal matter was emulsified in 0.85% saline and then passed through sieves with pore sizes of 355 μm, 180 μm, and 130 μm. The filtrate was centrifuged at 600 × *g* for 5 min, washed twice with saline, and centrifuged again. The sediment was resuspended in 1 mL of saline and transferred to Petri dishes for microscopic examination.

Egg identification was based on morphological characteristics using standard World Health Organization keys [24]. Observations were made under 10× and 40× magnification. This method provides a sensitivity and specificity of 70%–90%, depending on parasite burden and technician expertise [25, 26]. Sedimentation was preferred over flotation for detecting heavier eggs like those of *Fasciola* and *Schistosoma*.

The experimental design and flow of the processes in this study are illustrated in Figure 2.

Quality assurance procedures

To ensure analytical accuracy, at least 10% of processed samples were randomly selected for blinded re-examination by a senior parasitologist. If discrepancies were identified, a third independent review was conducted to reach consensus. All microscopy personnel received standardized training and participated in regular calibration exercises using reference slides. High-resolution images of parasite eggs were archived for consistency checks. These measures ensured methodological rigor and minimized observer bias.

Statistical analysis

All statistical analyses were performed using the Statistical Package for the Social Sciences version 27 (IBM Corp., Armonk, NY) and GraphPad Prism 9.0 (GraphPad Software Inc., Boston, USA). Prevalence was calculated as the proportion of infected cattle among total samples and expressed with 95% confidence intervals. Co-infections were categorized by parasite combinations. Chi-square tests were applied to evaluate associations between parasite prevalence and KRL location or lake proximity. Statistical assumptions – including independence and expected cell frequencies – were verified before analysis. Where applicable, non-parametric tests were used, and Bonferroni corrections were applied to account for multiple comparisons and reduce Type I error risk.

RESULTS

Cattle KRL profile

A total of 131 cattle from 13 KRLs across five communities in the Ga South District were examined and sampled in this study. The majority of cattle were female (n = 71, 54.20%), and over half (56.50%, n = 74) were between 1 and 3 years of age. The highest number of sampled cattle was located in the Manheam (Omega) community (n = 39, 29.80%). In addition, more than half of the cattle were identified as belonging to the West African Shorthorn breed (n = 64, 48.90%). Notably, 93.10% (n = 122) of all examined cattle had never been dewormed by their owners or caretakers. Details of the cattle KRL characteristics are provided in Table 1.

Prevalence of parasitic infections in the community

Out of 131 fecal samples analyzed, 105 tested positive for at least one intestinal parasite, resulting in an overall infection prevalence of 80.15% (Figure 3).

Table 1 : Demographic and management characteristics of cattle in the Ga South District.

Characteristics	Frequency	Percentage
Community		
Tomefa	20	15.27
Manheam (Omega)	39	29.77
Kalabule	22	16.79
Fulanitsekope	30	22.90
Domeabra	20	15.27
Sex of cattle		
Male	60	45.80
Female	71	54.20
Age (years)		
<1 year	10	7.60
1–3 years	74	56.50
>3 years	47	35.90
Breed of cattle		
N’Dama	41	31.30
Sanga (Keteku)	23	17.60
West African	64	48.90
Zebu	3	2.30
History of deworming		
Yes	9	6.90
No	122	93.10

Community-level prevalence rates were as follows: Tomefa – 24.14%, Fulanitsekope – 80.00%, and Kalabule – 77.27% (Table 2). At Manheam (Omega), 94.87% of cattle examined were infected, while all sampled cattle from Domeabra tested positive, indicating a 100% prevalence rate (Table 2).

Prevalence of specific parasitic infections

Eggs of SCH (*S. bovis* and *Schistosoma mansoni*) were identified in 45.03% of the fecal samples analyzed (Table 3). Specifically, *S. bovis* was found in 43.51% and *S. mansoni* in 1.53% of cattle samples. *Fasciola* spp. was detected in 77 cattle, accounting for a prevalence of 58.77%. Five species of STHs were observed (Table 3); hookworm was the most prevalent STH at 21.37% (28/131), followed by *Taenia* spp. at 14.50%. Only one sample contained TT, representing a prevalence of 0.76% (1/131) (Table 3).

Table 2: Community-level prevalence of cattle intestinal parasites with CIs.

Community	Total number of examined	Number of positives	Prevalence (%) (95% CI)
Tomefa	20	7	24.14 (12.28–42.28)^{a,b,c,d,e}
Fulanitsekope	30	24	80.00 (62.53–90.41)^{b,f}
Kalabule	22	17	77.27 (56.30–89.77)^{c,g}
Manheam (Omega)	39	37	94.87 (83.08–98.43)^{d,g}
Domeabra	20	20	100.00 (86.71–100.00)^{e,f}
Total	131	105	80.15 (72.49–86.06)

95% CI=95% confidence interval. Column values with the same superscript (a, b, c, d, e, f and g) differ significantly at $p < 0.05$

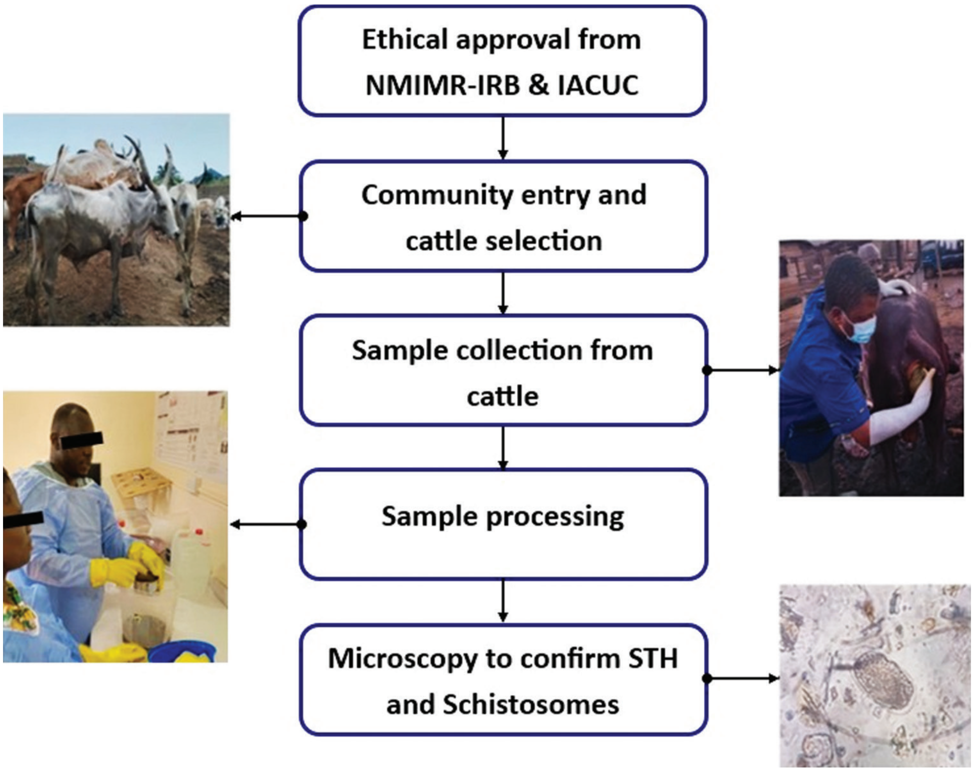

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Figure 2: Field and laboratory activities. Experimental design and process flow of the study.

Mixed infections and co-infection patterns

As shown in Figure 4a, 10.48% (11/105) of positive samples contained only SCH, and 4.76% were positive for a single STH parasite (sSTH only). No sample was positive for more than one STH species alone. Mixed infections involving SCH and STH (SCH-STH) were found in 11.43% (12/105) of samples. Infections involving only *Fasciola* spp. (FSC only) were also seen in 22.86% (24/105) of samples.

A further 22.86% of samples showed co-infection with *Fasciola* spp. and SCH. Mixed infections involving *Fasciola* spp. and STH were present in 16.19% (17/105), while 11.43% (12/105) had concurrent infection with *Fasciola* spp., SCH, and STH.

Among the SCH-STH mixed infections, 50.00% involved SCH and *Fasciola* spp. (Figure 4b). The triple combination of SCH–hookworm–*Fasciola* spp. was seen in 12.50%, while SCH–hookworm mixed infections accounted for 10.42% (5/48). In addition, 8.33% (4/48) of samples had SCH–*Taenia* spp. infections, and SCH–TT was the least common, at 2.08% (Figure 4b). The prevalence of SCH–*Fasciola* spp. co-infection significantly differed from SCH–*Fasciola* spp.–hookworm infection (χ^2 = 15.545, p < 0.001) and from SCH–hookworm infection (χ^2 = 17.647, p < 0.001).

As illustrated in Figure 4c, 60.00% (3/5) of sSTH infections were due to *Taenia* spp. and 40.00% (2/5) to hookworms. The prevalence difference between *Taenia* spp. and hookworm was not statistically significant (χ^2 = 0.360, p = 0.549).

In terms of *Fasciola*–STH mixed infections (Figure 4d), *Fasciola* spp.–hookworm accounted for 52.94%, while *Fasciola* spp.–*Taenia* spp. accounted for 11.76%. A single case (5.88%, 1/17) involved a combination of *Fasciola* spp., *Taenia* spp., and *A. lumbricoides*. The prevalence of *Fasciola* spp.–hookworm significantly differed from *Fasciola* spp.–*Taenia* spp. infection (χ^2 = 6.393, p = 0.012).

Environmental and geographic factors influencing infection

Higher infection prevalence was observed in KRLs located farther from the lake compared to those situated nearer (Figure 5). Grazing duration also played a role; cattle spending more time grazing near water sources were more likely to be infected with SCH (Figure 5).

In Tomefa, two KRLs were sampled. KRL 1 showed a prevalence of 45.45% (5/11) and KRL 2 had 22.22% (2/9); the difference was not statistically significant (χ^2 = 1.115, p = 0.291). In Fulanitsekope, three KRLs were studied. KRL 9 and KRL 10 both reported a prevalence of 70.00% (7/10), while KRL 11 had a prevalence of 100.00% (10/10). However, there was no significant difference in prevalence between KRL 11 and KRL 9 (χ^2 = 3.353, p = 0.067) or KRL 10 (χ^2 = 3.353, p = 0.067).

In Kalabule, KRLs 7 and KRL 8 showed prevalence rates of 60.00% and 91.67%, respectively; this difference was also not statistically significant (χ^2 = 2.974, p = 0.085).

Table 3: Prevalence of parasite species identified in cattle fecal samples.

Parasites	Total number of examined	Number of positives	Prevalence (%) (95% CI)
Flukes			
Schistosoma bovis	131	57	43.51 (35.31–52.08)
Schistosoma mansoni	131	2	1.53 (0.47–5.37)
Fasciola spp.	131	77	58.77 (50.20–66.84)
Soil-transmitted Helminths			
Taenia spp.	131	19	14.50 (9.51–21.56)
Hookworm spp.	131	28	21.37 (15.23–29.17)
Ascaris lumbricoides	131	2	1.53 (0.47–5.37)
Hymenolepis nana	131	2	1.53 (0.47–5.37)
Trichuris trichiura	131	1	0.76 (0.18–4.15)

95% CI=95% confidence interval. The reported prevalence is the overall number of positives identified and does not represent single-species infection per sample

At Manheam (Omega), four KRLs were assessed. KRL 4 and KRL 5 each had a 100.00% infection rate (10/10), while KRL 3 and KRL 6 recorded prevalence rates of 80.00% and 100.00%, respectively.

In Domeabra, two KRLs were examined, and both reported 100.00% infection prevalence (Table 4).

Table 5 provides a further breakdown:

- In KRL 5 (Fulanitsekope), 28.57% (n = 2) of samples had only SCH ova
- In KRL 8 and KRL 13 (Manheam – Omega), 30.00% (n = 3) and 44.44% (n = 4), respectively, had SCH only
- At Tomefa's KRL 2, all infections (100.00%, n = 2) were single-species STH infections
- Similarly, 57.14% (n = 4) of samples in KRL 4 (Fulanitsekope) had single-species STH infections
- The highest mixed STH prevalence occurred in KRL 6 (Fulanitsekope), with 80.00% (n = 8)
- In Tomefa (KRL 1) and Kalabule (KRL 3), all examined cattle (n = 5 and n = 6, respectively) were infected with both SCH and at least one STH species
- At Domeabra, KRL 12 and KRL 13 had mixed SCH–STH infection rates of 90.00% (n = 9) and 60.00% (n = 6), respectively
- Notably, 30.00% of KRL 13 infections were single-species STH, whereas KRL 12 had none (Table 5).

DISCUSSION

Zoonotic role of cattle and transmission complexity

This study provides compelling evidence that cattle in the Ga South District serve as important reservoirs for various parasitic infections, including zoonotic species such as *Fasciola hepatica* and SCH. The observed high overall prevalence (80.77%) and significant rate of mixed infections (61.90%) reflect

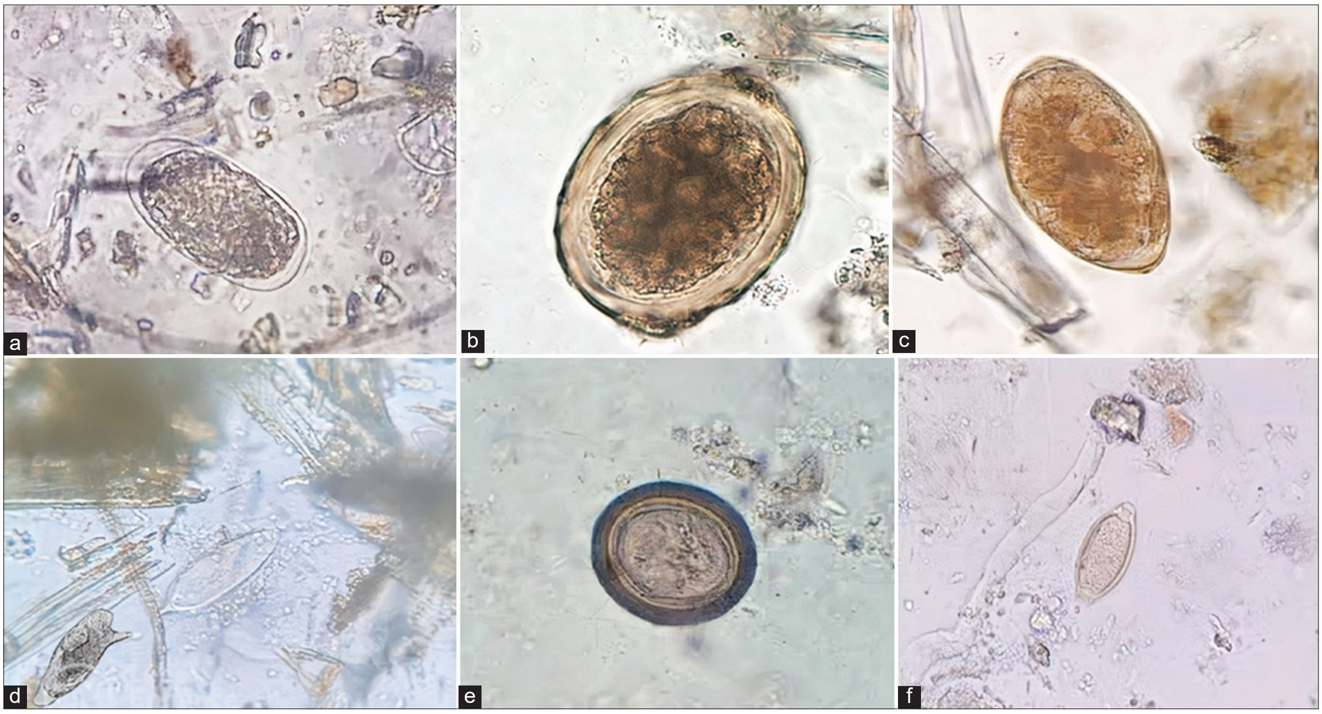

Figure 3: Illustrates parasites identified in fecal samples from cattle [a: Hookworm, b: *Ascaris lumbricoides*, c: *Fasciola* spp. d: *Schistosoma* spp., e: *Taenia* spp., f: *Trichuris trichuira*]. Ova of soil-transmitted helminths and *Schistosoma* spp. identified in cattle fecal samples at 40× magnification. The co-occurrence of zoonotic and gastrointestinal parasites emphasizes the role of cattle as reservoirs of local transmission.

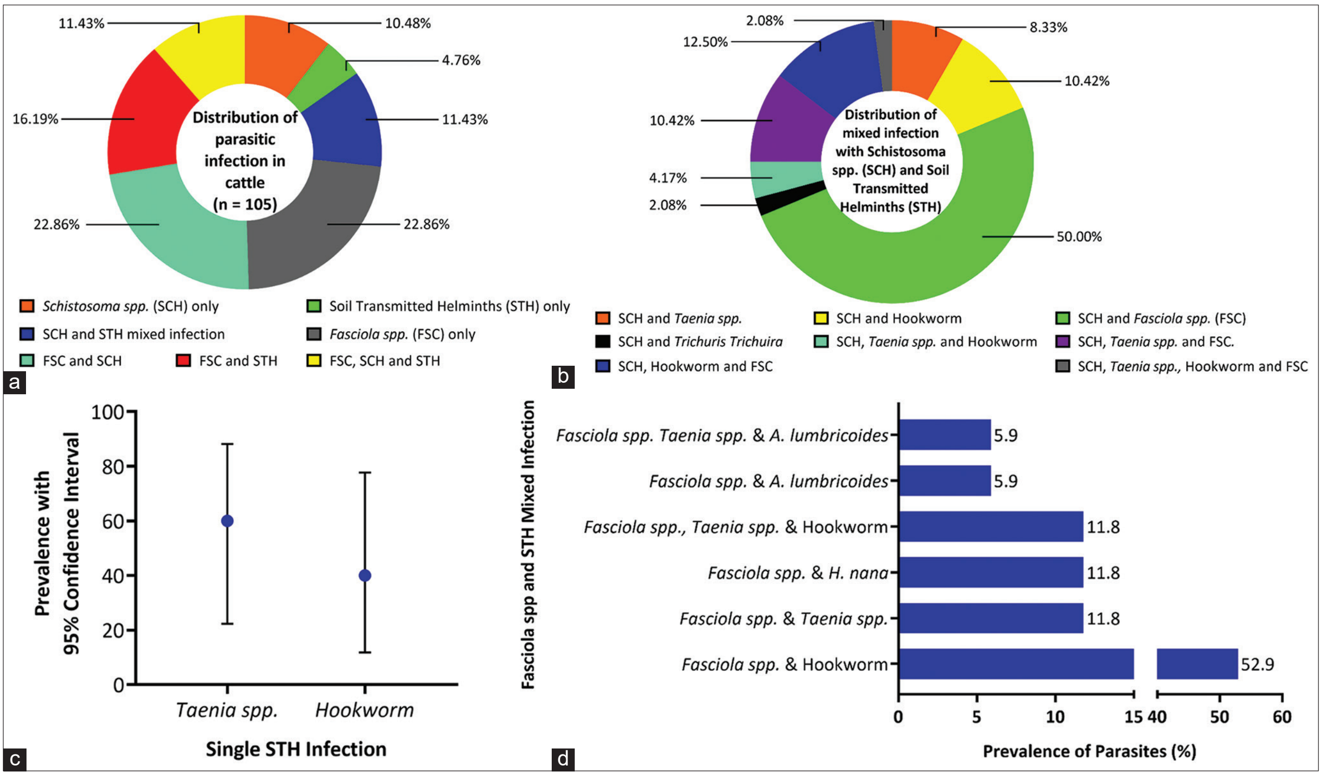

Figure 4: Classification of zoonotic parasitic infection among cattle kraals. ([a] Distribution of parasitic infection, [b] Distribution of mixed SCH, *Fasciola* spp. and STH infection, [c] Distribution of single STH infection, [d] Distribution of *Fasciola* spp. and STH infection). SCH=*Schistosoma* spp., STH: Soil-transmitted Helminths.

the complexity of parasite transmission dynamics in the area. These findings align with previous reports from other endemic regions, emphasizing the global relevance of zoonotic parasitic infections [27, 28].

The identification of SCH in cattle further supports the role of livestock as reservoirs in sustaining schistosomiasis transmission. Similar studies in sub-Saharan Africa have demonstrated the presence of

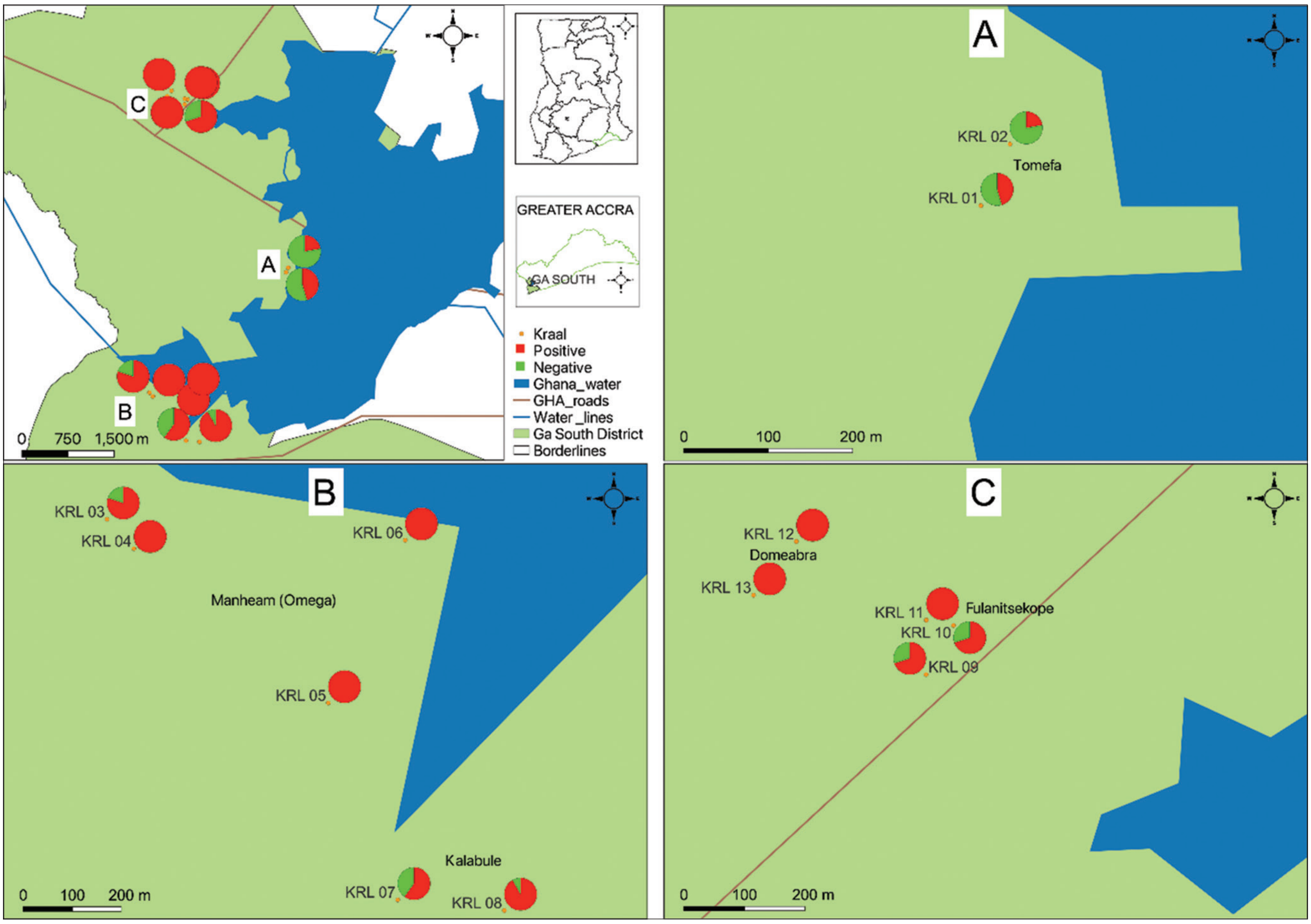

Figure 5: Kraal distribution and proximity to water source. (Distribution of kraal across selected communities with parasite prevalence. [A] Domeabra and Fulanitsekope, [B] Tomefa, and [C] Manheam [Omega] and Kalabule). [Source: Map generated using the geographical coordinates of each kraal and percentage positivity to infections, and processed in QGIS v3.28].

zoonotic *Schistosoma* species in animals grazing near water bodies, reinforcing the link between livestock and persistent transmission cycles [22, 29–31]. These animal reservoirs may contribute to human reinfection, complicating control efforts.

Of particular interest in this study was the detection of both *S. mansoni* and *S. bovis*, suggesting potential cross-species transmission. *S. mansoni* and *S. bovis* belong to two different evolutionary lineages of schistosomes; the *S. mansoni* and the *S. haematobium* groups, respectively. *S. mansoni* is known to infect humans, non-human primates or rodents, while *S. bovis* is known to infect livestock and rodents [32]. The presence of *S. mansoni* eggs in cattle is especially noteworthy, indicating a possible host adaptation by this human-specific species. To the best of our knowledge, this is the first report of *S. mansoni* in cattle in Ghana. Although previous studies have documented *S. mansoni* infections in domesticated and wild animals elsewhere [33, 34], only a few, such as the one by Barbosa *et al*. [35], have confirmed natural infection in cattle – with helminths found in the mesenteries and non-viable eggs observed in feces. Molecular and experimental studies are warranted to confirm viability and adaptation.

Hybridization and epidemiological implications

An important concern in schistosomiasis-endemic areas such as Ghana is the potential hybridization between human and animal schistosome species [36]. Hybrid forms of *S. mansoni* × *S. bovis* have been reported, capable of infecting both humans and cattle [4, 36–38]. These hybrids likely emerge in shared environments where definitive hosts – human and livestock – access the same water bodies, enabling co-infection of snail intermediate hosts. Environmental stressors such as land-use changes, climate variability, and host population shifts may further favor the survival of hybrid strains, enhancing their adaptability and infectivity.

Such hybridization events pose serious challenges to control programs by blurring species boundaries and complicating diagnosis and treatment strategies. Hybrid parasites may combine traits from both parent species, broadening their host range and increasing their resilience in environmental reservoirs [39]. Since MDA strategies typically focus on human populations, untreated animal reservoirs may continue the transmission cycle. This underscores the need for One Health strategies that address both human and animal hosts to effectively interrupt zoonotic transmission.

Fascioliasis burden and shared transmission pathways

The high prevalence of *F. hepatica* (59.23%) observed in this study is consistent with findings from other endemic regions, such as Ethiopia and Kenya, where livestock frequently grazes near waterlogged pastures or irrigation sites [40, 41]. These habitats, shared by animals and humans, facilitate the transmission of fascioliasis and other waterborne parasitic infections. Consequently, fascioliasis control should be included in both public health and veterinary health programs in such settings.

Table 4: Distribution of zoonotic parasitic infection by kraals.

Community	KRL ID	Total number of examined	Number of positives	Prevalence (95% CI)
Tomefa	KRL 01	11	5	45.45 (21.09–72.33)
	KRL 02	9	2	22.22 (6.67–55.61)
Manheam (Omega)	KRL 03	10	8	80.00 (51.62–95.94)
	KRL 04	10	10	100.00 (76.16–100.00)
	KRL 05	10	10	100.00 (76.16–100.00)
	KRL 06	9	9	100.00 (74.11–100.00)
Kalabule	KRL 07	10	6	60.00 (30.79–83.25)
	KRL 08	12	11	91.67 (68.11–99.50)
Fulanitsekope	KRL 09	10	7	70.00 (39.03–89.07)
	KRL 10	10	7	70.00 (39.03–89.07)
	KRL 11	10	10	100.00 (76.16–100.00)
Domeabra	KRL 12	10	10	100.00 (76.16–100.00)
	KRL 13	10	10	100.00 (76.16–100.00)

KRL=Kraal, 95% CI=95% confidence interval

Polyparasitism and its zoonotic risks

Mixed infections were a prominent feature of this study, particularly combinations involving *F. hepatica*, SCH, and hookworms. These findings are in line with studies from Uganda and Tanzania, where livestock exposed to contaminated aquatic environments exhibited similar polyparasitic profiles [42, 43]. Polyparasitism not only undermines livestock productivity but also increases the zoonotic transmission risk in areas with high human–animal interaction. The diverse range of parasite combinations seen in this study suggests that cattle in the Ga South District are exposed to multiple sources of infection, highlighting the need for integrated, multi-pathogen control approaches.

Environmental risk factors and spatial dynamics

Proximity to water sources was a significant determinant of infection prevalence. Cattle that grazed longer around lake areas showed higher infection rates. Interestingly, KRLs situated further from the lake exhibited greater prevalence, potentially because these animals spent extended time at the lake's edge due to a lack of nearby water access. In contrast, KRLs located closer to the lake may have had water directly fetched by owners, reducing cattle–lake contact. This pattern mirrors findings from Malawi and Egypt, where livestock grazing near freshwater environments had elevated infection risks [44, 45].

These results emphasize the influence of environmental variables – especially access to and use of water bodies – on parasite transmission. Implementing strategies such as controlled grazing, water access restrictions, and improved sanitation

Table 5: Pattern of infection by type among the cattle kraals

Community	KRL ID	N	SCH only n (%)	STH only n (%)	STH mixed infection n (%)	SCH-STH mixed infection n (%)
Tomefa	KRL 01	5	0 (0.00)	0 (0.00)	0 (0.00)	5 (100.00)
	KRL 02	2	0 (0.00)	2 (100.00)	0 (0.00)	0 (0.00)
Manheam (Omega)	KRL 03	8	0 (0.00)	4 (50.00)	1 (12.50)	3 (37.50)
	KRL 04	10	3 (30.00)	3 (30.00)	0 (0.00)	4 (40.00)
	KRL 05	10	0 (0.00)	5 (50.00)	0 (0.00)	5 (50.00)
	KRL 06	9	4 (44.44)	0 (0.00)	0 (0.00)	5 (55.56)
Kalabule	KRL 07	6	0 (0.00)	0 (0.00)	0 (0.00)	6 (100.00)
	KRL 08	11	0 (0.00)	5 (45.45)	3 (27.27)	3 (27.27)
Fulanitsekope	KRL 09	7	0 (0.00)	4 (57.14)	3 (42.85)	0 (0.00)
	KRL 10	7	2 (28.57)	1 (14.28)	2 (28.57)	2 (28.57)
	KRL 11	10	0 (0.00)	2 (20.00)	8 (80.00)	0 (0.00)
Domeabra	KRL 12	10	1 (10.00)	0 (0.00)	0 (0.00)	9 (90.00)
	KRL 13	10	1 (10.00)	3 (30.00)	0 (0.00)	6 (60.00)

The reported values are the total positive number of samples (N), the number of positives in subgroup (n). SCH=*Schistosoma* spp., STH: Soil-transmitted Helminths, STH only=Single species STH infection per fecal sample, STH mixed infection=More than one STH parasite per fecal sample, KRL=Kraal infrastructure could mitigate parasite exposure for both livestock and humans [40, 45]. Furthermore, establishing environmental surveillance systems to monitor contamination and infection prevalence in both human and animal populations is essential for targeted intervention planning.

One Health as a framework for integrated control

The One Health approach offers a comprehensive strategy to combat zoonotic parasitic infections by recognizing the interconnectedness of human, animal, and environmental health systems. The findings of this study reinforce the urgency of adopting this framework in endemic communities such as Tomefa, where humans and livestock frequently interact within shared environments [10].

The study's detection of zoonotic parasites in cattle – including human-specific species – further supports the need for integrated interventions. Sole reliance on human-focused strategies, such as MDA campaigns, is insufficient. Successful models from other regions, such as Cambodia, illustrate the benefits of combining human deworming with veterinary health measures, including livestock treatment [46]. This dual approach can reduce human reinfection rates while lowering the parasite load in animal reservoirs.

Moreover, the presence of human-associated parasites in cattle raises important questions about cross-species transmission. Further studies are needed to investigate infection patterns in cohabiting human populations and explore environmental pathways sustaining these dynamics. Environmental sampling will be key to understanding the broader transmission ecology.

Community engagement and policy implications

To ensure long-term success of parasite control in endemic areas, One Health strategies must incorporate community education on zoonotic diseases and their prevention. Promoting farmer-led initiatives such as rotational grazing and managed access to water points may help reduce transmission risks [42]. Community involvement is essential to ensure that interventions are locally appropriate, widely accepted, and sustainable.

Policymakers in Ghana should support One Health integration by fostering institutional collaboration among public health, veterinary, and environmental authorities. This could involve joint surveillance systems, dedicated funding for zoonotic disease control, and the inclusion of animal health considerations in national schistosomiasis elimination programs. Building local capacity – particularly at district and community levels – and investing in public education are also critical to program effectiveness and community compliance.

Limitations and mitigation strategies

This study acknowledged and addressed several methodological limitations. While convenience sampling could introduce bias, KRLs were deliberately selected to reflect varied proximity to environmental risk factors such as water bodies, enhancing representativeness. Seasonal fluctuations in parasite transmission were minimized by conducting sampling during the dry season. Nonetheless, future studies should span multiple seasons to assess temporal dynamics more robustly.

Another potential limitation is the underestimation of low-intensity infections due to the limited sensitivity of microscopy-based diagnostic techniques. To mitigate this, the study employed standardized protocols for sample processing and rigorous quality control – including cross-verification of results by senior parasitologists. These measures strengthened the validity of the findings and enhanced the reliability of parasite prevalence estimates within the study area.

CONCLUSION

This study provides strong epidemiological evidence that cattle in the Ga South District of Ghana serve as significant reservoirs for multiple parasitic infections, including zoonotic species such as *F. hepatica* and SCH. The high overall prevalence of infections (80.15%) and the frequent detection of mixed infections (61.90%) – particularly co-infections involving *Fasciola* spp., SCH, and STHs – underscore the complexity of parasite transmission dynamics within shared human–animal environments. Notably, the detection of *S. mansoni*, a human-specific parasite, in cattle for the first time in Ghana, highlights a potentially critical zoonotic transmission link that warrants further investigation.

From a practical standpoint, these findings challenge the effectiveness of current human-centric parasite control strategies, such as MDA, which do not address persistent reservoirs in livestock. The study illustrates the need for integrated parasite management programs that include regular veterinary deworming, targeted environmental interventions, and community engagement. Spatial analysis further revealed that proximity to and patterns of contact with water sources significantly influence infection risk, reinforcing the importance of environmental management as a complementary control measure.

A key strength of this study lies in its comprehensive One Health design, which considered environmental, animal, and spatial variables. Standardized parasitological techniques, quality-controlled diagnostics, and geospatial mapping collectively enhanced the reliability and policy relevance of the findings. In addition, the cross-sectional survey design enabled the identification of localized hotspots of infection and risk behaviors that may inform tailored intervention strategies.

Despite these strengths, the study also highlights several future directions. Longitudinal studies spanning different seasons are needed to capture temporal variation in infection dynamics. Molecular characterization of *Schistosoma* species in cattle and humans will be critical to confirming zoonotic transmission routes and potential hybridization. Furthermore, integrated surveillance systems encompassing both animal and human health data will enhance early detection and rapid response to emerging parasite threats.

This study reinforces the urgent need to incorporate livestock into national parasite control frameworks. Adopting a holistic One Health approach that bridges veterinary, public health, and environmental sectors is essential for breaking zoonotic transmission cycles and achieving sustainable elimination of NTDs in endemic regions like Ga South. Without such integrated efforts, reinfection will likely persist, undermining the long-term success of current control initiatives.

AUTHORS' CONTRIBUTIONS

YA, FTA, and DKD: Conceptualized the study, methodology, investigation, analyzed and interpreted data, and drafted, reviewed, and edited the manuscript. EKF, CD, PJ, TK, and CAD: Methodology, investigation, analyzed and interpreted data, and reviewed and edited the manuscript. IA and CQ: Methodology, formal analysis, and reviewed and edited the manuscript. All authors have read and approved the final manuscript.

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COMPETING INTERESTS

The authors declare that they have no competing interests.

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