



Prevalence and Distribution of Intestinal Parasites in Humans and Domestic Animals in Wa West District, Ghana: Implications for One Health Surveillance

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Abstract

Intestinal parasites are 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 detected 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 direct wet mounts, formol-ether concentration, flotation procedures, acid-fast staining and the McMaster technique. Socio-demographic and husbandry-related information was obtained using structured questionnaires. Among the sampled animals, parasite detection was 73.1% (320/438), while 67.7% (44/65) of human participants had at least one parasite taxon detected. Thirty-two morphologically identified taxa were recorded in animal samples and 17 taxa were recorded in human samples. Among animal categories, goats had the highest positivity (99.0%, 100/101), followed by cattle (75.0%, 15/20) and sheep (73.9%, 71/96). Among human participants, positivity was highest in children aged 0-5 years (93.8%, 30/32). Several taxa were recorded in both host groups. Because identification was based solely on morphology and the sampling was non-probabilistic at household/animal levels, the observed overlap should be interpreted as shared detection or possible shared environmental exposure rather than confirmed zoonotic transmission. These findings support integrated One Health surveillance, improved sanitation, veterinary care and health education.

The study identified a high frequency of intestinal parasite detection among sampled humans and domestic animals in Wa West District. All 100 participating households kept domestic animals and most used extensive animal-rearing systems. Although several morphologically identified taxa occurred in both humans and animals, the study did not establish cross-transmission because the samples were not fully matched and no molecular confirmation was performed. The findings therefore highlight opportunities for shared environmental exposure and the need for coordinated human, animal and environmental health surveillance. Future studies should use matched household sampling, larger probabilistic samples and molecular methods to verify unusual host-parasite associations.

Keywords: Intestinal parasites; Domestic animals; Parasite detection; Shared environmental exposure; One health; Ghana

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Introduction

Globally, zoonoses remain an important public-health concern because pathogens can move between people, animals and shared environments. WHO defines zoonoses as diseases or infections naturally transmissible between vertebrate animals and humans and emphasizes their importance in settings where people interact closely with animals [1]. One Health provides an integrated framework for addressing these interconnected risks by linking human, animal and environmental health [2,3].

Human activities, livestock production and close human-animal interfaces can create opportunities for pathogen exposure and spillover. One Health surveillance is therefore particularly relevant in rural settings where domestic animals, people and the environment interact closely [2,3]. Free-ranging animals and inadequate sanitation may increase opportunities for environmental contamination with faecal material, although the present study did not directly measure environmental contamination.

In Ghana, studies have documented zoonotic-disease awareness among pet owners and intestinal parasites in domestic animals [4-12]. Research from Ghana and other settings also demonstrates that intestinal parasites can occur where humans and domestic animals live in close proximity [9-12]. However, detection of the same morphological taxon in different hosts does not by itself demonstrate transmission between those hosts.

The Wa West District is predominantly rural and agricultural and many households keep domestic animals under extensive or semi-intensive systems. Close human-animal contact and the movement of animals around household compounds create plausible opportunities for shared environmental exposure to faecal parasites. Nevertheless, the extent and distribution of intestinal parasite detection among humans and domestic animals in this setting remain insufficiently documented.

Therefore, this study assessed the prevalence and distribution of intestinal parasites detected among humans and domestic animals in Wa West District, Ghana and described the occurrence of morphologically identified taxa across host groups within a One Health surveillance framework. The study was descriptive and cross-sectional; consequently, it was not designed to establish causal transmission pathways or confirm zoonotic transmission.

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

A descriptive cross-sectional design was used to describe intestinal parasite detection among sampled humans and domestic animals and to characterize household and animal-husbandry conditions. The sampling framework was multistage, but non-probability selection was used at the household and animal levels. Accordingly, prevalence estimates are presented as prevalence among sampled participants and animals rather than as population-representative estimates for the entire Wa West District.

Inclusion criteria for the study population

Human participants were permanent residents of the selected communities and were eligible if they could provide a faecal sample and where applicable, provide informed consent or have parental/guardian consent. Participants included children and adults. Individuals who were severely ill and unable to provide a sample, pregnant women, bedridden individuals and persons undergoing antiparasitic treatment at the time of data collection were excluded. The questionnaire age categories for mature respondents were reported separately from the laboratory age categories used for human parasite analysis.

Sampling techniques

A multistage sampling framework was used. The district was stratified into geographical clusters, after which communities and households were selected. Households with domestic animals were identified purposively. Available animals were selected by convenience according to accessibility and owner cooperation. Human participants were recruited from participating households according to the eligibility criteria and willingness to provide a faecal sample. Where two or more eligible household members were available, one was randomly selected from those available and willing to participate. This combination of purposive household selection, convenience animal selection and limited random selection of household members was treated as a non-probability sampling framework rather than a fully probability-based design.



Households were eligible when they owned at least one domestic animal, including pigs, dogs, cats, rabbits or poultry. Animal selection prioritized accessible animals that could be handled safely. These procedures may have introduced selection bias and therefore limit the generalizability of the findings.

A total of 100 households were included in the study. Human and animal samples were collected from the same participating households, providing a household-level One Health sampling framework. The laboratory dataset contained 65 human faecal samples and 438 animal faecal samples, giving 503 samples in total. The animal dataset included cats, cattle, dogs, ducks, goats, guinea fowl, pigs, poultry, rabbits and sheep.

Research instrument

A structured questionnaire contained sections on respondent characteristics, household composition, domestic-animal ownership, animal confinement and husbandry practices, veterinary services and knowledge of zoonoses. A checklist and observation schedule were used to record animal types, numbers, confinement, animal-human interactions, husbandry practices and visible animal faecal contamination within household compounds. A laboratory recording form was used for faecal sample collection and microscopy findings.

The English questionnaire was translated into Dagaare, Waale and Brefor. Face-to-face interviews were conducted with adult respondents. Parental or guardian assistance was used when information was required for children. The household checklist was completed during the visit and faecal samples were labelled with study identifiers before transport to the laboratory.

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 owner cooperation. Animals reared under extensive or semi-intensive systems were eligible irrespective of age or sex. Severely sick animals were excluded on the basis of available clinical observation. The animal dataset comprised cats, cattle, dogs, ducks, goats, guinea fowl, pigs, poultry, rabbits and sheep.

Faecal sample collection

Faecal samples from domestic animals were collected directly from the rectum or from freshly voided faeces.

Human faecal samples were collected in 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

Samples were transported on ice to the laboratory within 2-4 hrs of collection. Each sample was examined using a direct wet mount prepared with physiological saline, followed by formol-ether concentration. Approximately 1 g of faecal material was emulsified in 10% formalin, sieved and centrifuged with diethyl ether and the sediment was examined microscopically using $\times 10$ and $\times 40$ objectives. Parasite stages were assessed on the basis of morphology, including size, shape, shell or wall characteristics, opercula, internal structures and degree of embryonation, using standard parasitology references [5,6]. Centrifugal flotation procedures using sodium chloride, sodium nitrate, zinc sulfate and formal-ether solutions were used to improve recovery of ova, oocysts and larvae. Acid-fast staining was used for microscopic detection of *Cryptosporidium* oocysts and the McMaster technique was used to estimate faecal egg counts where applicable [7,8]. All slides were independently examined by two trained parasitologists. Discrepancies were resolved by joint re-examination and consensus. The source records did not document method-specific sample counts, McMaster analytical sensitivity or positive/negative control performance; these details were therefore not inferred in the revision. No PCR, sequencing or other molecular diagnostic method was used.

Parasitological identification

Parasite detection was based exclusively on microscopic morphology. Because several eggs, larvae and oocysts have overlapping morphological features, species-level identifications that could not be confidently supported by morphology were downgraded to genus-level or morphotype-level designations in the revised tables. Accordingly, unusual host-parasite associations are presented as morphological observations rather than confirmed species-level records. Two trained parasitologists independently examined the slides, with discordant findings resolved by consensus. No inter-observer agreement statistic was calculated; this is acknowledged as a limitation.

Data management and analysis

Data were analyzed using descriptive and inferential statistics. Frequencies, proportions and 95% Confidence Intervals (CIs) were used to summarize parasite detection and participant or animal characteristics. Wilson score intervals were used for proportions, including small cell sizes. Because individual animals could harbour more than one parasite taxon, taxon-specific percentages were



calculated using the total number of sampled animals (n=438) as the denominator and were interpreted as detection frequencies rather than mutually exclusive prevalence categories.

Chi-square tests without continuity correction were used for comparisons of categorical positivity where expected cell counts were adequate; Fisher’s exact test was used when expected counts were small. Comparisons included human sex and age categories and the overall proportions positive among sampled humans and animals. Statistical significance was set at $p<0.05$. No p-values were assigned to individual parasite taxa in the descriptive taxon table because no prespecified reference prevalence or between-group hypothesis was being tested for those individual frequencies. Because human and animal observations were collected from the same participating households, household clustering is a potential source of non-independence. A household-level clustered model and multivariable logistic regression were not performed because participant-level household identifiers and the complete individual-level dataset were not available in the materials accompanying this revision. Accordingly, household linkage is described as a feature of the sampling design, but no household-level association or transmission analysis is claimed.

The null hypothesis for each inferential comparison was that the proportions positive were equal across the groups being compared. Results are reported with exact sample sizes, percentages, 95% CIs and p-values where a formal comparison was performed. Missing data were not imputed; analyses used the available observations for each variable.

Data quality assurance: All reported sample totals, numerators, denominators and percentages in the revised analytical tables were checked for arithmetic consistency against the available aggregate laboratory records. Taxon-specific frequencies are reported descriptively and no unsupported species-level identifications or individual-taxon hypothesis tests were retained. Where participant-level household identifiers were unavailable in the materials accompanying this revision, no household-level inferential model was performed.

Results

Socio-demographic characteristics

Among the 100 questionnaire respondents, 64.0% were male and 36.0% were female. Most respondents were farmers (92.0%), 81.0% had no formal education and 69.0% reported household family sizes of at least 10 members. The mature respondent age distribution was 15.0% aged 18-25 years, 6.0% aged 26-34 years, 17.0% aged 35-40 years, 42.0% aged 41-49 years and 19.0% aged 50 years or older (**Table 1**). These questionnaire characteristics describe household respondents and

should not be confused with the age distribution of the 65 human faecal samples used for laboratory analysis.

Table 1: Socio-demographic characteristics of household respondents.

Variable	Frequency	Percentage (%)
Gender		
Male	64	64
Female	36	36
Age range		
18-25	15	15
26-34	6	6
35-40	17	17
41-49	42	42
50 years and above	19	19
Educational status		
Literate	19	19
Illiterate	81	81
Employment status		
Employed	6	6
Unemployed	91	91
Self-employed	3	3
Occupation		
Farmer	92	92
Teachers	6	6
Petty trader	2	2
Family size		
1-3	4	4
4-6	6	6
7-9	21	21
≥ 10	69	69
Children in the household		
1-2	20	20
3-4	42	42
5-6	25	25
≥ 7	12	12
Note: The age range in Table 1 refers to mature participants who signed the consent form and responded to the questionnaire.		

Animal ownership and husbandry practices

All 100 participating households reported keeping domestic animals. Extensive rearing was reported by 69.0% of households and semi-intensive rearing by 31.0%. Routine animal-health monitoring was reported by 46.0% of respondents, whereas 49.0% reported no routine monitoring and 5.0% reported monitoring animals sometimes. Most households (98.0%) allowed animals to roam and poultry (96.0%) and goats (91.0%) were the most commonly owned animal categories (**Table 2**).



Table 2: Animals and husbandry practice.

Variables	Frequency	Percentage (%)
Presence of animals in the household		
Yes	100	100
Number of animals you own		
Jan-19	9	9
20-39	12	12
40-69	3	3
70-80	76	76
Routine disease monitoring of animals		
Yes	46	46
No	49	49
Sometimes	5	5
Animals are allowed to roam about		
Yes	98	98
No	2	2
Form of rearing/raising the animals		
Semi-intensive	31	31
Extensive	69	69
Rear animals for commercial purposes		
Goats	63	63
Sheep	14	14
Cattle	10	10
Poultry	11	11
Pigs	2	2
Feed animals daily		
Yes	21	21
No	66	66
Sometimes	13	13
Animals you own		
Poultry	96	96
Goat	91	91
Dogs	54	54
Cats	49	49
Sheep	63	63
Cattle	17	17
Pigs	51	51

Among the 438 sampled domestic animals, 320 (73.1%; 95% CI: 68.7%-77.0%) had at least one parasite taxon detected. Community-level positivity ranged from 42.9% in Varinperi (12/28) to 90.6% in Kendeo (48/53). Community-level differences were statistically significant ($\chi^2=36.152$, $p<0.001$). By animal category, positivity was highest in goats (99.0%, 100/101; 95% CI: 94.0%-99.8%) and lowest in rabbits (0%, 0/1; 95% CI: 0%-79.3%). Animal-category differences were statistically significant ($\chi^2=56.369$, $p<0.001$). All percentages are based on the number examined within each community or animal category.

Table 3: Parasite detection among sampled domestic animals by community and animal category.

Level	Group	No examined	Positive no	Positivity % (95% CI)
Community	Bultuo	38	25	65.8% (49.9-78.8)
Community	Ga	37	33	89.2% (75.3-95.7)
Community	Grungu	57	42	73.7% (61.0-83.4)
Community	Kendeo	53	48	90.6% (79.7-95.9)
Community	Ponyenitanga	42	37	88.1% (75.0-94.8)
Community	Siiroo	52	34	65.4% (51.8-76.8)
Community	Tanvaare	37	23	62.2% (46.1-75.9)
Community	Varinperi	28	12	42.9% (26.5-60.9)
Community	Vieri	30	21	70.0% (52.1-83.3)
Community	Yeleyiri	64	45	70.3% (58.2-80.1)
Animal category	Cats	3	2	66.7% (20.8-93.9)
Animal category	Cattle	20	15	75.0% (53.1-88.8)
Animal category	Dogs	22	15	68.2% (47.3-83.6)
Animal category	Ducks	5	2	40.0% (11.8-76.9)
Animal category	Goats	101	100	99.0% (94.6-99.8)
Animal category	Guinea fowl	2	1	50.0% (9.5-90.5)
Animal category	Pigs	38	25	65.8% (49.9-78.8)
Animal category	Poultry	150	89	59.3% (51.3-66.9)
Animal category	Rabbit	1	0	0.0% (0.0-79.3)
Animal category	Sheep	96	71	74.0% (64.4-81.7)
Overall	All sampled animals	438	320	73.1% (68.7-77.0)

Parasite taxa detected in domestic animals

Thirty-two morphologically identified parasite taxa or morphotypes were recorded in the 438 animal samples. The most frequently recorded were *Trichostrongylus* sp. (83 detections; 18.95%), *Eimeria* sp. (78; 17.81%), *Strongyloides* sp. (62; 14.16%), *Bunostomum* sp. (49; 11.19%), *Oesophagostomum* sp. (39; 8.90%) and *Ancylostoma* sp. (35; 7.99%). Because individual animals could harbour more than one taxon, these taxon-specific percentages are not expected to sum to 100%. Species-level names that were not considered sufficiently secure from morphology alone were downgraded to genus-level or morphotype-level designations in the revised table.



Table 4 presents descriptive taxon frequencies with 95% CIs. Individual p-values have been removed because the original manuscript did not specify a meaningful null hypothesis for those tests. Taxon frequencies should therefore be interpreted descriptively.

Table 4: Morphologically identified parasite taxa detected among domestic animals (n=438).

Parasite taxon/morphotype	Positive n	Detection % (95% CI)
<i>Ancylostoma sp.</i>	35	7.99% (5.80-10.91)
<i>Ascaridia sp.</i>	6	1.37% (0.63-2.96)
<i>Balantidium sp.</i>	17	3.88% (2.44-6.13)
<i>Bunostomum sp.</i>	49	11.19% (8.57-14.48)
<i>Diocotophyma sp.</i>	4	0.91% (0.36-2.32)
<i>Echinococcus sp.</i>	2	0.46% (0.13-1.65)
<i>Fasciola sp.</i>	15	3.42% (2.09-5.57)
<i>Filaroides sp.</i>	1	0.23% (0.04-1.28)
<i>Haemonchus sp.</i>	5	1.14% (0.49-2.64)
<i>Heterakis sp.</i>	4	0.91% (0.36-2.32)
<i>Linguatula sp.</i>	2	0.46% (0.13-1.65)
<i>Muellerius sp.</i>	2	0.46% (0.13-1.65)
<i>Moniezia sp.</i> (morphotype 1)	2	0.46% (0.13-1.65)
<i>Moniezia sp.</i> (morphotype 2)	3	0.68% (0.23-1.99)
<i>Nanophyetus sp.</i>	1	0.23% (0.04-1.28)
<i>Nematodirus sp.</i>	9	2.05% (1.08-3.86)
<i>Oesophagostomum sp.</i>	39	8.90% (6.58-11.94)
<i>Cryptosporidium sp.</i>	13	2.97% (1.74-5.01)
<i>Eimeria sp.</i>	78	17.81% (14.51-21.67)
<i>Isospora sp.</i>	6	1.37% (0.63-2.96)
<i>Alaria sp.</i> (ova)	2	0.46% (0.13-1.65)
<i>Paragonimus sp.</i>	5	1.14% (0.49-2.64)
<i>Platynosomum sp.</i>	7	1.60% (0.78-3.26)
<i>Schistosoma sp.</i>	4	0.91% (0.36-2.32)
<i>Stephanurus sp.</i>	9	2.05% (1.08-3.86)
<i>Strongyloides sp.</i>	62	14.16% (11.20-17.73)
<i>Strongylus sp.</i>	13	2.97% (1.74-5.01)
<i>Toxocara sp.</i> (morphotype 1)	5	1.14% (0.49-2.64)
<i>Toxocara sp.</i> (morphotype 2)	7	1.60% (0.78-3.26)
<i>Toxascaris sp.</i>	8	1.83% (0.93-3.56)
<i>Trichostrongylus sp.</i>	83	18.95% (15.56-22.88)
<i>Trichuris sp.</i>	13	2.97% (1.74-5.01)

Parasite detection among human participants

Among the 65 human faecal samples, 44 were positive for at least one parasite taxon (67.7%; 95% CI: 55.6-77.8%). No statistically significant difference was detected between the proportions positive in the sampled human group (44/65, 67.7%) and sampled animal group (320/438, 73.1%) ($\chi^2=0.815$, $p=0.367$). This comparison should not be interpreted as evidence that the two

populations have equivalent parasitological burdens because the sampling frames, host composition and sample sizes differed (**Table 5**).

Table 5: Parasite detection among human participants by sex, age and community.

Variable	No examin ed	Positi ve no	Positivi ty %	95% CI	P- value
Overall	65	44	67.7	55.6- 77.8	
Sex					
Male	32	20	62.5	45.3- 77.1	0.538
Female	33	24	72.7	55.8- 84.9	
Age					
0-5 years	32	30	93.8	79.9- 98.3	<0.00 1
6-10 years	15	6	40	19.8- 64.3	
11-15 years	10	4	40	16.8- 68.7	
16-25 years	4	2	50	15.0- 85.0	
26 years and above	4	1	25	4.6- 69.9	
Community					
Berinyasi	7	5	71.4	35.9- 91.8	0.596
Ponyenita nga	3	3	100	43.9- 100.0	
Siiroo	1	0	0	0.0- 79.3	
Tanvaare	12	8	66.7	39.1- 86.2	
Varinperi	10	6	60	31.3- 83.2	
Vieri	28	20	71.4	52.9- 84.7	
Yeleviri	4	2	50	15.0- 85.0	

Among human participants, positivity was 62.5% (20/32; 95% CI: 45.3%-77.1%) in males and 72.7% (24/33; 95% CI: 55.8%-84.9%) in females; the difference was not statistically significant ($\chi^2=0.379$, $p=0.538$). Positivity differed significantly across age groups ($\chi^2=22.013$, $p<0.001$), with the highest observed proportion in children aged 0-5 years (93.8%, 30/32; 95% CI: 79.9%-98.3%). Community estimates were unstable in groups with very small sample sizes, including 100% in Ponyenitanga (3/3) and 0% in Siiroo (0/1) and should not be interpreted as population-level differences. The human and animal samples were collected from the same participating households; therefore, the observed overlap in taxa should be interpreted as household-level co-occurrence/shared detection rather than evidence of cross-transmission. A detailed human taxon-by-community cross-tabulation is not presented because the



aggregate source table available for this revision did not preserve sufficient participant-level information for independent verification of each cell.

Shared morphological detection in human and animal samples

Table 6 summarizes parasite taxa or morphotypes detected among humans and domestic animals sampled from the participating households. Shared detection is presented descriptively and should not be interpreted as evidence of cross-transmission. Because the human and animal samples were collected within the same participating household framework, the overlap is relevant to household-level co-occurrence and shared environmental exposure; however, the present aggregate data do not establish that a parasite detected in a human and an animal came from the same transmission chain. Where morphology did not support species-level confidence, identifications have been expressed at genus level. Molecular characterization would be required to confirm unusual host-parasite associations and assess genetic relatedness.

Table 6: Parasite taxa or morphotypes detected among humans and domestic animals sampled from participating households.

Taxon/morphotype	Animal no	Animal %	Human no	Human %	Identification level
<i>Ancylostoma sp.</i>	35	7.99	1	1.54	Genus-level
<i>Ascaridia sp.</i>	6	1.37	1	1.54	Genus-level
<i>Bunostomum sp.</i>	49	11.19	5	7.69	Genus-level
<i>Fasciola sp.</i>	15	3.42	1	1.54	Genus-level
<i>Haemonchus sp.</i>	5	1.14	1	1.54	Genus-level
<i>Heterakis sp.</i>	4	0.91	1	1.54	Genus-level
<i>Cryptosporidium sp.</i>	13	2.97	5	7.69	Genus-level
<i>Eimeria sp.</i>	78	17.81	5	7.69	Genus-level
<i>Alaria sp. (ova)</i>	2	0.46	1	1.54	Genus-level / ova
<i>Platynosomum sp.</i>	7	1.6	3	4.62	Genus-level
<i>Strongyloides sp.</i>	62	14.16	3	4.62	Genus-level
<i>Strongylus sp.</i>	13	2.97	5	7.69	Genus-level
<i>Toxocara sp.</i>	12	2.74	1	1.54	Genus-level
<i>Toxascaris sp.</i>	8	1.83	1	1.54	Genus-level
<i>Trichuris sp.</i>	13	2.97	3	4.62	Genus-level

Discussion

This study documented substantial parasite detection among sampled domestic animals and humans in Wa West District. All 100 participating households kept domestic animals, with poultry and goats being the most commonly owned categories and extensive rearing reported by 69.0% of households. These conditions provide a relevant context for One Health surveillance because human, animal and environmental health are closely interconnected [2,3].

Parasite detection occurred in 73.1% of sampled animals and 67.7% of sampled humans. Animal positivity varied by community and animal category, with goats showing the highest observed proportion positive. These estimates describe the sampled animals and should not be generalized to all domestic animals in Wa West District because households were selected purposively and animals were selected by convenience. Similar studies have documented intestinal parasites among humans and livestock living in rural settings, supporting the value of integrated surveillance, although differences in host composition, diagnostic methods and sampling design limit direct comparison [9-12].

Seventeen morphologically identified parasite taxa were recorded in the human dataset, while 32 taxa or morphotypes were recorded among animals. Several taxa were detected in both host groups. Such overlap is compatible with shared environmental exposure, particularly where humans and animals occupy the same household environment, but it does not establish transmission between hosts. The use of morphology alone is especially important when interpreting unusual host associations because morphologically similar eggs, larvae and oocysts may be difficult to distinguish reliably to species level. The revised manuscript therefore uses genus-level or morphotype-level designations where species-level certainty was not justified. Molecular characterization would be required to test whether organisms detected in different hosts are genetically identical or part of a common transmission pathway.

Study limitations

Several limitations should be considered. First, the human sample was relatively small (65) compared with the animal sample (438) and several human age and community strata had very small denominators. Second, purposive household selection and convenience selection of available animals may have introduced selection bias; therefore, the estimates are not population-representative. Third, although human and animal samples were collected from the same participating households, animal records covered ten communities whereas human samples were available from seven communities, limiting direct community-level comparability. Fourth, observations from the same



household may not be statistically independent, but participant-level household identifiers were not available for clustered modelling in this revision. Fifth, parasite identification relied entirely on morphology, limiting taxonomic resolution and making unusual host-parasite associations uncertain without molecular confirmation. Sixth, a detailed human parasite-by-community taxon cross-tabulation was not used for inferential claims because the aggregate source table available for this revision did not preserve sufficient participant-level information for independent verification of each cell. Finally, the study did not directly test environmental contamination, hygiene behaviour or causal transmission pathways, so these mechanisms should be treated as hypotheses rather than demonstrated explanations.

Conclusion

The study demonstrated substantial parasite detection among the sampled domestic animals and humans in Wa West District, with 73.1% (320/438) of animals and 67.7% (44/65) of humans positive for at least one morphologically identified parasite taxon. Thirty-two taxa or morphotypes were recorded among animals and 17 among humans. Several taxa occurred in both host groups, but because identification was morphological and sampling was not fully matched or probability-based, the findings indicate shared detection and possible shared environmental exposure rather than confirmed zoonotic transmission. The findings support coordinated One Health surveillance involving human health, veterinary health and environmental health sectors.

Recommendation

A coordinated One Health approach is recommended. Priority actions should include improved household sanitation and safe disposal of animal faeces, hand hygiene and food-safety education, routine veterinary assessment of domestic animals and coordinated surveillance among health, veterinary and environmental officers. Antiparasitic treatment should be guided by confirmed parasite identification and applicable human-health or veterinary guidelines rather than by the present cross-sectional findings alone. Future studies should use larger probability-based samples, molecular methods to confirm unusual host-parasite associations, household-level linkage analysis using participant/animal identifiers, environmental sampling and longitudinal designs where feasible to investigate potential transmission pathways.

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). Written permission was obtained from the Wa West District Assembly before sample

collection. Participants received information about the study objectives, procedures, potential risks and benefits, voluntary participation and the right to withdraw. Written informed consent was obtained from adult participants, with parental/guardian consent for minors as applicable.

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Availability of Supporting Data

All data used for this manuscript are available upon reasonable request, subject to applicable ethical and data-protection requirements.

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.

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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