DOI 10.24425/pjvs.2026.3595

Original article

Status of parasitic infections in migratory birds in selected areas of Bangladesh

K.S. Islam[1], Anisuzzaman[1], J.P. Juthy[2], S.S. Bushra[2], M.Z. Alam[1], A.R. Dey[1]

[1] Department of Parasitology, Faculty of Veterinary Science, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh
[2] Department of Aquaculture, Faculty of Fisheries, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh

Correspondence to: A.R. Dey, e-mail: anitadey@bau.edu.bd

Abstract

Migratory birds are a source of natural beauty and help in maintaining ecosystems, pest control and pollination. However, as with other pathogens, gastrointestinal (GI) parasites residing within migratory birds consequently contaminate the environment through their droppings. The study was aimed at identifying and estimating the prevalence and spatial distribution of GI parasites in migratory birds. To do this, 265 fecal samples were collected, (Bangladesh Livestock Research Institute (BLRI) Lake, Dhaka (203) and Tanguar Haor, Sunamganj (62) during October 2022 to March 2023. Samples were processed and examined using flotation and sedimentation techniques. Overall prevalence of parasites was 19.2% (51 out of 265). Parasites belonging to ten genera were identified, including Ascarid (2.3%), *Capillaria* (2.3%), *Echinuria* (0.8%), *Heterakis* (0.8%), nematode larva (3.4%), *Strongyloides* (1.9%), *Tetrameres* (0.8%), Echinostome (4.5%), *Raillietina* (1.1%), *Eimeria* (2.6%) and *Isospora* (2.3%). We detected the highest infections caused by nematodes (10.9%), followed by protozoa (4.9%), trematodes (4.5%), and cestodes (1.1%). Infections were almost equal in Tanguar Haor (19.4%) and the BLRI lake (19.2%). Statistically significant variation among nematode, trematode, cestode and protozoan infections were detected at the BLRI lake ($p<0.001$) but were insignificant ($p>0.05$) at Tanguar Haor. Most importantly, we also detected zoonotic parasites (4.5%), suggesting potential zoonotic relevance. This indicates that strict guidelines regarding hygienic measures while visiting areas densely populated with migratory birds should be followed.

Keywords: BLRI lake, migratory birds, parasitic infections, Tanguar Haor, zoonotic parasite

Introduction

Migratory birds are an important component of the ecosystem and approximately 11,032 extant species of birds have been estimated around the world (Gill et al. 2023). In Bangladesh, a total of 712 species of birds are available; of which 320 are migratory birds. The migratory birds that visit Bangladesh include lesser whistling teal, greater whistling teal, cotton pygmy geese, pochard, darters (snakebirds), pintail ducks, herons, comb ducks, kingfishers, egrets, bitterns, storks and flycatchers (Khatun et al. 2024).

Migratory birds inhabit a diverse range of ecosystems, relying on Arctic/temperate regions for summer breeding and warmer, southern coastal/inland wetlands, rivers and forests for wintering. However, due to rapid urbanization, loss of wetland, environmental pollution and climate change, these habitats are severely reduced; thus the birds are forced to migrate to other suitable zones (Hurlbert and Liang 2012). Among the world's nine recognized flyways used by migrating birds during their annual trip, the geographic position of Bangladesh covers two important flyways, the East Asian–Australasian Flyway (EAAFP) and the Central Asian Flyway (CAF) (Rabbi et al. 2020). Birds migrate to Bangladesh over the year during the winter, summer and spring mainly for food and suitable habitats while facing challenges in their original habitats (Alfonzo et al. 2013, Zurell et al. 2018).

Seasonal migration can intensely affect interactions between hosts and pathogens (Altizer et al. 2011). In addition, migrations enhance the geographical spread of pathogens and introduce a wide range of parasites as the birds move annually between breeding and wintering grounds. Long-distance migration can have profound consequences for species interactions, including for the ecology of infectious diseases (Satterfield et al. 2018). Stressed conditions the higher energy cost of migration make the birds more susceptible to greater range of infections than domestic or non-migratory birds (Nebel et al. 2012, Koprivnikar and Leung 2015). They cause the spread of a wide range of pathogens including helminths, bacteria, viruses, rickettsia and protozoa (Hubalek 2004). Among parasites, trematodes such as *Echinostoma*, *Paramonostomum, Catatropis*, *Metorchis* and *Microphallus*; cestode including *Raillietina* and *Hymenolepis*; nematodes such as *Amidostomum*, *Tetrameres*, *Strongyloides*, *Syngamus*, *Capillaria*, *Porrocaecum*, *Polymorphus* and ascarid; protozoa such as *Plasmodium*, *Haemoproteus* and *Leucocytozoon* and coccidia, and Acanthocephala have been reported in migratory birds in different parts of the world (Mascarenhas et al. 2009, Birmani et al. 2011). These migratory birds intermingle with domestic birds at their temporary residence and potentially share common species of pathogens (Smith and Ramey 2015, Ramey et al. 2016, Viana et al. 2016).

According to Parsa et al. (2023), 20.0% wild passerines are infected with intestinal helminths (*Syngamus,* 33.1% and *Capillaria*, 27.2%) and protozoa (*Isospora,* 32.0%) in Britain and Ireland. *Amidostomum nodulosum* is abundant in the Mallard and has proven lethal for the host in heavy infections. Haemosporidian parasites (34.8%) including *Leucocytozoon* (28.5%), *Plasmodium* (8.1%) and *Haemoproteus* (0.3%) were detected in the grey-cheeked thrush in North and Central America, the Santa Marta mountains, the Andes and the Amazon (Pulgarin-R et al. 2019). Also, predatory and racing birds are infected with different parasites including protozoa (*Avispora* and *Trichomonas*) and nematodes (*Porrocaecum* sp. and *Capillaria*) (Bobrek et al. 2017, Pratnicka et al. 2024).

Migratory birds play an important role in spreading zoonotic parasites. Defecation of migratory birds on crops, various drinking water sources, recreational waters, or direct contact with humans are a source of infections of pathogens (Egan et al. 2024). Among these, water is the main sources of zoonotic parasites, especially *Cryptosporidium* and *Giardia*. Another important zoonotic trematode, transmitted by the ingestion of raw snails, fishes, and amphibians that harbor the infective stage is echinostome which is mostly prevalent in humans in Southeast Asia and the Far East (Chantima et al. 2013).

In winter, many migratory birds visit Bangladesh from Russia and China. In the last few years, many studies have been conducted on the genetic diversity of various viruses as well as drug resistant bacterial strains (Hasan et al. 2012, Khatun et al. 2024). However, information regarding parasitic infections in migratory birds in Bangladesh is lacking and yet to be addressed. Therefore, the present study was designed to report gastro-intestinal parasitic infections in migratory birds in Bangladesh in two areas of Bangladesh.

Materials and Methods

Study area

Two migratory resident sites at Bangladesh Livestock Research Institute (BLRI), situated in the central part of the country in Dhaka division and at Tanguar Haor (wetland ecosystem), located in the eastern part of the country, in the Sunamganj district of the Sylhet division were surveyed for the detection of parasitic infections (Fig. 1). Migratory birds visit these locations in the winter season including the months of December,

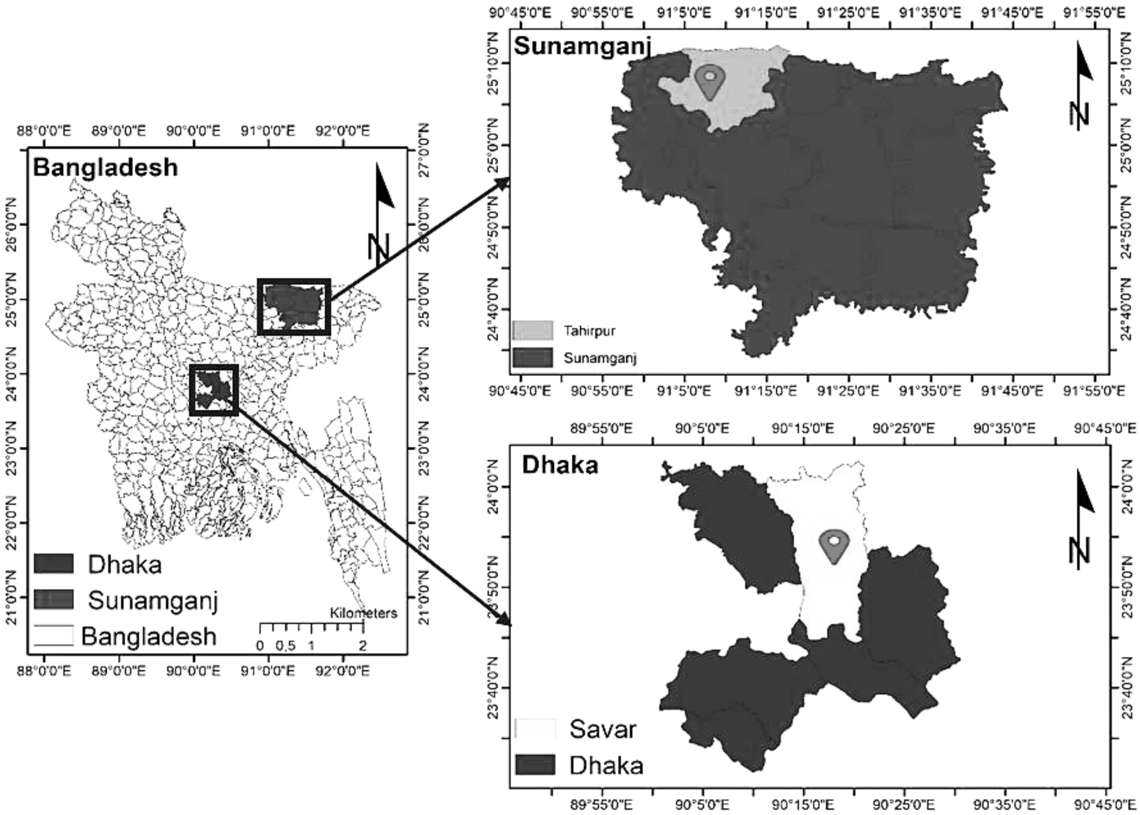

Fig. 1. Map of study area from where the fecal samples of migratory birds were collected.

January and February when the temperature ranges from 10°C to 20°C.

Tanguar Haor consists of a mosaic of permanent wetlands (beels), flooded grasslands, reed swamps and remnant swamp forests. It is a vital wintering ground for over 30,000-40,000 migratory birds where lesser whistling-duck, comb duck, red-crested pochard, northern pintail etc. are mostly available . Tanguar Haor offers diverse habitats key for migratory waterfowl including submerged vegetation, free-floating plants, and rooted floating plants.

The lake at BLRI serves as an essential winter habitat for various migratory bird species including lesser whistling teal, greater whistling teal, cotton pygmy goose, pochard, darters (snakebird), pintail duck, garganey, mallard duck, northern shoveler and the African comb duck etc. The area typically features aquatic vegetation, including floating, submerged and emergent plants that provide food and shelter, while adjacent terrestrial vegetation offers roosting sites.

Collection of fecal samples

The current law of Bangladesh, the Wildlife Conservation and Security Act of 2012 (Chapter-3, Article no. 6), strictly prohibits the catching, trapping, hunting or killing of any wildlife animal. However, for the common practice of working with migratory birds, scientists collect feces from the birds' dwelling places (Khatun et al. 2024). In the present study, a team of researchers stayed in the focal area of the migratory birds to observe the activities of the birds gathered. Freshly voided feces were collected from grass blades or along the banks of lakes and wetlands in the very early morning before sunlight. The inclusion criteria for sample collection were freshness, sufficient amount and free from environmental contamination. Otherwise, samples were not considered for this study.

Approximately 2 g of each dropping was collected using a laboratory spoon and placed in a 15-ml sterile Falcon tube containing 10% formalin for preservation and transported to the laboratory, Department of Parasitology, Bangladesh Agricultural University maintained at 4°C in an icebox. A total of 265 samples were collected from Tanguar Haor (n=62), Sunamgonj and the Bangladesh Livestock Research Institute Lake (n=203), Savar, Dhaka. Samples were collected once in a week from each location. Samples were examined as early as possible to avoid the effects of preservative on the developmental stage of parasites.

Examination of samples and identification of parasites

Samples were examined under a microscope following simple sedimentation and flotation techniques

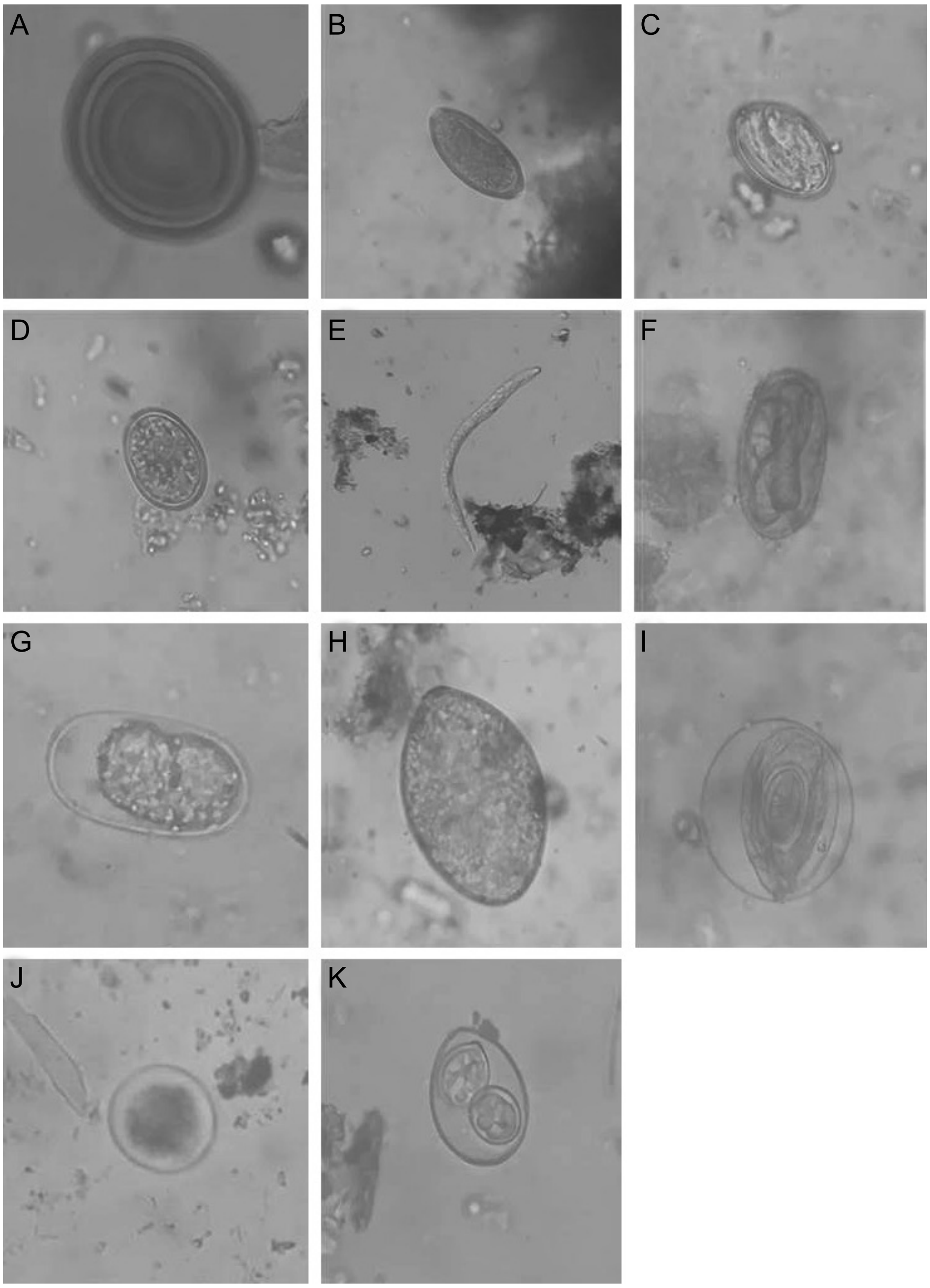

Fig. 2. Identified eggs, larvae and oocysts of parasites from fecal samples of different migratory birds. The detected parasites were (A) egg of Ascarid, (B) egg of *Capillaria* spp., (C) egg of *Echinuria* spp., (D) egg of *Heterakis* spp., (E) nematode larva, (F) egg of *Strongyloides* spp., (G) egg of *Tetrameres* spp., (H) egg of Echinostome, (I) egg of *Raillietina* spp., (J) unsporulated oocyst of *Eimeria* spp. and (K) sporulated oocyst of *Isospora* spp.

Briefly, in the simple sedimentation technique, 1 g of droppings was mixed thoroughly with water to prepare a homogeneous suspension and then filtered to remove coarse particles. Following filtration, the suspension was allowed to stand for 30 minutes, and the sediment was examined using a microscope. Briefly, 1g of fecal pellet was gradually mixed with 10 ml flotation solution (saturated salt solution, specific gravity: 1.200). The suspension was thoroughly stirred and allowed to pass through a sieve to remove coarse particles. The suspension was then poured into a test tube and more flotation fluid was added to fill up to the brim, a coverslip was placed on the top of the tube and the suspension was allowed to stand for 10-15 min to float all parasitic eggs, cysts and oocysts. The coverslip was then removed, placed on a slide and examined under a microscope (Olympus CX21LEDFS1, Tokyo, Japan) using 10X and 40X magnification. Three slides were examined from each sample to minimize error. The eggs, larvae and oocysts of parasites were identified according to the key morphological features as described by Thienpont et al. (1986).

Table 1. Overall prevalence of identified parasites in migratory birds in Bangladesh.

Category of parasite	Identified Parasites	No. of infected birds	Prevalence (%)	95% (CI of prevalence
Nematode	Ascarid	6	2.3	0.84-4.86
	Capillaria spp.	6	2.3	0.84-4.86
	Echinuria spp.	2	0.8	0.09-2.70
	Heterakis spp.	2	0.8	0.09-2.70
	Nematode larva	9	3.4	1.56-6.35
	Strongyloides spp.	5	1.9	0.61-4.35
	Tetrameres spp.	2	0.8	0.09-2.70
	Sub total	**29**	**10.9***	**7.45-15.34**
Trematode	Echinostome	12	4.5	2.36-7.78
Cestode	*Raillietina* spp.	3	1.1	0.23-3.27
Protozoa (coccidia)	*Eimeria* spp.	7	2.6	1.07-5.37
	Isospora spp.	6	2.3	0.84-4.86
	Sub total	**13**	**4.9**	**2.64-8.24**
Co-infection		**10**	**3.8**	**1.82-6.83**
Overall infection (n= 265)		**51**	**19.2**	**14.68-24.52**

CI, Confidence Interval; *, significant variation among nematode, trematode, cestode and protozoan infections (p<0.001)

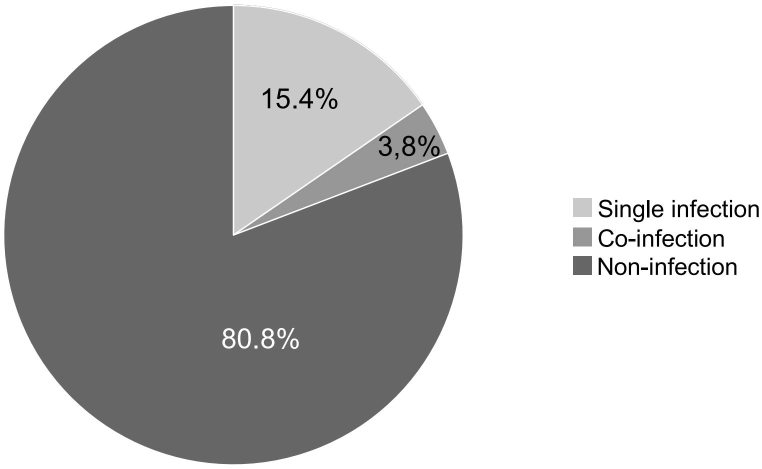

Fig. 3. Pie diagram representing the prevalence of single infection, co-infections and non infection.

Data analysis

The data were processed and analyzed using computer program, SPSS 26.0 software. The Chi-square test was performed to determine the level of significance using SPSS 26.0 software.

Results

Prevalence of parasitic infections in migratory birds of Bangladesh

A total of 265 fecal samples were collected and examined, of which, 51 samples were found to be infected with one or more species of parasites and the estimated overall prevalence was 19.2%. The identified parasites were ascarid (2.3%), *Capillaria* spp. (2.3%), *Echinuria* spp. (0.8%), *Heterakis* spp. (0.8%), nematode larva (3.4%), *Strongyloides* spp. (1.9%), *Tetrameres* spp. (0.8%) as nematodes; Echinostome (4.5%) as trematode; *Raillietina* spp. (1.1%) as cestode; *Eimeria* spp. (2.6%) and *Isospora* spp. (2.3%) as protozoa (Fig. 2). A statistically significant ($p<0.001$) variation was detected among nematode (10.9%), trematode (4.5%), cestode (1.1%) and protozoan (4.9%) infections (Table 1). Among the examined samples single infection was found in 15.4% and mixed infections in 3.8% of the samples (Fig. 3).

Prevalence and spatial distribution of parasitic infections in migratory birds

We found no significant variation in overall infections in the two study areas. In the present study, out of

Table 2. Overall prevalence of identified parasites in migratory birds at BLRI in Bangladesh.

Category of parasite	Identified Parasites	No. of infected birds	Prevalence (%)	95% (CI of prevalence
Nematode	Ascarid	5	2.5	0.8-5.65
	Capillaria spp.	5	2.5	0.8-5.65
	Echinuria spp.	2	1	0.12-3.51
	Heterakis spp.	2	1	0.12-3.51
	Nematode larva	7	3.4	1.4-6.98
	Strongyloides spp.	3	1.5	0.31-4.26
	Tetrameres spp.	2	1	0.12-3.51
	Sub total	**22**	**10.8***	**6.92-15.95**
Trematode	Echinostome	9	4.4	2.05-8.25
Cestode	*Raillietina* spp.	3	1.5	0.31-4.26
Protozoa	*Eimeria* spp.	7	3.4	1.4-6.98
	Isospora spp.	4	2	0.54-4.97
	Sub total	**11**	**5.4**	**2.74-9.49**
Co-infection		**8**	**3.9**	**1.72-7.62**
Overall infection (n= 203)		**39**	**19.2**	**14.03-25.31**

CI, Confidence Interval; *, significant variation among nematode, trematode, cestode and protozoan infections ($p<0.001$)

203 samples collected from the BLRI lake, 39 were found to be infected with one or more species of parasites with an overall prevalence of 19.2%. The identified parasites were ascarid (2.5%), *Capillaria* spp. (2.5%), *Echinuria* spp. (1.0%), *Heterakis* spp. (1.0%), nematode larva (3.4%), *Strongyloides* spp. (1.5%), and *Tetameres* spp. (1.0%) as nematodes; Echinostome (4.4%) as trematode; *Raillietina* spp. (1.5%) as cestode; *Eimeria* spp. (3.4%) and *Isospora* spp. (2.0%) as protozoa (Table 2). Among the examined samples, co-infection was found in 3.9% of samples.

In Tanguar Haor, from 62 collected samples, 12 were found to be infected with one or more species of parasites with an overall prevalence of 19.4%. The identified parasites were ascarid (1.6%), *Capillaria* spp. (1.6%), nematode larva (3.2%) and *Strongyloides* spp. (3.2%) as nematodes; Echinostome (4.8%) as trematode; *Isospora* spp. (3.2%) as protozoa (Table 3). Among the examined samples, co-infection was found in 3.2% of samples. Statistically significant variations among nematode, trematode, cestode and protozoan infections were detected in the BLRI lake ($p<0.001$) but were insignificant ($p>0.05$) in Tanguar Haor.

Co-occurring parasite species found in migratory birds

In this study, co-infection was found in 3.8% of samples where 3.9% were in the BLRI lake and 3.2% in Tanguar Haor. A total of nine combinations were found and are presented in Table 4.

Prevalence of zoonotic parasites

Among the identified parasites, Echinostome has zoonotic potential. Out of 265 samples, 12 samples were found to be infected with Echinostome with an overall prevalence of 4.5%, with 4.4% detected in the BLRI lake and 4.8% in Tanguar Haor.

Discussion

Migratory birds play an important role in the transmission of parasites among species at breeding and wintering grounds (Waldenstrom et al. 2002, Klaassen et al. 2012, Levin et al. 2013). It has been speculated that variation in migratory strategies and behaviors among migrant species might affect host-parasite interactions and eventually the transmission cycle of parasites (Altizer et al. 2011, Moller and Szep 2011, Clark et al. 2016).

In this study, about 19.2% examined birds were infected with a wide range of helminth and protozoan parasites such as ascarid, *Capillaria*, *Echinuria*, *Heterakis*, nematode larva, *Strongyloides*, *Tetrameres* as nematodes; Echinostome as trematode; *Raillietina* as cestode; *Eimeria* and *Isospora* as protozoa. All the above parasite species have been reported in different studies in migratory birds around the world (Calvete et al. 2003, Millan et al. 2004, Khan et al. 2008, Mascarenhas et al. 2009). In Bangladesh, ascarids, *Capillaria*, *Heterakis*, *Echinostoma*, *Raillietina* and *Eimeria* have been detected from domestic fowls (Alam et al. 2021, Siddiqui et al. 2024, Noor et al. 2025).

Table 3. Overall prevalence of identified parasites in migratory birds at Tanguar Haor in Bangladesh.

Category of parasite	Identified Parasites	No. of infected birds	Prevalence (%)	95% (CI of prevalence
Nematode	Ascarid	1	1.6	0.04-8.66
	Capillaria spp.	1	1.6	0.04-8.66
	Echinuria spp.	0	0	-
	Heterakis spp.	0	0	-
	Nematode larva	2	3.2	0.39-11.17
	Strongyloides spp.	2	3.2	0.39-11.17
	Tetrameres spp.	0	0	-
	Sub total	**7**	**11.3^{NS}**	**4.66-21.89**
Trematode	Echinostome	3	4.8	1.01-13.5
Cestode	*Raillietina* spp.	0	0	-
Protozoa	*Eimeria* spp.	0	0	-
	Isospora spp.	2	3.2	0.39-11.17
	Sub total	**2**	**3.2**	0.39-11.17
Co-infection		**2**	**3.2**	0.39-11.17
Overall infection (n= 62)		**12**	**19.4**	**10.42-31.37**

CI, Confidence Interval; NS, statistically insignificant variation among nematode, trematode, cestode and protozoan infections (p>0.05)

Table 4. Co-occurring parasite species found in migratory birds in Bangladesh.

SL. No.	Co-occurring parasite species	No. of cases
1.	Ascarid and nematode larva	1
2.	Ascarid, nematode larva and Echinostome	1
3.	Nematode larva and Echinostome	2
4.	Echinostome and *Raillietina*	1
5.	*Strongyloides* and *Capillaria*	1
6.	*Capillaria* and *Isospora*	1
7.	Ascarid and Echinostome	1
8.	*Strongyloides* and *Eimeria*	1
9.	Echinostome and *Isospora*	1

Studies on the prevalence of parasitic infection are important for both economic and zoonotic aspects. In the present study, 2.3% of migratory birds were infected with ascarid parasites. This finding is much lower than Faizullah et al. (2022) and Youssef and Mansour (2014), who reported 52.17% and 28.7% intestinal infection with *Ascaridia* species in quails in Baluchistan Pakistan and Egypt, respectively. A similar kind of study was also carried out by Rosa et al. (2017) in Brazil in which the prevalence of *A. galli* was 20.0% in quail. Difference in prevalence between the present and previous studies might be due to difference in bird species, method of examination, duration of migration period and difference in ecological and environmental factors.

According to the life cycle pattern of helminth species, climatic condition affects their prevalence, intensity and geographical distribution of helminths (Mas-Coma et al. 2008). The life history and ecological traits of the hosts play an important role in distribution and diversity of the helminth parasites (Poulin and Morand 2000). The geographical location and climatic condition of Bangladesh is suitable for migratory birds (Dey et al. 2020); thus they enhance the spread of a wide range of parasitic infections among the humans and domestic birds.

Migratory strategies and behaviors potentially affecting the transmission of infections are difficult to study (Pulgarin-R et al. 2019). The present study examined the dynamics of infection with different nematode parasites from long-distance migratory birds. These findings are in line with the earlier study of Islam et al. (2024) who reported *Ascaridia*, *Heterakis* and *Capillaria* from 21 species of wild birds (dead birds for museum specimens) in Bangladesh. Coccidia, important protozoan parasites are highly host-specific (Garedaghi et al. 2011). However, coccidian parasites including *Eimeria* (2.6%) and *Isospora* (2.3%) were recorded in this study in different species of migratory birds. Among various species of *Eimeria*, *E. tenella* (72.2%) was reported in long-distance migratory birds, quails, and *Coturnix japonica* in Balochistan, Pakistan (Khan et al. 2022). *E. tenella* was also documented in Japanese quails in Mosul, Iraq (49.9%) and Azerbaijan (52.0%) (Khan et al. 2022). The lower prevalence in the present study might be due to variation in bird species, method of examination and difference in ecological and environmental factors.

In this study, the prevalence of parasitic infections was more or less similar in the two different studied areas, BLRI Lake, Savar (19.4%) and Tanguar Haor, Sunamganj (19.2%). This might be due to the same species of birds, climatic condition and habitats of migratory birds in the two studied locations. According to Rabbi et al. (2020), different species of migratory birds visit these places every winter and stay there during the pick of the winter season.

Echinostome, the extensively distributed member of the family Echinostomatidae have a complex life cycle involving a wide range of definitive hosts, particularly aquatic birds and various mollusks or amphibians which act as intermediate hosts. Some echinostomatid species cause disease in humans in specific foci in East and Southeast Asia through ingestion of raw or undercooked molluscs, fish, crustaceans and amphibians infected with metacercariae (Enabulele et al. 2023). In the present study, Echinostome, the zoonotic parasite, was reported in migratory birds.

Migratory birds act as natural hosts and vectors for transmitting a wide range of zoonotic pathogens over the world. The rate of transmission of zoonotic diseases depends on cross-species transmission of diseases among humans, animals and birds, frequent movement of humans into the natural habitats of wild birds and domestication of wild birds as pets or game birds. A recent study revealed that 1,438 wild bird species were associated with transmitting 760 pathogens including 387 emerging and 212 zoonotic pathogens (Qiu et al. 2025). In Bangladesh, Echinostomes have previously been reported in indigenous ducks (Anisuzzaman et al., 2005) and semi- scavenging indigenous chickens (Noor et al. 2025). Domestic water fowl managed by scavenging and semi- scavenging systems share common water sources including, wetlands and post-harvest rice paddy fields with migratory birds, thus providing opportunities for transmission of pathogens. These water sources, therefore, act as potential foci for various zoonotic parasites. Enabulele et al. (2023) reveal that the genetic flow of the zoonotic parasite *E. revolutum* (s.s.) in Eurasia is probably due to movements of migratory waterfowl. Although Echinostome infections in humans is yet to be reported in Bangladesh, it is well documented in Nepal (Sah et al. 2018), Indonesia, China, Thailand and India where they cause severe damage to intestinal mucosa, intestinal perforation, marked malnutrition and anemia (Sohn et al. 2011).

Conclusions

To the best of our knowledge, this is the first report documenting parasitic infections in migratory birds in Bangladesh. The present study revealed that parasitic infections are prevalent (19.2%) in migratory birds and ten genera of parasites were detected including Ascarid, *Capillaria*, *Echinuria*, *Heterakis*, nematode larva, *Strongyloides*, *Tetrameres*, Echinostome, *Raillietina*, *Eimeria* and *Isospora*. Prevalence of parasitic infections was almost equal in the two selected areas. Nematode, trematode, cestode and protozoan infections varied significantly ($p<0.001$) in the BLRI but were insignificant ($p>0.05$) in Tanguar Haor. Echinostome, the zoonotic parasite, was identified in the present study. In this study, it was not possible to collect fecal samples from individual birds due to restrictions on catching, trapping, hunting, or killing of any wildlife animal according to the current law of Bangladesh, and only microscopic examination was performed which confirmed genus level identification. Therefore, further detailed epidemiological investigation with greater sample sizes as well as genetic diversity pattern of parasitic infections in migratory birds in Bangladesh is recommended.

Acknowledgements

The authors thanks the Bangladesh Agricultural University (Project No.: 2019/759/BAU) for funding the research.

Author Declarations

Ethical statement

During the conduct of this research, the authors maintained all possible ethical standards in their work. The Animal Welfare and Ethical Committee of Bangladesh Agricultural University (AWEEC/BAU/2022 (3)) approved the research work.

Use of generative artificial intelligence

The authors declare that no generative artificial intelligence (AI) tools were used in the preparation of the manuscript.

Conflict of interest

The authors declare no conflict of interests.

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