



ORIGINAL ARTICLE

MORPHOLOGICAL DETECTION OF GASTROINTESTINAL PARASITES AND MOLECULAR CHARACTERIZATION OF *CAPILLARIA ANATIS* OF DOMESTIC TURKEYS IN OYO STATE, NIGERIA

Nkeiruka Fortunate Ogbonna¹, Olanrewaju Samuel Olaifa^{2*}, Adetolase Azizat Bakre³, Ayomi-kun Elizabeth Oyesiji², Ezekiel Ayomide Adebawale⁴

¹Department of Veterinary Parasitology, Faculty of Veterinary Medicine, University of Ibadan, Oyo State, Nigeria; ²Department of Veterinary Pathology, Faculty of Veterinary Medicine, University of Ibadan, Oyo State, Nigeria; ³Department of Veterinary Medicine, Faculty of Veterinary Medicine, University of Ibadan, Oyo State, Nigeria; ⁴Department of Veterinary Microbiology, Faculty of Veterinary Medicine, University of Ibadan, Oyo State, Nigeria

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*Correspondence: os.olaiifa@ui.edu.ng

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Ethical considerations: When reporting experiments on animals Observation of the ARRIVE guidelines 2.0: Updated guidelines for reporting animal research, published on July 14, 2020 (DOI: 10.1371/journal.pbio.3000410), is applied. The authors ensure that all procedures were performed in compliance with the guidelines for animal care of their institutions or with national/international guidelines.

ABSTRACT

This study investigated the prevalence, diversity, and molecular identification of gastrointestinal parasites in domestic turkeys raised under rural and semi-intensive systems. A total of 77 faecal samples were examined, revealing a gastrointestinal parasite prevalence of 62.34%, with *Heterakis* sp. being the most frequently identified helminth (41.56%), followed by protozoans such as *Eimeria* sp. (15.58%) and *Balantidium coli* (12.99%). Notably, Nigerian indigenous turkey breeds had a 100% infection rate compared to only 12.12% in Hybrid Converter Turkey (HTC) breeds, indicating significant breed-specific susceptibility ($P < 0.05$). Age was also a significant determinant, with younger turkeys (2–6 months) exhibiting higher infection rates than older birds ($P < 0.05$). Single infections were most prevalent, though mixed infections occurred in several combinations, amplifying the risk of compounded morbidity. Molecular characterization via amplification of the 18S rRNA gene and phylogenetic analysis confirmed the presence of *Capillaria anatis*, reinforcing the importance of molecular tools in parasite surveillance. These findings highlight the urgent need for improved parasite control, routine molecular diagnostics, and targeted management strategies in backyard and smallholder poultry systems. The study provides vital data for veterinarians, poultry farmers, and public health stakeholders aiming to enhance turkey health and productivity through integrated parasitological monitoring and intervention.

Keywords: bird diseases; *Capillaria*; feces; gastrointestinal parasites; nematoda; polymerase chain reaction

INTRODUCTION

Parasitic infections continue to pose a major obstacle in turkey production, contributing significantly to diminished performance, compromised health, and economic setbacks, as emphasized by Ola-Fadunsin et al. [1]. In Nigeria, where poultry farming is integral to food security and income generation, turkey production is especially vulnerable. This vulnerability stems from weak biosecurity, substandard management practices, and climatic factors that promote parasite proliferation, as noted by Lawal et al. [2] and further supported by the observations of Adeyemi et al. [3]. Among the most frequently encountered nematodes in turkeys across Nigeria are species of *Capillaria*. According to Benisheikh et al. [4], prevalence rates can reach as high as 29% in Borno State, with *Capillaria retusa*, *C. columbae*, *C. bursata*, and *C. contorta* being the dominant species. In contrast, a separate investigation conducted by Jallailudeen et al. [5] in the same region reported a considerably lower prevalence of 6.8%, suggesting that seasonal variations and management factors may influence infection rates. These findings are consistent with global reports by Shifaw et al. [6], who documented high *Capillaria* prevalence in free-range birds, particularly in humid environments.

Another significant nematode, *Heterakis gallinarum*, which resides in the ceca, has been reported by Patil et al. [7] to occur in 13.1% of turkeys in northern Nigeria. This species is particularly concerning due to its role in transmitting *Histomonas meleagridis*, the protozoan responsible for histomoniasis, as explained by McDougald [8] and further supported by the findings of Cupo and Beckstead [9]. Additional helminths, including *Ascaridia galli* (17.7%), *Raillietina tetragona* (6.8%), and *Strongyloides avium* (3.7%), have been identified in turkeys, as detailed by Jallailudeen et al. [5]. Of particular concern is *A. galli*, which is known to cause intestinal obstruction and impair nutrient absorption, as described by Sharma et al. [10]. The co-occurrence of multiple parasitic species underscores the complexity of managing such infections, a challenge that ElKhawas [11] highlights as contributing to worsened clinical outcomes. These parasites not only irritate the birds but also serve as vectors for secondary infections and contribute to blood loss.

Effective control begins with accurate parasite identification. Benisheikh et al. [4] and Yevstafieva et al. [12]

describe the importance of morphometric studies in distinguishing *Capillaria* species, using features such as egg size, esophageal structure, and reproductive anatomy. For example, *C. retusa* produces eggs measuring 50–60 µm in length, whereas *C. columbae* eggs are smaller, typically ranging from 45–50 µm, a distinction clearly presented in the seminal parasitology work of Soulsby [13]. Moreover, Holterman et al. [14] emphasize the value of molecular techniques like PCR, which are increasingly used alongside morphology to enhance diagnostic accuracy.

Free-range turkeys tend to exhibit significantly higher nematode infection rates; 56.3% compared to 25.2% in intensively reared birds; primarily due to increased exposure to contaminated soil and intermediate hosts [5]. While confinement systems offer more control, Permin and Hansen [15] caution that inadequate hygiene can still allow for persistent infections. Rainy seasons further aggravate the situation, with parasite prevalence surging to 61.8% compared to 20.6% during dry seasons, a pattern also noted by Jallailudeen et al. [5]. This seasonal trend has been similarly documented in other tropical regions, reinforcing the recommendation by Sharma et al. [10] for implementing deworming protocols aligned with climatic changes. Susceptibility also appears to vary with age and sex. Lawal et al. [2] observed that older turkeys and females are more prone to infection, likely due to longer exposure periods and physiological stress. Although juvenile birds tend to have lower infection rates, they are more susceptible to severe pathological consequences, as highlighted by Reed et al. [16]. Parasitic infections cause multiple pathological effects. For instance, *H. gallinarum* has been shown by McDougald [8] to induce caecal wall thickening and hemorrhage while facilitating secondary infections with *Histomonas meleagridis*, which can lead to hepatic necrosis. *Capillaria* species, on the other hand, cause inflammation of the intestinal mucosa, goblet cell proliferation, and nutrient malabsorption, as recently documented by Perrucci et al. [17]. Chronic helminthiasis significantly reduces feed efficiency and renders turkeys more vulnerable to opportunistic infections, further corroborated by the work of Sharma et al. [10]. To control these infections, farmers commonly administer anthelmintics such as pyrantel pamoate, flubendazole, and toltrazuril. ElKhawas [11] underscores the importance of rotating these drugs to prevent the emergence of resistance. Beyond pharmaceutical interventions, herbal alternatives are gaining attention;

for instance, neem (*Azadirachta indica*) has shown potential as a complementary therapy, according to Ademola and Eloff [18]. Strategic management practices are equally crucial. Routine deworming at regular time intervals is necessary to maintain low parasite loads [19, 20]. Additionally, Permin and Hansen [15] advise separating different age groups to limit cross-contamination, and Adeyemi et al. [3] advocate for deep litter management to reduce environmental parasite burden and enhance bird welfare.

Robust biosecurity remains vital. Soulsby [13] emphasizes the efficacy of simple protocols like footbaths and disinfectants at farm entrances in reducing parasite transmission, while Akter [21] notes the added benefit of quarantining new birds to prevent the introduction of infections. When combined with pharmacological and husbandry strategies, these biosecurity measures offer a holistic approach to improving turkey health and productivity.

In summary, parasitic infections continue to constrain turkey production across Nigeria through complex host-parasite-environment interactions. However, integrating anthelmintic regimens, evidence-based management practices, and stringent biosecurity can mitigate these losses. Continued research and education are essential for equipping farmers with tools for sustainable parasite control. Therefore, this study focuses on identifying the predominant gastrointestinal parasites affecting turkeys in Oyo State, Nigeria, while exploring their distribution, pathological impact, and control strategies.

MATERIALS AND METHODS

Study Area

This study was conducted on turkeys sourced from various facilities within Ibadan, a city in southwestern Nigeria. Geographically, Ibadan lies between latitudes 7°32'50"N and 7°45'83"N and longitudes 3°8'00"E and 3°9'75"E. Spanning approximately 3,000 square kilometers, the city consists of 11 Local Government Areas (LGAs) and has an estimated population of about 4 million, making it the third-largest city in Nigeria (<https://worldpopulationreview.com/cities/nigeria/ibadan>). The region experiences a humid tropical climate characterized by distinct wet and dry seasons, with average temperatures ranging from 21.9 °C to 23.8 °C and a mean monthly rainfall of 78.38 mm (World Population Prospects, [22]).

Sample Collection

In this study, freshly voided faecal samples from 33 Hybrid Converter Turkey (HTC) and 44 Nigerian indigenous breeds of turkeys were randomly collected from January to May 2025 for screening. Turkeys of different age groups, sexes, free-range and deep litter systems were included. The age of the turkeys was classified into two groups: (A) 2–6 months and (B) 6–10 months (Table 1). The samples were collected from the floor with a spatula, which was washed after each collection to prevent contamination. Each sample was placed in a sterile sample bottle and labelled with the date of collection, sex, age, breed, and the method of keeping and stored at 4 °C. All samples were processed at the Department of Veterinary Parasitology and Entomology research laboratory, University of Ibadan, following standard parasitological procedures.

Parasitological Examination

Faecal samples were first examined macroscopically and then subjected to simple flotation and sedimentation techniques, using saturated salt solution and distilled water, respectively, to screen for helminth eggs, larvae, whole worms, gravid segments, and protozoan oocysts at x10 and x40 objective lenses ([13, 23]). Identification of parasite eggs or oocysts was based on their morphology and size. The eggs or oocysts per gramme of faeces were obtained using the McMaster counting technique [24]. Data obtained from the external and gastrointestinal parasites of the different breeds of turkeys were analyzed using simple descriptive statistics.

DNA Extraction, Polymerase Chain Reaction and Sequencing of *Capillaria anatis*

A total of 100 g of feces from one of the free-range turkeys, highly positive for *Capillaria* species by microscopy, was homogenized, and total DNA was extracted using the QIAamp Fast DNA Stool Mini Kit (Qiagen, Germany), in accordance with the manufacturer's guidelines. The faecal sample was picked because of the zoonotic potential of some *Capillaria* species. The extracted DNA was then stored at -20 °C prior to PCR amplification.

A 1000 bp segment of the 18S rRNA gene from nematodes was amplified using primers 18S-F (CCTGAGACGGCTACTACTT) and 81R (GGCATCGCAGACCTGTTATT). The PCR reaction took place in a 50 µL volume, which included 10 µL of 5x GoTaq colorless

reaction mix, 3 μL of 25 mM MgCl_2 , 1 μL of 10 mM dNTPs, and 1 μL of each 10 pmol primer. The amplification was performed on the GeneAmp 9700 PCR System Thermocycler (Applied Biosystem Inc., USA). The PCR protocol started with an initial denaturation at 94 °C for 5 minutes, followed by 34 cycles comprising 30 seconds of denaturation at 94 °C, 30 seconds of annealing at 52 °C, 60 seconds of extension at 72 °C, and concluded with a final extension at 72 °C for 7 minutes.

The amplified product underwent verification through gel electrophoresis on an agarose gel. The integrity of the amplified 1000 bp gene fragment was assessed using a 1.5% agarose gel prepared with 1X TAE buffer. The agarose suspension was heated in a microwave until boiling for five minutes. After cooling to 60 °C, 3 μL of 0.5 g/ml ethidium bromide was added to the molten agarose. Combs were inserted into the slots of the casting tray, and the molten agarose was poured. The gel was allowed to solidify for 20 minutes to create the wells. Next, 1X TAE buffer was added to the gel tank until the gel was just covered. Following this, a 100 bp DNA ladder was loaded into well 1 of each PCR product, and 2 μL of 10X blue gel loading dye were combined with 4 μL of each PCR product to facilitate sample loading and monitor gel progression. Electrophoresis was conducted at 120V for 45 minutes, after which the gel was visualized under UV trans-illumination. The sizes of the PCR products were determined by comparing the mobility of the 100 bp molecular weight ladder to the experimental samples on the gel.

The PCR reagents were eliminated from the amplicon through an ethanol purification process. In a new, sterile 1.5 ml Eppendorf tube, each 40 μL of PCR-amplified product was mixed with 7.6 μL of 3M sodium acetate and 240 μL of 95% ethanol. These mixtures were vortexed thoroughly, then the tubes were stored at -20 °C for at least 30 minutes. The pellet was washed by adding 150 μL of 70% ethanol, mixed, and centrifuged for 15 minutes at 7500 g and 4 °C after discarding the supernatant by inverting the tube over the trash for 10 minutes at 13000 g and 4 °C. Next, resuspend the tube with 10 μL of sterile distilled water and store it at -20 °C before sequencing. Again, discard the supernatant (invert the tube over the trash), place the tube on a paper towel, and allow it to dry in the fume hood at ambient temperature for 10-15 minutes. The purified fragment was quantified using a NanoDrop 2000 from Thermo Scientific and analyzed on a 1.5% agarose gel run

at 110V for approximately an hour, as previously done, to confirm the presence of the purified product.

The amplified fragments were sequenced in both directions on a Genetic Analyzer 3130xl sequencer from Applied Biosystems, in accordance with the manufacturer's instructions. The sequencing kit utilized was the BigDye Terminator v3.1 Cycle Sequencing kit. DNA sequences were viewed and edited using Chromas 2.6.6 (Technelysium - <http://www.technelysium.com.au/Chromaslite.html>) [25]. To identify the sequences and obtain similar sequences from GenBank, the NCBI nucleotide BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) [26] was utilized. A phylogenetic tree was created through multiple sequence alignments of the nucleotide sequence from the 18S rRNA gene along with sequences obtained from GenBank, using MEGA version 11.0.10 [27].

RESULTS

Out of 77 faecal samples examined from domestic turkeys, this study revealed a gastrointestinal parasite prevalence of 62.34%, either as single or mixed infections (Table 1). Among the helminths identified (Fig. 1), *Heterakis* sp. emerged as the most prevalent (41.56%), followed distantly by *Ascaridia* sp. and nematode larvae (3.90% each) and *Capillaria* sp. (1.30%). Protozoan parasites identified included *Eimeria* sp. (15.58%), *Balantidium coli* (12.99%), and *Entamoeba* sp. (2.60%). The calculated parasite loads (Table 2) were highest in *Capillaria* sp. (51×10^2 eggs per gram), followed by *Eimeria* sp. (31×10^2 oocysts per gram) and *Heterakis* sp. (5×10^2 eggs per gram), while the lowest values were noted for nematode larvae (1×10^2 larvae per gram) and *Entamoeba* sp. (2×10^2 cysts per gram). These findings underscore a substantial parasitic burden that could potentially impair turkey health and productivity, especially in the absence of routine parasite monitoring or control.

Notably, all 44 (100%) turkeys from the Nigerian indigenous breed tested positive for gastrointestinal parasites, compared to only 4 (12.12%) of the 33 Hybrid Converter Turkey (HTC) breeds examined—demonstrating a statistically significant disparity ($P < 0.05$). This suggests a likely genetic or environmental susceptibility among Nigerian indigenous breeds. Though males (71.43%) showed a relatively higher infection rate than females (57.14%), the difference was not statistically significant ($P > 0.05$).

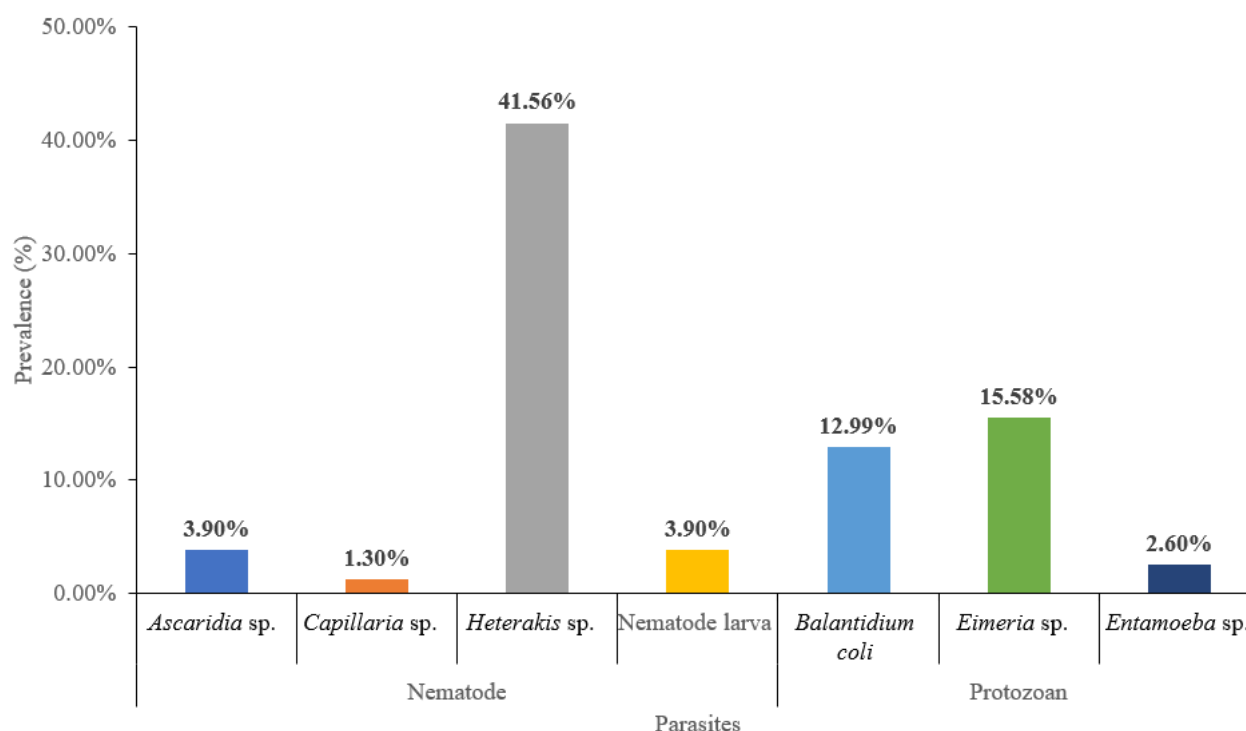


Fig. 1. Prevalence of gastrointestinal helminths and protozoans of examined turkeys

Age, however, was a significant factor: younger birds (2–6 months) had markedly higher infection rates (84.85%) than those aged 6–10 months (45.45%), indicating heightened vulnerability during early growth phases, which may be linked to immature immune defenses or increased exposure during early foraging behaviors (Table 1).

Infection patterns further revealed that single parasite infections were most common (42.86%), with *Heterakis* sp. accounting for the majority (Table 3). Mixed infections, though less frequent, were diverse, involving combinations like *Eimeria* sp. with *Heterakis* sp., and triple co-infections were rare, occurring in only one sample (Fig.

2). A pictorial display of the parasites is presented in Fig. 3. These co-infection profiles emphasize the complex parasitological interactions turkeys face in natural or backyard settings. Importantly, the high burden and diversity of parasites, particularly in Nigerian indigenous and younger turkeys, indicate the urgent need for regular deworming programs, improved sanitation, and targeted control strategies. These findings contribute valuable insights to veterinary parasitology by highlighting the epidemiological dynamics of gastrointestinal parasitism in turkeys raised under typical rural or semi-intensive systems.

Table 1. Prevalence of GIT parasites in turkeys based on sex, breed/management system and age groups of turkeys

	Breed		Sex		Age		Total
	Hybrid Converter Turkey (HTC)	Nigerian indigenous	Female	Male	2–6 Months	6–10 Months	
Number Positive	4	44	28	20	28	20	48
Number Tested	33	44	49	28	33	44	77
Prevalence (%)	12.12	100.00	57.14	71.43	84.85	45.45	62.34
Chi-Sq. Stat	65.03 (p-value < 0.0001)		1.55 (p-value > 0.10)		12.46 (p-value < 0.0001)		

Table 2. Gastrointestinal parasite load in faecal samples of turkeys

AVERAGE EGGS PER GRAMME /OOCYSTS PER GRAMME OF FAECES						
<i>Ascaridia</i> sp. x10 ²	<i>Balantidium coli</i> x10 ²	<i>Capillaria</i> sp. x10 ²	<i>Heterakis</i> sp. x10 ²	Nematode larva x10 ²	<i>Eimeria</i> sp. x10 ²	<i>Entamoeba</i> sp. x10 ²
3	3	51	5	1	31	2

Table 3. Prevalence of individual parasites across categories of turkeys examined

Parasites		Categories					
		Sex		Age		Breed	
		Female	Male	2–6 months	6–10 months	Hybrid Con- verter Turkey (HTC)	Nigerian indigenous
Nematode	<i>Ascaridia</i> sp.	3 (6.12%)	-	-	3 (6.82%)	-	3 (6.82%)
	<i>Capillaria</i> sp.	-	1 (3.57%)	1 (3.03%)	-	-	1 (2.27%)
	<i>Heterakis</i> sp.	23 (46.94%)	9 (32.14%)	19 (57.58%)	13 (29.55%)	2 (6.06%)	30 (68.18%)
	Nematode larva	3 (6.12%)	-	1 (3.03%)	2 (4.55%)	-	3 (6.82%)
Protozoan	<i>Balantidium coli</i>	2 (4.08%)	8 (28.57%)	6 (18.18%)	4 (9.09%)	2 (6.06%)	8 (18.18%)
	<i>Eimeria</i> sp.	6 (12.24%)	6 (12.24%)	9 (27.27%)	3 (6.82%)	1 (3.03%)	11 (25.00%)
	<i>Entamoeba</i> sp.	2 (4.08%)	-	1 (3.03%)	1 (2.27%)	-	2 (4.55%)

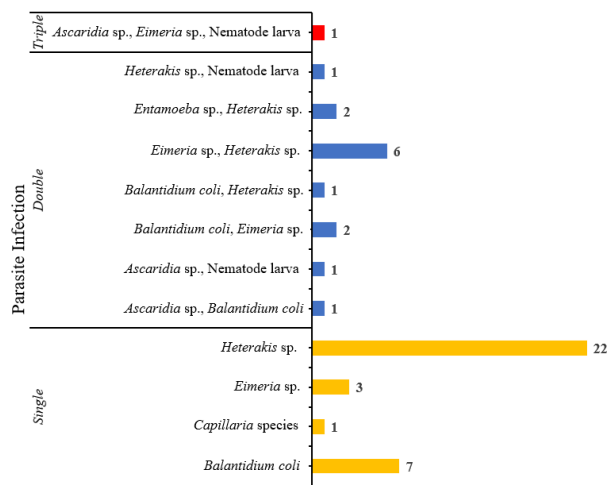


Fig. 2. Prevalence of single and mixed GIT parasite infections in turkeys

The agarose gel electrophoresis results (Fig. 4) confirmed the successful amplification of a 1000 base pair fragment of the 18S rRNA gene, indicating the presence of nematode DNA in the sample. Subsequent phylogenetic analysis placed this amplified sequence within a clade comprising *Capillaria anatis* reference sequences from GenBank (Fig. 5). The phylogenetic tree was generated through multiple sequence alignments of the obtained sequence with homologous nematode sequences, using the maximum likelihood method and validated by 1000 bootstrap replicates. The sequence in question, labeled SM4, clustered reliably with known *Capillaria anatis* entries, confirming its identity.

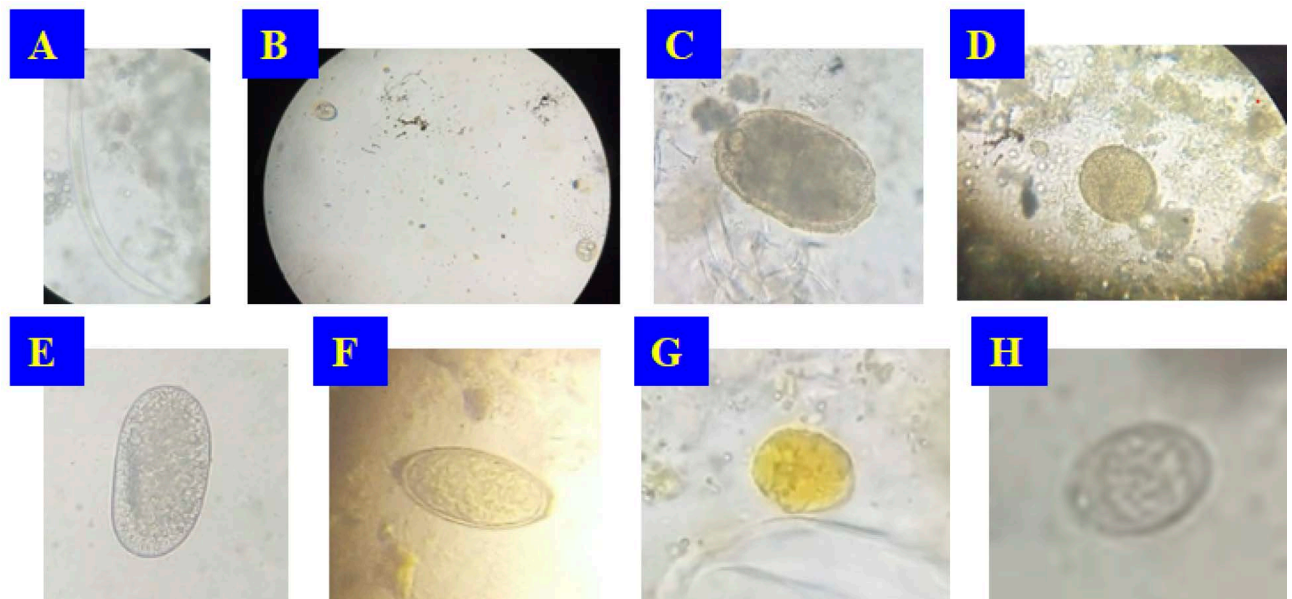


Fig. 3. [A] Nematode larva; [B] *Eimeria* species (sporulated oocysts); [C] *Ascaridia* sp. (egg); [D] *Balantidium coli* (cyst); [E] *Heterakis* species (egg); [F] *Capillaria anatis* (egg); [G] *Entamoeba* sp. (cyst); [H] *Eimeria* species (unsporulated oocyst)

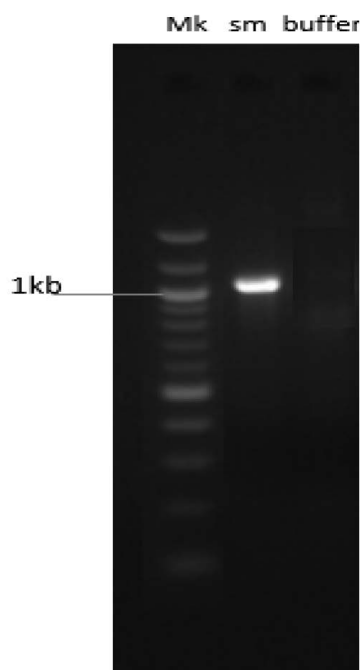


Fig. 4. Agarose gel electrophoresis displaying a 1000 bp segment of the suspected 18S rRNA gene of nematodes. Lane 1: Molecular marker; lane 2: Stork (SM); lane 3: Negative control (buffer).

DISCUSSION

The study's findings on gastrointestinal parasitism in domestic turkeys provide valuable insights into avian health, particularly within rural and semi-intensive farming systems where biosecurity is often lax. A notably high prevalence rate of 62.34% was recorded, with *Heterakis* species emerging as the most dominant helminth at 41.56%. This observation is consistent with previous reports by Cupo and Beckstead [9], who identified *Heterakis gallinarum* as a prevalent nematode in poultry, often linked to the transmission of *Histomonas meleagridis*, the causative agent of histomoniasis. The detection of protozoans such as *Eimeria* species and *Balantidium coli* highlights the diverse parasitic threats faced by turkeys, especially in environments where poor hygiene and inadequate management are common. These findings reinforce the multifactorial nature of gastrointestinal infections in poultry raised outside intensive systems.

Breed-specific susceptibility was another significant finding of this study. Nigerian indigenous turkey breeds showed a 100% infection rate, in stark contrast to the 12.12% recorded in Hybrid Converter Turkey (HTC) breeds. This disparity may be attributed to genetic differences or, more plausibly, to divergent husbandry practices.

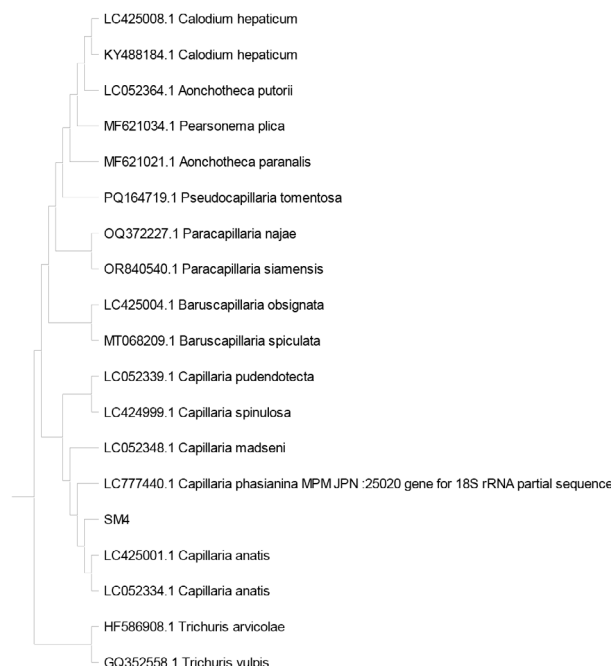


Fig. 5. Phylogenetic analysis of the *Capillaria anatis* sequence from this study alongside other nematode sequences from GenBank

As noted by Montes-Vergara et al. [28], local breeds are typically reared in free-range systems, exposing them to contaminated soil, feces, and intermediate hosts—factors that substantially elevate the risk of parasitic infection. Age-related vulnerability also played a key role in infection prevalence. Turkeys aged between 2 and 6 months exhibited the highest infection rates, which may be due to immature immune systems and greater environmental exposure during the early stages of foraging and exploration. Tompkins et al. [29] similarly reported increased parasitic susceptibility in juvenile birds, attributing this to underdeveloped immunity and higher environmental interaction. Infection pattern analysis revealed that single infections were more common than mixed infections, with *Heterakis* species dominating the single-infection group. Although less frequent, co-infections—such as those involving *Eimeria* species in combination with *Heterakis*—pose a greater threat by compounding clinical symptoms and reducing growth rates and productivity. This compounding effect of parasitic co-infections has been previously discussed by Clayton and Moore [30], who emphasized their synergistic impact on host health and performance.

Capillaria species, although detected at a lower prevalence, remain of clinical relevance. Their presence aligns with earlier studies, including those by Ola-Fadunsin et

al. [31], who reported *Capillaria* as a persistent nematode in poultry flocks. The relatively low detection rate in the present study may reflect differences in environmental conditions, intermediate host availability, or regional management practices.

A key advancement in this study was the molecular identification of *Capillaria anatis* using the 18S rRNA gene. This finding supports earlier work by Holterman et al. [14], who validated this gene as a robust marker for nematode taxonomy and phylogenetics. The use of maximum likelihood analysis coupled with strong bootstrap values adds confidence to the molecular identification process. This taxonomic approach, as demonstrated in similar studies by Holterman et al. [14], enables the differentiation of closely related helminths with high precision.

The confirmation of *Capillaria anatis* in domestic turkeys carries important implications for flock health and management. Its occurrence in semi-intensive or backyard production systems—where environmental sanitation is often inadequate—likely facilitates parasite transmission. Moreover, infections with *Capillaria anatis* have been shown to cause enteritis, nutrient malabsorption, and reduced feed conversion efficiency, as detailed by Afia et al. [32], thereby contributing to significant economic losses in turkey farming. Given these findings, molecular surveillance emerges as a crucial tool for early detection, epidemiological mapping, and the formulation of targeted control strategies in avian populations. Regular monitoring not only aids in controlling outbreaks but also supports broader health management efforts.

The broader implications of this study extend to poultry farming, veterinary medicine, and public health. For farmers, adopting regular deworming protocols, improving litter hygiene, and transitioning to controlled feeding systems are critical steps in reducing parasitic loads. Veterinarians play a vital role by conducting routine parasite screenings and educating flock owners on best practices for parasite control. Animal scientists, meanwhile, can explore the genetic basis of resistance in Hybrid Converter Turkey (HTC) turkey breeds, with a view to incorporating such traits into local populations for improved resilience. From a public health standpoint, special attention should be given to zoonotic parasites such as *Balantidium coli*. Its control is imperative in preventing cross-species transmission, particularly in communities where close contact between humans and poultry is common.

CONCLUSION

This study provides compelling evidence of a high gastrointestinal parasite burden in domestic turkeys reared in rural and semi-intensive settings, with a striking overall prevalence of 62.34%. The predominance of *Heterakis* sp., a helminth often linked with the transmission of *Histomonas meleagridis*, underscores a significant threat to turkey health and farm productivity. The concurrent presence of protozoans such as *Eimeria* sp. and *Balantidium coli* reflects complex parasitic interactions and environmental contamination risks, especially under management systems that lack biosecurity and routine health monitoring.

The stark contrast in infection rates between Nigerian indigenous turkeys and Hybrid Converter Turkey (HTC) breeds, with a 100% infection rate among Nigerian indigenous turkeys, reveals potential genetic susceptibility or exposure linked to extensive husbandry systems. Similarly, the heightened vulnerability observed in younger turkeys suggests a critical window for targeted intervention, particularly in the early growth stages when immune development is still underway. Mixed parasitic infections, while less frequent, present a layered challenge due to their potential to cause synergistic pathological effects.

The molecular confirmation of *Capillaria anatis* using 18S rRNA gene sequencing strengthens the case for integrating molecular diagnostics into routine veterinary practice. This not only improves accuracy in species identification but also enhances the understanding of parasite epidemiology in avian hosts. Our findings align with emerging literature that advocates for DNA-based tools in detecting gastrointestinal nematodes, especially in field conditions where morphological differentiation can be challenging.

In conclusion, this study contributes meaningful insights to veterinary parasitology and poultry health management. It emphasizes the necessity for multifaceted control strategies, including regular anthelmintic administration, improved sanitation, genetic resistance research, and farmer education. For veterinarians and animal scientists, these results reinforce the value of proactive parasite surveillance and the implementation of evidence-based interventions. From a public health standpoint, managing zoonotic parasites such as *Balantidium coli* is essential to safeguard both animal and human health in shared environments. Ultimately, this research underscores the interconnectedness of animal husbandry practices, parasite ecology, and health outcomes, offering a scientific foun-

data for sustainable poultry production in resource-limited settings.

Data Availability Statement

The raw data of this article will be made available by the authors, without undue reservation.

Ethical Statement

This study involved non-invasive collection of freshly voided faecal samples and did not require direct handling or disturbance of the birds; therefore, no formal ethical approval was required. Verbal consent was given by the poultry farmers for access to farm location and use of faecal matter for research purposes.

Conflict of Interest

The authors do not have any known conflict of interest and have all given consent to the submission and publication.

Generative AI Statement

AI assisted technology was used to ensure grammatic consistency of the manuscript.

Authors' Contributions

Ogbonna N. F. conceived the study and performed parasitological analyses, with support from Oyesiji A. E., Bakre A. A. and Adebawale E. A. carried out the molecular analyses and wrote that section of the manuscript. Olaiya O. S. and Ogbonna N. F. drafted the manuscript and conducted the literature review. All authors read, critically revised, and approved the final version of the manuscript and acknowledge the research is original.

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