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Prevalence and Distribution of Intestinal Parasites in Humans and Domestic Animals in Wa West District, Ghana: A One Health Perspective

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Research Article

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Abstract

Intestinal parasites pose an important One Health concern in rural communities where humans and domestic animals live in close proximity. This study assessed the prevalence and distribution of intestinal parasites among humans and domestic animals in the Wa West District of Ghana. A descriptive cross-sectional design was used, involving 503 faecal samples comprising 438 animal samples and 65 human samples. Samples were examined using standard microscopy-based diagnostic techniques, including direct wet mounts, concentration and flotation methods, the McMaster technique, and acid-fast staining for Cryptosporidium oocysts. Socio-demographic and husbandry-related data were obtained using structured questionnaires.

The majority (64.0%) of household heads were male, 69.0% of households used an extensive animal-rearing system, and 49.0% reported that they did not routinely monitor animal health. Parasitic infection was detected in 73.1% (320/438) of domestic animals and 67.69% (44/65) of humans. Thirty-two parasite taxa were recorded in animal samples and 17 taxa in human samples. Among animals, goats had the highest infection prevalence (99.1%), followed by sheep (73.9%), cattle (75.0%), dogs (68.2%), cats (66.7%), pigs (65.8%), poultry (59.3%), guinea fowl (50.0%), ducks (40.0%), and rabbits (0%). Community-level animal prevalence was highest in Kendeo (90.5%), followed by Ga (89.2%) and Ponyenitanga (88.1%). In humans, prevalence was highest among children aged 0–5 years (93.8%). Several parasite taxa occurred in both humans and animals. Because identification was based solely on morphology, these findings indicate shared occurrence and potential zoonotic exposure rather than confirmed cross-transmission. Molecular confirmation is recommended to resolve unusual host-parasite associations and investigate possible transmission pathways.

Author Summary

Zoonotic parasitic infections pose a significant public health challenge in rural communities where humans and domestic animals share living spaces. This study used a One Health approach to investigate intestinal parasites in humans and domestic animals in the Wa West District of Ghana. A total of 503 faecal samples (438 from animals and 65 from humans) were examined using standard microscopy-based parasitological techniques. Infection was detected in 73.1% of animals and 67.69% of humans. Thirty-two parasite taxa were recorded in animal samples and 17 in human samples, with several taxa occurring in both hosts. The observed overlap may reflect shared environmental exposure, but morphology alone cannot establish active cross-transmission. The findings support integrated One Health surveillance, improved sanitation, veterinary care, and health education in rural communities.

1. Introduction

Globally, zoonotic diseases are increasing and constitute a significant public health threat in recent times [1]. Over 60.0% of human diseases are infectious, with approximately 75.0% originating from animal sources [2]. However, the dynamics of human-domestic animal interaction play a pivotal role in the spillover of infectious pathogens of zoonotic importance [3]. More than 2.5 billion cases of zoonosis occur each year, with about 2.7 million deaths worldwide. [4]. Moreover, emerging and re-emerging zoonoses such as COVID-19, Monkeypox disease, Ebola virus disease, and Avian influenza highlight the ongoing threat posed by pathogens originating from animal reservoirs [5].

In Africa, the interaction between humans and domestic animals is commonplace and is influenced by several factors, including cultural, environmental, and socio-economic factors [6]. The African continent has witnessed about a 63.0% increase in cases of zoonotic diseases over the last decades [7]. Over 70.0% of the African population, however, relies on backyard animal rearing for their livelihoods and often coexist closely with these domestic animals [8]. However, the proximity and interaction between humans, domestic animals, and wildlife increase the potential for the transmission of pathogens of zoonotic importance [9].

Moreover, most of the annual millions of deaths in Sub-Saharan Africa are due to limited access to healthcare services, close contact with animals, and environmental conditions conducive to the transmission of infectious diseases [10]. Nearly 25.0% and 70.0% of these diseases are zoonotic, which are linked to domestic and wild animals, respectively [11]. This, therefore, highlights the critical role domestic and wild animals contribute to the transmission of zoonotic pathogens of public health importance [12].

About 70% of Ghana's population engages in agriculture, including backyard animal farms with high human-animal interactions, which makes them vulnerable to zoonotic diseases [13]. Reports in Ghana show rabies is endemic due to the failure to vaccinate dogs [14], resulting in human mortality estimated at 1000 annually [15], especially in rural areas [16]. Furthermore, 6.7% and 92.0% of brucellosis and toxoplasmosis were recorded in cattle and humans, respectively, in rural Ghana [17]. In addition, the intimate interactions among humans, domestic animals, and wild animals are more prevalent in rural areas, creating a unique interface for zoonotic disease transmission [18]. This highlights the One Health concept, which emphasizes the interconnection and interplay among human and animal health and well-being, as well as their interactions with the environment.

In Ghana, several studies focused on different zoonotic parasites, including the knowledge of zoonoses [19], tick-borne parasites in livestock [20], giardiasis, and helminths in cattle and dogs [21]. However, these studies did not examine the interaction between humans and domestic animals in rural communities and the potential of parasitic zoonoses. Meanwhile, there is a high risk of infectious pathogens being transmitted from animals to humans via environmental pathways. Moreover, there is limited literature on parasitic zoonoses in the Wa West District. Moreover, in this district,

most households maintain backyard farms and practice free-range animal husbandry. There are reports of zoonosis in this study area with uncertain sources [22]. This has become imperative, necessitating an urgent assessment of interactions and coexistence between humans and domestic animals in household settings, as well as the associated risks of parasitic zoonoses. This is crucial for informing evidence-based interventions and policy considerations [23]. Therefore, this study sought to assess the prevalence of parasites in domestic animals and humans, their coexistence in household settings, and the risk of parasitic zoonoses within the One Health concept in the Wa West District of Ghana.

2. Materials and Methods

Study Area

This study was conducted in the Upper West Region of Ghana, with Wa as its administrative capital. The study was conducted in the Wa West District, which borders Côte d'Ivoire to the west, the Nadowli/Kaleo District to the north, the Wa Municipality to the east, and the Sawla/Tuna/Kalba District to the south. Wechiau is the administrative capital. The district is predominantly agricultural, and households commonly keep poultry, goats, sheep, cattle, pigs, dogs, and cats. The animal sampling dataset contained records from ten communities: Bultuo, Ga, Grungu, Kendeo, Ponyenitanga, Siiroo, Tanvaare, Varinperi, Vieri, and Yeleyiri. Human samples were available from seven communities: Berinyasi, Ponyenitanga, Siiroo, Tanvaare, Varinperi, Vieri, and Yeleyiri.

Research design

In a One Health concept, a descriptive cross-sectional design assessed human-domesticated animal interactions and the risk of parasitic zoonosis. This design was preferred because it measured multiple variables and analyzed the relationship between exposures and outcomes.

Inclusion Criteria for the Study Population

Human participants were eligible if they were permanent residents of the selected communities and aged 0–50 years, a high-risk group for intestinal parasitic infections in rural settings. Both male and female participants, including their occupations and household characteristics, were included. Individuals were selected with or without clinical symptoms, allowing inclusion of both asymptomatic and symptomatic persons. However, individuals with severe illness who were unable to provide stool samples were excluded. Pregnant women, bedridden individuals, and those undergoing antiparasitic treatment at the time of data collection were excluded to avoid bias.

Sampling techniques

A multistage sampling approach was used. The district was stratified into geographical clusters, after which communities and households were selected. Households with domestic animals were identified purposively, and available animals were selected according to accessibility and owner cooperation. Human participants were recruited from participating households according to the eligibility criteria and willingness to provide stool samples.

In the third stage, purposive sampling was used to identify households that owned at least one domestic animal (e.g., pigs, dogs, cats, rabbits, or poultry). Fourthly, animal selection was conducted using convenience sampling, prioritizing animals that were accessible and accustomed to human handling to minimize stress and injury.

Lastly, household members were selected using a total-population sampling approach in which all available individuals were invited to participate. When two or more eligible members were present, one was randomly selected from those available and willing to provide consent (or whose parents/guardians consented for minors) and to provide a stool sample, irrespective of age, sex, occupation, or household characteristics.

A total of 100 households were included in the study. The raw laboratory dataset contained 65 human stool samples and 438 animal faecal samples, giving 503 faecal samples in total. The animal dataset included cats, cattle, dogs, ducks, goats, guinea fowl, pigs, poultry, rabbits, and sheep.

Research instrument

A structured questionnaire was developed in five sections: demographics and household members and characteristics; number and types of domesticated animals and levels of confinement; animal husbandry practices; veterinary services; and knowledge of zoonoses. Additionally, a checklist was developed and used in conjunction with observation to record the number and types of backyard farm animals, levels of confinement, animal-human interactions, husbandry practices, and the presence of animal droppings in the household compound. Lastly, a laboratory tool was developed for faecal sample collection and microscopy examination results.

Data collection procedure

The English questionnaire was translated into local dialects, including Dagaare, Waale, and Brefor. Face-to-face interviews were conducted to elicit responses from study participants using questionnaires. A checklist was used to collect data on the types of animals, numbers, and levels of

confinement from each household. However, to ensure ethical handling and adequate data collection from children, parental assistance was required.

Animal Sampling

Domestic animals were selected according to availability and the cooperation of owners. The animal dataset comprised cats, cattle, dogs, ducks, goats, guinea fowl, pigs, poultry, rabbits, and sheep. Animals reared under extensive and semi-intensive systems were included irrespective of age or sex. Severely sick animals were excluded based on available clinical observation.

Stool Sample Collection

Faecal samples from domestic animals were collected directly from the rectum or from freshly voided faeces. Human stool samples were collected using clean, labelled containers. Approximately 80 g of fresh faecal material was collected where sufficient material was available. Animal and human characteristics, including age and sex, were recorded.

Laboratory Methods

Stool samples were collected and transported on ice to the laboratory within 2–4 hours of collection. Upon arrival, each sample was first examined using a direct wet mount prepared with physiological saline to detect motile protozoa. To increase diagnostic sensitivity, the formol-ether concentration technique was subsequently applied. Approximately 1 g of stool was emulsified in 10% formalin, sieved, and centrifuged with diethyl ether. The resulting sediment was examined microscopically using ×10 and ×40 objectives. Parasite eggs, larvae, cysts, and oocysts were identified based on morphological characteristics, including size, shape, shell or cyst wall thickness, presence of opercula, internal cell structures, and degree of embryonation. Identification followed standard parasitology keys [26–28]. Additionally, the flotation technique was employed to enhance parasite recovery. The centrifugal flotation method using sodium chloride, sodium nitrate, zinc sulfate, and formal-ether solutions was applied to recover ova, oocysts, and larvae according to their specific gravity, as previously described [29]. Zinc sulfate solution was handy for recovering Ancylostoma spp. and Toxocara sp. Acid-fast staining was performed to facilitate microscopic detection of Cryptosporidium sp. The McMaster technique was also used to estimate parasite burden by quantifying the number of parasite eggs per gram of stool, following the method reported earlier [30]. For quality control and diagnostic accuracy, all slides were examined independently by two trained parasitologists. Any discrepancies in identification were resolved through joint re-examination until consensus was reached. No molecular diagnostic methods were employed in this study.

Parasitological Identification

All stool samples were examined using standard microscopic parasitological techniques. Direct wet mounts were used to observe motile protozoa, followed by formol-ether concentration to improve recovery of helminth eggs and protozoan cysts. Additional flotation procedures and acid-fast staining were used as described above. Parasite identification was based on morphological characteristics, including egg or oocyst shape, size, shell or wall characteristics, larval features, and internal structures, using established parasitological identification keys [31, 32]. No molecular diagnostic tools (e.g., PCR or sequencing) were used for confirmation. Two trained parasitologists independently examined the slides, and discrepancies were resolved by joint re-examination and consensus.

Data Management and Analysis

Data were analyzed using descriptive and inferential statistics. Descriptive statistics (frequencies and percentages) were used to summarize parasite prevalence and demographic characteristics.

Chi-square tests were used to compare categorical infection outcomes across communities and between human and animal groups. Fisher's exact test was considered where expected cell frequencies were small. Statistical significance was set at $p < 0.05$. Because infection status was categorical, one-way ANOVA was not used as the primary test of prevalence differences.

Chi-square (χ^2) tests were used to compare prevalence between humans and domestic animals and across age categories. This test was appropriate because the variables were categorical (infected vs. non-infected). The null hypothesis was that infection prevalence was equal between the groups compared. Statistical significance was considered at $p < 0.05$ for all analyses.

Ethical Review and Clearance

Ethical clearance was obtained from the Committee on Human Research, Publications, and Ethics at the Kwame Nkrumah University of Science and Technology (Ref: CHRPE/AP/851/23). Prior to sample collection, written permission was obtained from the Wa West District Assembly. Each participant received a detailed verbal explanation of the study's objectives, procedures, potential risks, and benefits. They were also informed of their right to participate voluntarily and the freedom to withdraw from the study at any time without any consequences. After the briefing, participants who agreed to take part signed a written informed consent form, confirming their voluntary participation.

3. Results

Socio-Demographic Characteristics

Table 1 shows that 64.0% and 36.0% of household heads were male and female, respectively. Additionally, 42% of respondents were aged 41–49, and 6.0% were aged 26–34. Most (83.0%) respondents were married; 7.0%, 9.0%, and 1.0% were single, divorced, and widowed, respectively. Most participants (81.0%) had no formal education, whereas 19.0% had at least a primary education. The majority (64.0%) of the respondents were Christians, 22.0% were Muslims, and 14.0% were Traditionalists. Also, 92.0% of the respondents were farmers, 6.0% were teachers, and 2.0% were petty traders. Most (69.0%) households had a large family of more than 10 members, while 42.0% had 3–4 children (See Table 1).

Table 1
Socio-Demographic Characteristics of the Respondents

Variable	Frequency	Percentage (%)
Gender		
Male	64	64.0
Female	36	36.0
Age Range		
18–25	15	15.0
26–34	6	6.0
35–40	17	17.0
41–49	42	42.0
50-above	19	19.0
Educational Status		
Literate	19	19.0
Illiterate	81	81.0
Employment status		
Employed	6	6.0
Unemployed	91	91.0
Self-employed	3	3.0
Occupation		
Farmer	92	92.0
Teachers	6	6.0
Petty Trader	2	2.0
Family Size		
1–3	4	4.0
4–6	6	6.0
7–9	21	21.0
≥ 10	69	69.0
Children in the Household		
1–2	20	20.0
3–4	42	42.0
5–6	25	25.0
≥ 7	12	12.0

Note: The age range in Table 1 refers to mature participants who signed the consent form and responded to the questionnaire.

Animals and Husbandry Practice

Table 2
Animals and Husbandry Practice

Variables	Frequency	Percentage (%)
Presence of animals in the household		
Yes	100	100.0
Number of animals you own		
1–19	9	9.0
20–39	12	12.0
40–69	3	3.0
70–80	76	76.0
Routine disease monitoring of animals		
Yes	46	46.0
No	49	49.0
Sometimess	5	5.0
Animals are allowed to roam about		
Yes	98	98.0
No	2	2.0
Form of rearing/raising the animals.		
Semi-intensive	31	31.0
Extensive	69	69.0
Rear animals for commercial purposes		
Goats	63	63.0
Sheep	14	14.0
Cattle	10	10.0
Poultry	11	11.0
Pigs	2	2.0
Feed animals daily		
Yes	21	21.0
No	66	66.0
Sometimes	13	13.0
Animals you own		
Poultry	96	96.0
Goat	91	91.0
Dogs	54	54.0
Cats	49	49.0
Sheep	63	63.0
Cattle	17	17.0
Pigs	51	51.0

Table 2 shows that all the respondents had animals in their homes, using either an extensive system (69.0%) or a semi-intensive system (31.0%) for rearing them. However, 49.0% of respondents do not routinely monitor animals, whereas 46.0% and 5.0% are monitored regularly and sometimes, respectively, for diseases. Most respondents (98.0%) indicated that their animals were not confined, and 66.0% did not feed them at home; 21.0% and 13.0% fed their animals daily and occasionally, respectively. Concerning the type of animals reared, 96.0% kept poultry, 91.0% kept goats, while 63.0%, 54.0%, and 51.0% kept sheep, dogs, and pigs, respectively. Also, 49.0% and 17.0% kept cats and cattle, respectively, as shown in Table 2. The

majority (63.0%) of respondents raised goats, while 14.0%, 11.0%, 10.0%, and 2.0% reported raising sheep, cattle, poultry, and pigs for commercial purposes, respectively.

Table 3
Parasitic Infection Rates among Communities and Animals

Community	Cats n (%)	Cattle n (%)	Dogs n (%)	Ducks n (%)	Goats n (%)	Guinea fowl n (%)	Pigs n (%)	Poultry n (%)	Rabbit n (%)	Sheep n (%)	Positive n (%)	P-value
Bultuo	1 (2.63%)	2 (5.26%)	5 (13.15%)	0	1 (2.63%)	0	3 (7.89%)	4 (10.5%)	0	9 (23.7%)	25 (65.8%)	
Ga	0	1 (2.70%)	2 (5.41%)	0	15 (40.5%)	0	0	8 (21.6%)	0	7 (18.9%)	33 (89.2%)	
Grungu	1 (1.75%)	1 (1.75%)	2 (3.51%)	0	13 (22.8%)	0	5 (8.77%)	18 (31.6%)	0	2 (3.51%)	42 (73.7%)	
Kendeo	0	0	2 (3.77%)	0	23 (43.4%)	0	0	15 (28.3%)	0	8 (15.1%)	48 (90.5%)	
Ponyenitanga	0	1 (2.38%)	2 (4.76%)	1 (2.38%)	11 (26.3%)	0	3 (7.14%)	10 (23.8%)	0	9 (21.4%)	37 (88.1%)	
Siiroo	0	10 (19.2%)	0	1 (1.92%)	8 (15.4%)	0	0	12 (23.1%)	0	3 (5.77%)	34 (65.4%)	
Tanvaare	0	0	1 (2.70%)	0	8 (21.6%)	0	2 (5.41%)	8 (21.6%)	0	4 (10.8%)	23 (62.2%)	
Varinperi	0	0	0	0	8 (28.6%)	0	1 (3.57%)	2 (7.14%)	0	1 (3.57%)	12 (42.8%)	
Vieri	0	0	0	0	4 (13.3%)	1 (3.33%)	0	11 (36.7%)	0	5 (16.7%)	21 (70.0%)	
Yeleyiri	0	0	1 (1.56%)	0	9 (14.1%)	0	11 (17.2%)	1 (1.56%)	0	23 (35.9%)	45 (70.3%)	
Total	2 (66.7%)	15 (75.0%)	15 (68.2%)	2 (40.0%)	100 (99.1%)	1 (50.0%)	25 (65.8%)	89 (59.3%)	0 (0%)	71 (73.9%)	320 (73.1%)	< 0.001

Table 3 shows an overall parasite prevalence of 73.1% (320/438) among the sampled domestic animals. Kendeo recorded the highest community-level prevalence (90.5%), followed by Ga (89.2%) and Ponyenitanga (88.1%). Prevalence was also high in Grungu (73.7%), Yeleyiri (70.3%), Vieri (70.0%), Siiroo (65.4%), Bultuo (65.8%), Tanvaare (62.2%), and Varinperi (42.8%). Among animal categories, goats had the highest prevalence (99.1%), followed by cattle (75.0%), sheep (73.9%), dogs (68.2%), cats (66.7%), pigs (65.8%), poultry (59.3%), guinea fowl (50.0%), ducks (40.0%), and rabbits (0%). Overall differences in infection prevalence across communities were statistically significant ($\chi^2 = 36.152$, $p < 0.001$), as were differences across animal categories ($\chi^2 = 56.369$, $p < 0.001$). Overall parasite prevalence among domestic animals was 73.1% (320/438). Prevalence differed significantly across communities ($\chi^2 = 36.152$, $p < 0.001$) and animal categories ($\chi^2 = 56.369$, $p < 0.001$). Goats showed the highest prevalence (99.1%), followed by cattle (75.0%) and sheep (73.9%).

Prevalence of Parasite Isolates among Domesticated Animals

The animal parasite dataset contained 32 morphologically identified taxa. The most frequently recorded taxa were Trichostrongylus spp. (83 infections; 18.95%), Eimeria spp. (78; 17.81%), Strongyloides spp. (62; 14.16%), Bunostomum spp. (49; 11.19%), Oesophagostomum spp. (39; 8.90%), and Ancylostoma caninum (35; 7.99%). Other taxa occurred less frequently. Because identification was morphological, species-level assignments should be interpreted cautiously.

The 438 animal samples yielded 32 morphologically identified parasite taxa. Because individual animals could harbour more than one taxon, the sum of parasite-positive observations exceeds the number of animals examined. Percentages in Table 4 use 438 as the denominator.

Table 4
Prevalence of morphologically identified parasite taxa among domestic animals (n = 438)

Parasite	Animal infection (n)	Percentage (%)	P-value
Ancylostoma caninum	35	7.99	< 0.001
Ascaridia sp.	6	1.37	0.0086
Balantidium coli	17	3.88	< 0.001
Bunostomum sp.	49	11.19	< 0.001
Dioctophyma renale	4	0.91	0.839
Echinococcus sp.	2	0.46	0.245
Fasciola sp.	15	3.42	< 0.001
Filaroides osleri	1	0.23	0.563
Haemonchus contortus	5	1.14	< 0.001
Heterakis galliae	4	0.91	< 0.001
Linguatula serata	2	0.46	0.543
Muellerius capillaris	2	0.46	0.432
Moniezia benedeni	2	0.46	< 0.001
Moniezia expansa	3	0.68	0.453
Nanophyetus salmincola	1	0.23	< 0.001
Nematodirus sp.	9	2.05	< 0.001
Oesophagostomum sp.	39	8.90	0.002
Cryptosporidium sp.	13	2.97	< 0.001
Eimeria sp.	78	17.81	< 0.001
Isospora sp.	6	1.37	< 0.001
Alaria sp. *(ova)*	2	0.46	0.563
Paragonimus kellicotti	5	1.14	0.078
Platynosomum fastosum	7	1.60	< 0.001
Schistosoma bovis	4	0.91	0.002
Stephanurus dentatus	9	2.05	0.034
Strongyloides sp.	62	14.16	< 0.001
Strongylus spp.	13	2.97	< 0.001
Toxocara canis	5	1.14	< 0.001
Toxocara cati	7	1.60	< 0.001
Toxascaris leonina	8	1.83	< 0.001
Trichostrongylus sp.	83	18.95	< 0.001
Trichuris vulpis	13	2.97	< 0.001

Prevalence of Parasites among Participants in the Study Sites

Table 5
Prevalence of Parasites among Participants in the Study Sites

Variable	Total samples	Positivity Rate	Percentage (%)	χ^2	P-value
TOTAL	**65**	**44**	**67.69%**	**14.892**	**0.0001**
Sex					
Male	32	20	62.5	0.379	0.537
Female	33	24	72.7		
Age					
0–5	32	30	93.8	22.013	0.0002
6–10	15	6	40.0		
11–15	10	4	40.0		
16–25	4	2	50.0		
26 and above	4	1	25.0		
Community					
Berinyasi	7	5	71.4	4.599	0.5961
Ponyenitanga	3	3	100		
Siiroo	1	0	0.00		
Tanvaare	12	8	66.7		
Varinperi	10	6	60.0		
Vieri	28	20	71.4		
Yeleyiri	4	2	50.0		

Note: The age range in Table 5 applies to participants who provided stool samples for laboratory analysis.

A chi-square test comparing infection prevalence between humans (67.69%, 44/65) and domestic animals (73.1%, 320/438) showed no statistically significant difference ($\chi^2 = 0.815$, $p = 0.367$). Thus, the study did not demonstrate a statistically significant difference in overall infection prevalence between the two sampled host groups.

Among humans, parasite prevalence was 67.69%. Females had a higher prevalence (72.7%) than males (62.5%), although the difference was not statistically significant ($\chi^2 = 0.379$, $p = 0.537$). Prevalence was highest among participants aged 0–5 years (93.8%) and lowest among those aged 26 years and above (25.0%), with a statistically significant difference across age groups ($\chi^2 = 22.013$, $p = 0.0002$). Human community-level prevalence was 100% in Ponyenitanga, 71.4% in Berinyasi and Vieri, 66.7% in Tanvaare, 60.0% in Varinperi, 50.0% in Yeleyiri, and 0% in Siiroo.

Parasites recovered from Humans and Domesticated Animals, and the Risk of Zoonosis.

Table 6 summarizes parasite taxa recorded in both human and animal samples. The occurrence of the same morphologically identified taxa in different hosts may indicate shared environmental exposure or potential zoonotic risk; however, it does not establish cross-transmission. Because parasite identification was based on morphology, unusual host–parasite associations should be interpreted cautiously and confirmed using molecular methods in future studies.

Table 6
Parasite taxa recorded in both animal and human samples. Shared occurrence is presented descriptively and should not be interpreted as evidence of cross-transmission.

Parasite taxon	Animal infections (n)	Animal (%)	Human infections (n)	Human (%)
Ancylostoma caninum /Ancylostoma sp.	35	7.99	1	1.54
Ascaridia sp.	6	1.37	1	1.54
Bunostomum sp.	49	11.19	5	7.69
Fasciola sp.	15	3.42	1	1.54
Haemonchus sp.	5	1.14	1	1.54
Heterakis galliae	4	0.91	1	1.54
Cryptosporidium sp.	13	2.97	5	7.69
Eimeria sp.	78	17.81	5	7.69
Alaria spp. (ova)	2	0.46	1	1.54
Platynosomum fastosum	7	1.60	3	4.62
Strongyloides sp.	62	14.16	3	4.62
Strongylus spp.	13	2.97	5	7.69
Toxocara canis	5	1.14	1	1.54
Toxascaris leonina	8	1.83	1	1.54
Trichuris vulpis	13	2.97	3	4.62

4. Discussions

This study found that all 100 participating households kept domestic animals. Poultry (96.0%) and goats (91.0%) were the most commonly owned animal categories, followed by sheep (63.0%), dogs (54.0%), pigs (51.0%), cats (49.0%), and cattle (17.0%). Most households (69.0%) used an extensive rearing system. These patterns indicate substantial human–animal contact and provide an important context for a One Health assessment of intestinal parasite exposure.

The extensive rearing system and limited routine animal-health monitoring may increase opportunities for environmental contamination with animal faeces and subsequent human exposure. However, the present cross-sectional design cannot establish that animal infections caused human infections. The findings therefore support integrated surveillance and preventive measures rather than attribution of a specific transmission pathway. Parasitic infection was detected in 73.1% of the 438 domestic animals examined. Prevalence varied markedly by animal category, ranging from 0% in the single sampled rabbit to 99.1% in goats. The animal dataset contained 32 morphologically identified parasite taxa. *Trichostrongylus* spp., *Eimeria* sp., *Strongyloides* sp., *Bunostomum* sp., *Oesophagostomum* sp., and *Ancylostoma caninum* were among the most frequently recorded taxa. Differences from other studies may reflect differences in host composition, environmental conditions, husbandry systems, sample size, and diagnostic methods. In humans, 44 of 65 participants (67.69%) were positive for at least one intestinal parasite. Prevalence was significantly associated with age, with the highest proportion observed among children aged 0–5 years (93.8%). The higher prevalence in young children may be compatible with increased exposure to contaminated environments and less developed hygiene practices, although these mechanisms were not directly tested in the present analysis.

The human dataset contained 17 parasite taxa. Several taxa were recorded in both human and animal samples, including *Ancylostoma, Ascaridia, Bunostomum, Fasciola, Haemonchus, Heterakis, Cryptosporidium, Eimeria, Alaria, Platynosomum, Strongyloides, Strongylus, Toxocara/Toxascaris*, and *Trichuris*. Such overlap is compatible with shared environmental exposure, particularly where humans and animals live in close proximity, but morphology alone cannot establish that the organisms in the different hosts are genetically identical or that transmission occurred between them. The overall infection prevalence was not significantly different between humans and domestic animals ($\chi^2 = 0.815$, $p = 0.367$). This indicates comparable levels of infection in the sampled groups, but it should not be interpreted as evidence of a common transmission pathway. The substantial occurrence of intestinal parasites in both host groups nevertheless supports integrated One Health surveillance involving human health, veterinary health, sanitation, and environmental management. Several parasite taxa were recorded in hosts outside their usual or expected host associations. Because the study relied exclusively on morphological identification, these findings may reflect shared environmental exposure, limitations in morphological discrimination, or misidentification. They should therefore not be interpreted as confirmed cross-species transmission. Molecular characterization would be required to verify species identity and investigate possible transmission linkages. Morphological identification was the principal diagnostic approach in this study. Although microscopy is practical and widely used in field-based parasitological surveys, it has limitations in sensitivity and taxonomic resolution. The unusually broad host range reported for some taxa reinforces the need for molecular

confirmation in future studies. The co-occurrence of intestinal parasites in humans and domestic animals highlights the interconnected nature of human, animal, and environmental health. A One Health framework is therefore appropriate for coordinating surveillance, sanitation, veterinary services, health education, and preventive interventions. The present data support this integrated approach but do not demonstrate active cross-transmission. Interventions should therefore focus on reducing opportunities for environmental contamination and human exposure. These include improved household sanitation, safe disposal of animal faeces, routine veterinary care, appropriate antiparasitic treatment, hand hygiene, food safety, and coordinated surveillance across human, animal, and environmental health sectors. This study highlights the high burden of intestinal parasites in rural Ghanaian communities, with significant overlap between humans and domestic animals. The findings underscore the need for integrated One Health surveillance, improved sanitation, veterinary care, and health education.

Study Limitations

Several limitations should be considered when interpreting the findings. First, some participants were unwilling to participate, contributing to the relatively small human sample (65 compared with 438 animal samples). Second, purposive household selection and convenience-based selection of available animals may have introduced selection bias. Third, the animal and human community datasets were not identical: animal records covered ten communities, whereas human samples were available from seven communities. Fourth, the study relied exclusively on morphological identification, which limits diagnostic sensitivity, specificity, and taxonomic resolution. Consequently, unusual host–parasite associations cannot be considered definitive without molecular confirmation. Finally, the raw human parasite-by-community table contained internal inconsistencies between row sums and reported totals; because those discrepancies could not be resolved without the original participant-level records, that detailed distribution was not used to generate new claims in the revised manuscript. The small human sample size relative to animals, reliance on morphology without molecular confirmation, and potential misclassification of taxa. Future studies should incorporate molecular diagnostics to confirm host-parasite associations and clarify zoonotic transmission pathways.

5. Conclusion

The study revealed a high prevalence of intestinal parasitic infection among domestic animals and humans in the Wa West District. Overall prevalence was 73.1% among animals (320/438) and 67.69% among humans (44/65). Thirty-two parasite taxa were morphologically identified in animal samples and 17 in human samples, with several taxa occurring in both host groups. Because identification was based solely on morphology, the findings indicate shared occurrence and potential zoonotic exposure rather than confirmed cross-transmission. Molecular studies are recommended to confirm parasite identity and investigate possible transmission pathways. The findings support coordinated One Health surveillance involving human health, animal health, and environmental health sectors.

6. Recommendation

A coordinated One Health approach is recommended to address the observed patterns of human–animal co-infection. This includes synchronized community deworming for both humans and domestic animals, strengthened veterinary outreach for routine faecal screening, treatment, and owner education, and improved household sanitation practices such as safe disposal of animal faeces and increased latrine use. Targeted health education on hand hygiene, food safety, and safe animal handling is essential, as are environmental management measures, such as proper waste disposal and improved drainage, to minimize soil contamination. Finally, integrated surveillance involving health, veterinary, and environmental officers is crucial for monitoring parasite transmission and guiding timely interventions.

Declarations

Consent for publication

We have all read the final manuscript and consented to it for publication.

Conflict of interest

The authors declared no conflict of interest.

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Authors' Contributions

JKZ was responsible for data collection, data analysis, and manuscript drafting. DDY played a pivotal role in conceptualizing and developing the manuscript, provided critical edits, contributed to data analysis and interpretation, and ensured its intellectual rigour and clarity. NYAB reviewed the

manuscript and approved it for publication. All authors read and approved the final manuscript.

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Availability of supporting data

All data used for this manuscript are available upon a reasonable request.

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