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Gastrointestinal parasite infection and the first molecular detection of strongyle infection in cattle of the Ayeyarwaddy Division, Myanmar

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ABSTRACT

Background: Gastrointestinal parasites (GI) are a group of pathogens that infect the digestive tract of a wide range of animals and cause significant infections in cattle worldwide. Nematodes at the order level Strongylida have the highest prevalence in livestock farming. In Myanmar, cattle production plays a critical role in the rural lifestyle. However, baseline data on GI parasitic infection in cattle from Myanmar remain scarce.

Aim: This study is the first report to identify the most abundant GI parasites in cattle from this country using microscopic identification, followed by species identification of egg-positive samples through molecular methods targeting the internal transcribed spacer (*ITS*) region.

Methods: A total of 219 cattle were involved in this cross-sectional study. Fecal flotation and formalin-ether centrifugal sedimentation techniques were used for conventional microscopic analysis. A fragment of the ITS gene was analyzed genetically in five samples identified as single-species infections.

Results: Microscopy revealed an overall infection rate of 79.5% with intestinal parasites. Regarding results, strongyles were the most frequently detected parasites, followed by *Eimeria* spp. and *Toxocara* spp. Concretely, two species from the family Trichostrongylidae were found in the study area, *Haemonchus contortus* and *Trichostrongylus colubriformis*.

Conclusion: This study provides the first molecular evidence of GI parasites in cattle in Myanmar, highlighting the high risk of parasitic infections in this area. Molecular analysis of five samples showed single-species infections: four with *H. contortus* and one with *T. colubriformis*, both likely widespread and dominant in Myanmar. These findings suggest that cattle may contribute to local transmission. The high prevalence underscores the necessity for sustained surveillance, implementation of effective control strategies, intersectoral collaboration between veterinary and public health authorities, and enhancement of public awareness to prevent and manage significant GI parasitic infections in Myanmar.

Keywords: Cattle, Gastrointestinal parasites, Microscopy, Myanmar, Strongyle.

Introduction

Livestock is vital to national economies and rural livelihoods, offering milk, meat, inputs for crop production, soil enrichment, and raw materials for industry and serving as a form of living insurance for farmers. The importance of dairy products and meat as essential protein sources for humans has led to an increase in cattle farming (Pighin *et al*., 2016). However, at the same time, significant adverse challenges, such as parasitic diseases, antimicrobial resistance, and climatic disasters, have also arisen (Soe *et al.*, 2024). In Myanmar, over 70% of the population resides in rural areas, with more than 58% raising cattle, goats, and chickens as primary or supplementary sources of income for household expenses (Belton and Fang, 2022). The country has an estimated population of over 9.6 million draught cattle and approximately 129,000 crossbred dairy cattle. Cattle farming in Myanmar is threatened by numerous pathogenic threats, such as limited veterinary services, lack of knowledge, poor health practices, and the absence of preventive measures against parasitic infections.

When a livestock population arises, pathogens and their diseases pose critical concerns for human and animal health. Either livestock or farm animals may act as sources of infections for humans or vice versa (Pradhan

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and Karanth, 2023), so the fight against these zoonoses must be carried out using a One Health approach (Sinclair, 2019). Regarding parasitic diseases, beyond causing high morbidity in both humans and animals, they result in considerable economic loss on a global scale associated with weight loss, reduced meat and milk production, abortions, and sterility (Lopes *et al.*, 2016). In fact, herd mortality can exceed 40% due to either internal or external parasitic infections, particularly among young animals, and annual weight losses of 6–12 kg per animal have been reported (Sykes, 1994). While parasites are a highly diverse group of organisms, gastrointestinal (GI) parasites are of particular relevance in the context of cattle farming in Myanmar. GI parasites represent a major global burden, particularly affecting livestock health and productivity in tropical and subtropical regions, including Myanmar (Krecek and Waller, 2006; Pisarski, 2019). GI parasitism in ruminants occurs year-round, with higher intensity during the rainy season, as temperature and humidity have been mentioned as key factors that influence the development and survival of eggs, larvae, cysts, and oocysts in pastures (Terfa *et al.*, 2023). Helminths, such as *Strongyloides* spp., which inhabit the small intestine or cecum, are the primary cause of GI parasitism in cattle, linking to sudden death in severe cases (Thamsborg *et al.*, 2017). GI parasitism poses a significant threat to cattle farming in Myanmar, compounding existing challenges such as limited access to veterinary services, inadequate parasite control measures, and the absence of routine deworming practices. Understanding the epizootiology of parasitism is essential for sustainable parasitic control because it depends on interactions between the host, climate, management practices, and production conditions. However, the health status of the cattle population in the Ayeyarwaddy Division remains unclear, despite it being the second largest cattle-producing region in Myanmar, and to the author's knowledge, no previous investigations have been conducted.

The primary diagnostic method for parasitic infection is fecal microscopic examination. However, this technique requires the expertise of a skilled technician (Playford and Besier, 2024). Although microscopic examination of strongyle eggs in fecal samples is straightforward, the egg morphology does not permit species identification. For this purpose, internal transcribed spacer (*ITS*) regions in rDNA can be used to identify nematodes (Chilton, 2004). Genetic markers within the *ITS* enable accurate species-level identification of nematodes (Gasser *et al.*, 1996; Newton *et al.*, 1998). Recent studies of cattle GI parasites in other countries have revealed high prevalence rates and fluctuating diversity across them (Huang *et al.*, 2014; Ahmed *et al.*, 2015; Das *et al.*, 2018; Income *et al.*, 2021). Until now, updated baseline data on bovine GI parasites at the country level are still needed in Myanmar. The aims of the current study, therefore, are i) screen for major GI parasites in cattle fecal samples using a light microscopic technique and ii) the further molecular identification of nematode species based on *ITS* genetic markers. In addition, phylogenetic analyses between the isolates identified in the current study and other global isolates will be performed. These findings will serve as baseline data and contribute to developing effective strategies to tackle the health challenges associated with cattle farming practices in Myanmar.

Materials and Methods

Sampling area and farming characteristics

A cross-sectional study was conducted for approximately 4 months between August and November 2022. The sampling map, geographic coordinates, and livestock husbandry system of the Ayeyarwaddy Division are shown in Figure 1. The Ayeyarwaddy Division, located in the southern part of Myanmar, experiences tropical weather, with summer temperatures ranging from 24° to 36°C and winter temperatures from 19° to 31°C. Moreover, it is a low-lying delta region with extensive floodplains. The area is characterized by rivers, wetlands, and fertile agricultural land, making it one of Myanmar's most important regions for rice production. Unlike the mountainous regions in the North and East of Myanmar, the Ayeyarwady Division has relatively flat topography. Livestock farming in the Ayeyarwaddy Division is predominantly practiced on a small scale and is integrated with crop production. The region is characterized by high humidity and seasonal flooding and is considered favorable for parasite transmission. Several challenges are commonly encountered, including limited access to veterinary care, irregular deworming practices, low input systems, and financial constraints, which contribute to suboptimal animal health and productivity. The study targeted 21 farms, of which each farm housed more than 10 cattle. A total of 219 cattle fecal samples were collected. These cattle were crossbreed (approximately two-third of population) and indigenous breeds, and they were raised using traditional method with semi-intensive farming practices when grazing pastures were available. Feeding practices included roughage, such as rice straw and natural grass and concentrated feeds such as rice bran and sesame cake chosen based on socioeconomic factors.

Questionnaires survey

A questionnaire was designed to gather signalment data related to the history of the sampled animals. The questionnaire covered information on age (<1 year, 1–3 years, and >3 years), sex (male/ female), breed (crossbred/ indigenous), feeding system (grazing/ cut and carry), and anthelmintics usage (routine practice/ not regular). The age of the cattle was estimated using dentition, following the method described by Sten (1989). Cattle over 3 years old were classified as mature, as breeding (natural or artificial) is typically completed in Myanmar by this age. Accordingly, the cattle were categorized into three age groups, and all sampled cattle were identified using ear tags.

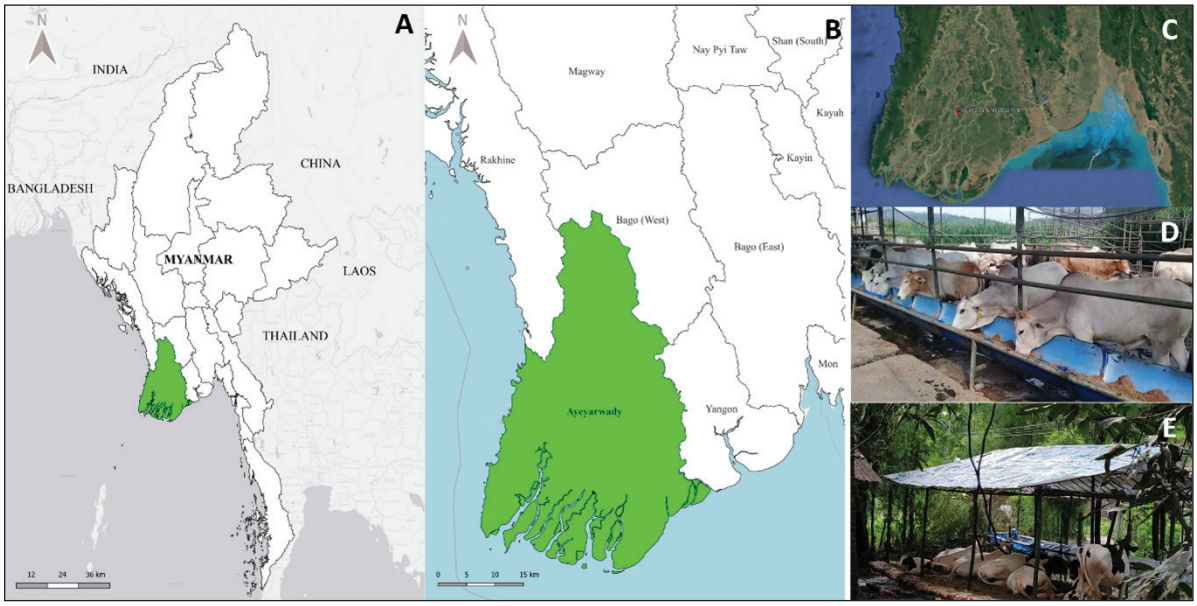

Fig. 1. (A, B, and C) Map and geographic coordinates of sampling sites in Ayeyarwaddy Division, southern part of Myanmar. (D and E). The figures demonstrate cattle livestock husbandry systems nearby residential areas and grazing pastures. The map was drawn by QGIS (version 3.36.3). The satellite image was modified from the Google Earth Website.

Fecal sample collection, microscopic identification, and statistical analysis

Fecal samples were collected directly from the rectum using sterile plastic bags. Thereafter, the samples were placed in cool ice boxes and transported to the Laboratory of Molecular Detection, Livestock Upgrading Section, Mingaladon, Yangon, where fecal examination was conducted within 24 hours. For fecal flotation, 2 g of feces was mixed with 10 ml of saturated NaCl solution and transferred into a 15 ml corning tube by passing through a sterile cotton gauze. The tube was then filled with saturated NaCl until a convex meniscus formed at the top and was covered with a coverslip. After standing for 10–15 minutes, the coverslip was examined under a light microscope (Dryden *et al.*, 2005). In formalin-ether centrifugal sedimentation, approximately 2 g of feces was mixed with 10 ml of 10% formalin and filtered through sterile cotton gauze into a 15 ml corning tube. The volume was adjusted to 10 ml by adding 10% formalin, followed by the addition of 2 ml of ether. The mixture was then shaken vigorously and centrifuged at 500 × *g* for 2 minutes. The sediment was then transferred to a glass slide, covered with a coverslip, and subsequently examined under a light microscope (Zajac and Conboy, 2012).

Statistical analysis

A Pearson chi-square test was conducted using SPSS version 28.0 (IBM Corp., NY, USA), to assess associations between the occurrence of infection, as determined by microscopic identification, and selected parameters: age, sex, breed, feeding system, and anthelmintic use. In addition, multiple regression analyses were conducted to evaluate the simultaneous effects of these variables on each parasite infection status. The analysis was performed using a 95% confidence interval, with a p-value <0.05 considered statistically significant.

DNA extraction and polymerase chain reaction (PCR) amplification

DNA was extracted from five microscopically positive samples which showed a high number of fecal eggs using the QIAamp Fast DNA Stool Mini Kit (Qiagen, Germany), according to the manufacturer's protocol. Briefly, the *ITS* region of the nematode was amplified using the primers (ITSF 5′-CTCGCTCTCAGTGTTTTCGT-3′) and (ITSR 5′-TTGACAAGTTAAGCAGCTTC-3′), as described by Gasser *et al.* (1996). PCR amplification was performed under the following conditions: initialization at 94°C for 5 minutes, 40 cycles of denaturation at 98°C for 10 seconds, annealing at 55°C for 15 seconds, extension at 68°C for 1 minute, and a final extension at 68°C for 5 minutes (Sato *et al.*, 2014). The PCR products were analyzed using 1% agarose gel electrophoresis in 1× TBE buffer at 100 V for 30 minutes, and positive bands were checked using 1,000 bp DNA ladder (Thermo Fisher Scientific Inc., Waltham, MA).

Sequencing and phylogenetic analyses

The amplified PCR products were sent to a commercial sequencing company (Macrogen, Seoul, South Korea). The resulting nucleotide sequences were then checked using a BLASTn search tool (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Reference sequences were retrieved from GenBank for phylogenetic analyses. Briefly, multiple sequence alignment was performed with Molecular Evolutionary Genetics Analysis, software

version 11, and a phylogenetic tree was generated using the maximum-likelihood method with the IQ-TREE web server (http://iqtree.cibiv.univie.ac.at/), employing 10,00 bootstrap replicates. The optimal substitution model was determined (Trifinopoulos *et al.*, 2016). The phylogenetic tree was visualized using FigTree (software version 1.4.4) (http://tree.bio.ed.ac.uk/software/figtree/).

Haplotype networks

Haplotype networks were constructed using 32 sequences of *Trichostrongylus colubriformis*, *Oesophagostomum* species, and *Haemonchus* species. The number of haplotypes was determined using DnaSP software (version 5.10.1). Representative haplotype sequences were manually arranged before visualization with the TCS network in PopART (https://popart.maths.otago.ac.nz/). These sequences were obtained from Myanmar, Laos, New Zealand, Italy, Iran, Ireland, Egypt, China, Denmark, the USA, and India.

Ethical approval

Not needed for this study.

Results

Microscopic identification

In the present study, the overall rate of infection with intestinal parasites was 79.5% (174/219), indicating a high level of GI parasitic infection. The most common parasites were strongyles (95.4% (166/174), followed by *Eimeria* spp. 36.8% (64/174) and *Toxocara* spp. 33.3% (58/174). The coinfection of strongyles with either *Eimeria* spp. or *Toxocara* spp. was identified in 58% (101/174) of the cattle. The parasite stages detected via microscopy are shown in (Fig. 2), and the distribution of GI parasites relating to signalment data is shown in Table 1. According to the Pearson's chi-square test, the prevalence of GI parasites was significantly higher in cattle older than 3 years ($\chi^2 = 86.4$; $p = 0.0001$), females ($\chi^2 = 13.87$; $p = 0.0001$), indigenous breeds ($\chi^2 = 8.97$; $p = 0.02$), animals with a feeding system based on grazing ($\chi^2 = 9.36$; $p = 0.002$), and those animals whose farmers did not routinely use anthelmintics ($\chi^2 = 34.35$; $p = 0.0001$).

Molecular identification and phylogenetic analyses

Only five representative fecal samples were submitted for molecular amplification targeting the *ITS* gene, and amplicons were subsequently sent for Sanger sequencing. As a result, four sequences revealed 99.64% sequence identity with *H. contortus* sequence (accession no. AB908962) in ruminant fecal samples from Lao PDR. The remaining sequence showed 100%

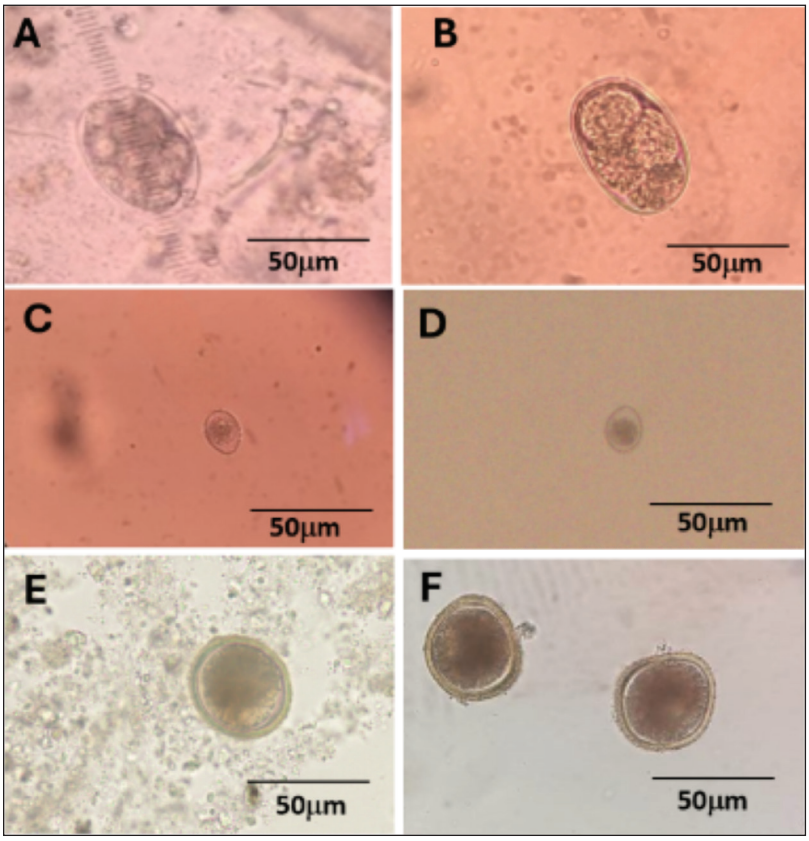

Fig. 2. GI parasite stages in cattle fecal sample in the present study. (A and B) Strongyles eggs, (C and D) *Eimeria* spp. oocyst, and (E and F) *Toxocara* spp. eggs observed under light microscope. A, C, E: sedimentation; B, D, F: flotation.

Table 1. Distribution of GI parasites via microscopy.

Factors	No. of animals	No. of positive (%)	p-value	Strongyles	p-value	Eimeria spp.	p-value	Toxocara spp.	p-value	Co-infection: S+ (E or T)	p-value
Age			0.0001*		0.00001*		0.22		0.00001*		0*
< 1 year	56	27 (48.2)		22		18		8		20	
1–3 years	27	12 (44.4)		11		2		-		3	
>3 years	136	135 (99.2)		133		44		50		78	
Sex			0.0001*		0*		0.29		0.99		0.26
Male	88	59 (67)		53		22		23		45	
Female	131	115 (87.8)		113		42		35		56	
Breed			0.002*		0.39		0.0004*		0.40		0.45
Indigenous	34	34 (100)		28		19		11		18	
Crossbred dairy	185	140 (75.7)		138		45		47		83	
Feeding system			0.002*		0.01*		0*		0.61		0.13
Grazing	62	58 (93.5)		54		32		18		34	
Cut and carry	157	116 (73.9)		112		32		40		67	
Anthelmintics			0.0001*		0.00001*		0.08		0.02		0.01*
Routine practice	55	28 (50.1)		27		11		8		17	
Not regular	164	146 (89)		139		53		50		84	
Total	219	174 (79.5)		166		64		58		101	

S: Strongyles., E: *Eimeria* spp., T: *Toxocara* spp.

*significantly different.

identity with *T. colubriformis* sequence (accession no. AB908960) from a ruminant fecal sample obtained from Lao PDR. The resulting five sequences were submitted to GenBank under accession number (PV069068-PV069072). Phylogenetic analyses were conducted to investigate closely related sequences (Fig. 3).

Haplotype networks

Herein, a total of 15 identical haplotypes were identified in this study. The sequences from this study belonged to haplotype 14 (H14), representing *T. colubriformis*, and haplotype 15 (H15), representing *H. contortus*. Briefly, H14 was grouped with sequences from Myanmar, Laos, New Zealand, Italy, Iran, Ireland, and Egypt. Similarly,

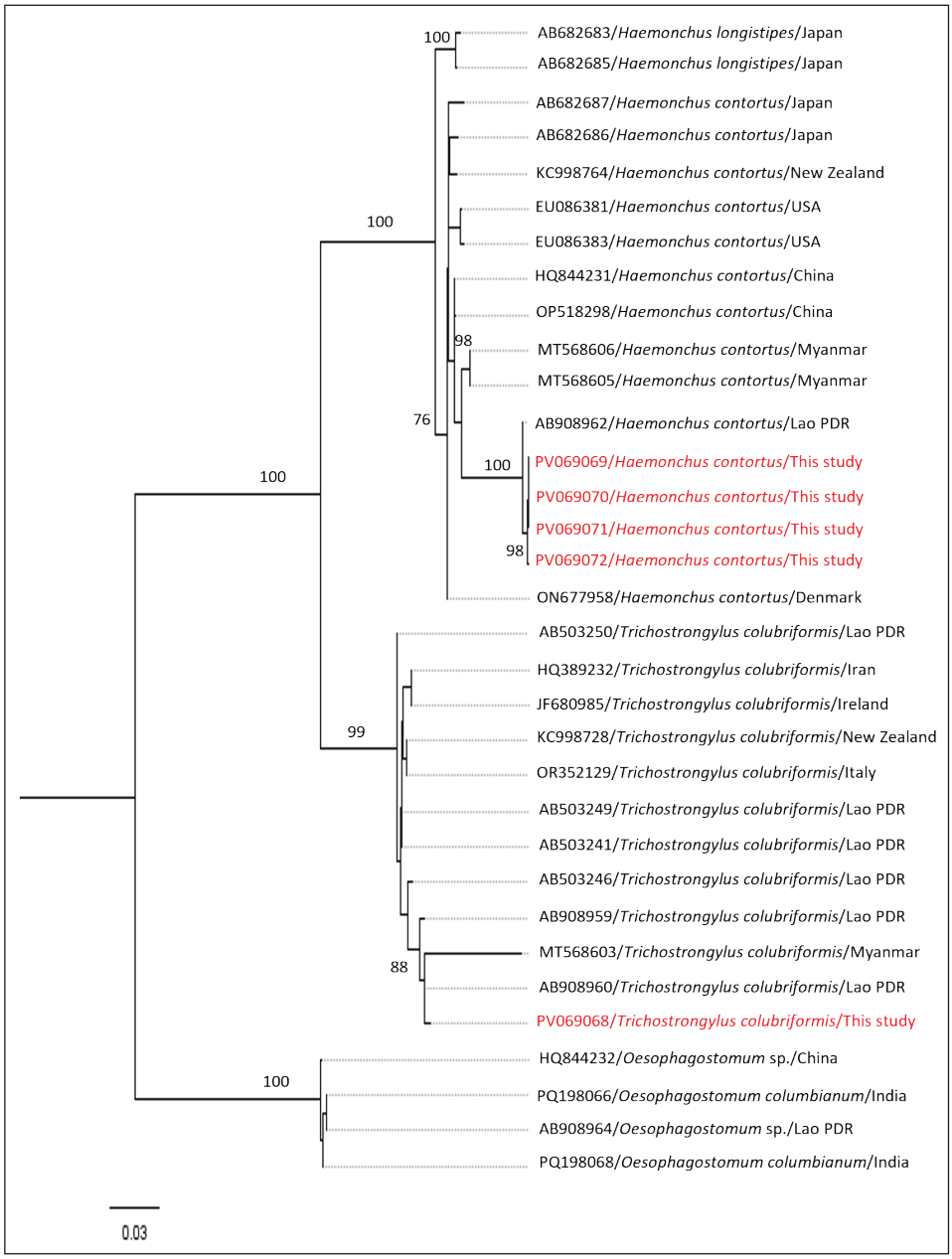

Fig. 3. A phylogenetic analysis was performed using five sequences from this study and 28 reference sequences retrieved from GenBank, including two *Oesophagostomum* species, two *Oesophagostomum columbianum*, 11 *T. colubriformis*, and 13 *H. contortus* sequences. The maximum likelihood method, based on the TPM2+F+G4 model, was applied with 1,000 bootstrap replicates in IQTree software. Branch lengths in the tree represent the number of substitutions per site. Sequences from this study are highlighted in red.

an identical H15 was clustered with *Haemonchus* spp. sequences from Egypt, Myanmar, China, Denmark, and the USA. Based on our analyses, no sequences from this study were related to *Oesophagostomum* species. Nucleotide variation was observed within each parasite group, particularly in *Haemonchus* spp. (Fig. 4).

Discussion

Understanding the dynamics of parasitism is essential for efficient preventive measures in managing GI parasites (Cable *et al.*, 2017). The relatively high prevalence rate (35.7%–86.9%) of GI parasitic infections in the livestock industry in Myanmar's neighboring countries highlighted the need for public awareness and a treatment regime plan (Huang *et al.*, 2014; Ahmed *et al.*, 2015; Das *et al.*, 2018; Income *et al.*, 2021). To date, nematodes have been investigated as the most dominant GI parasites all over the world compared to trematodes and coccidia infection (Charlier *et al.*, 2018). Although various GI parasites infect either livestock or farm animals, only strongyles, coccidia, flukes, and *Moniezia* spp. cause major GI problems, leading to chronic economic losses by reducing animal production rather than causing mortality (Jittapalapong *et al.*, 2011). From GI nematodes, strongyles infection had been previously shown as the most common (Jittapalapong *et al.*, 2011; Income *et al.*, 2021).

This study provides information about GI parasites in cattle farming areas in Ayeyarwaddy Division, Myanmar. The results revealed a high prevalence of GI parasites, with an overall rate of 79.5%. The different prevalence rates could be due to the presence or absence of some of the identified risk factors or the study design. For example, using more than one fecal sample from each individual, it is possible to improve diagnostic sensitivity, as single sampling for coprological techniques may result in an underestimation of the prevalence due to intermittent egg shedding of some parasites (Ferreira-Sá *et al.*, 2024). In addition, cross-sectional study design does not assess the intensity and persistence of infections over time (Møller *et al.*, 2003). In our study, the most abundant parasite stages were strongyle-type eggs 95.4% (166/174), followed by *Eimeria* spp. oocysts 36.8% (64/174) and *Toxocara* spp. eggs 33.3% (58/174). Co-infection of strongyles with either *Eimeria* spp. or *Toxocara* spp. was detected in 58% (101/174) of the cattle. The noticeable prevalence rate in the selected sampling division, which is situated near rivers, canals, and lakes, is consistent with previous findings showing that humidity and water sources play crucial roles in the parasite lifecycle (Jittapalapong *et al.*, 2011). The infective stages of *Toxocara* spp. are shed in feces and require several days to weeks in the environment to embryonate and become infective. Therefore, high humidity and moist environments promote egg survival and embryonation, facilitating transmission through the ingestion of contaminated material (Mizgajska, 2001). In *Eimeria*, sporulation of oocysts occurs to become the infective stage, and sporulation is highly dependent on environmental

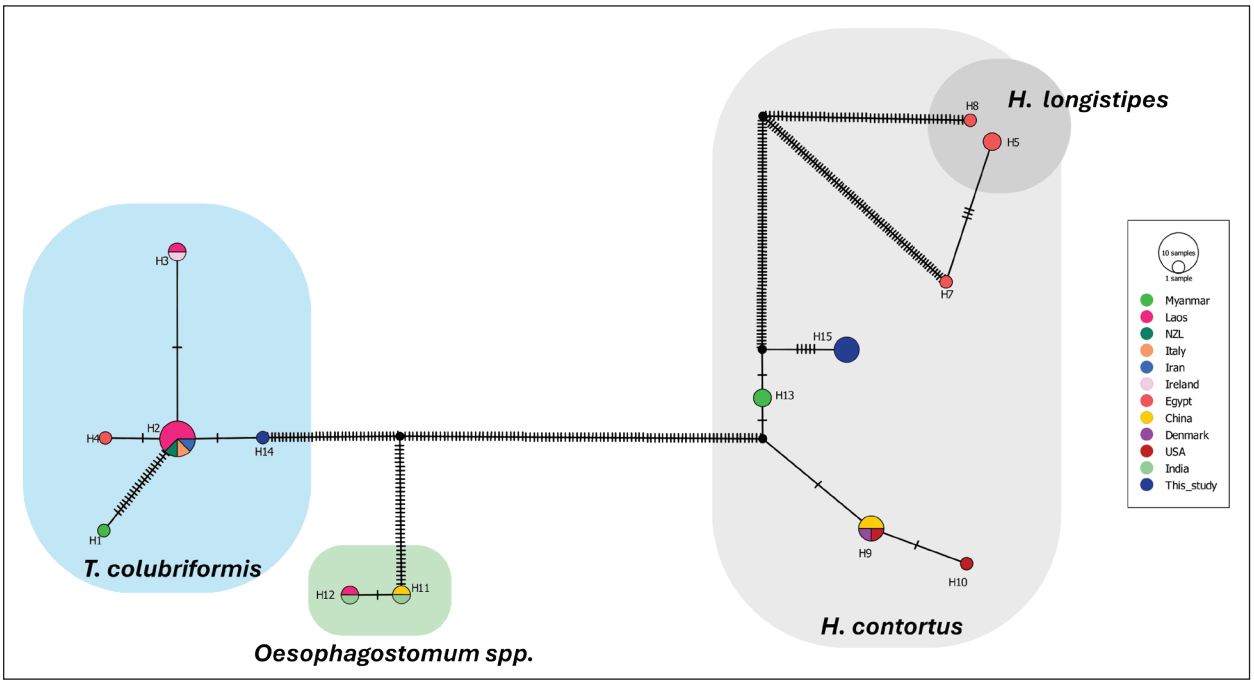

Fig. 4. Haplotype network (TCS network) of *T. colubriformis*, *Haemonchus* spp., and *Osesophagostomum* spp. sequences. The network illustrates the relationships among 15 identical haplotypes, with sequences from this study belonging to haplotype 14 (H14) for *T. colubriformis* and haplotype 15 (H15) for *H. contortus* (colored by dark blue).

conditions from which humid conditions favor the persistence and infectivity of oocysts (Sánchez *et al.*, 2008). In strongyle nematodes, warm and humid environments with adequate moisture enhance larval development and migration onto vegetation, increasing the likelihood of host ingestion (Stromberg, 1997). In the sampling area, the Ayeyarwaddy River served as the main water reservoir for this division. Therefore, this river acts as a natural source for spreading these parasitic diseases, as it is located near villages where eggs from reservoir hosts can be shed (Vanhove *et al.*, 2022). In this study, high GI parasitic infections, such as strongyles, *Eimeria* spp., and *Toxocara* spp. infection, might result from poor hygiene in housing pens, mixed crop-livestock systems, and contaminated environments, contributing to reinfection and high parasite burdens (Jittapalapong *et al.*, 2011). Without proper sanitation, parasites are likely to pose a significant threat in the study area. Traditionally, cattle farming practices were commonly observed nearby residential areas (15–40 m) from the farm owner's house; therefore, the distribution of infections appeared to be capable under poor hygienic behavior (Wangboon *et al.*, 2024). Although strongyles are known to be primarily parasitized herbivores, sporadic human cases have been documented globally (Sato *et al.*, 2010; Aung *et al.*, 2017). Therefore, a broader systematic investigation of strongylosis is necessary given that free-roaming practices can increase the risk of parasitic diseases in humans. Intensive group housing further increases the risk of transmission within herds. Coccidiosis, caused by *Eimeria* spp., is a global intestinal disease in livestock that can cause anemia, diarrhea, and electrolyte imbalances (Jittapalapong *et al.*, 2011). *Eimeria* species vary in pathogenicity, host specificity, and site of infection. Up to date, over 20 *Eimeria* spp. have been reported in cattle with most regarded as non-pathogenic or the animals have developed immunity after previous infection (Cornelissen *et al.*, 1995). However, *Eimeria bovis* and *Eimeria zuernii* are known to be highly pathogenic in cattle (Munyua and Ngotho, 1990). Therefore, further molecular or morphological identification is necessary to distinguish between *Eimeria* species and evaluate their respective pathogenic potential in the study population. In the present study, *Eimeria* spp. were detected mainly in crossbred females over 3 years of age, indicating ongoing exposure and possible subclinical infection. In addition, the lack of regular deworming may have contributed to the persistence of environmental oocysts. Since adult cattle can act as reservoirs, there is a need for continued monitoring and parasite control across all age groups. Environmental contamination of potentially infectious sources, such as contaminated pastures and water reservoirs, can facilitate oocyst transmission to young animals. Infection with *Eimeria* is considered a risk factor when animals experience stress, such as transportation or underfeeding, which can weaken the immune system and result in the proliferation of *Eimeria* in the intestine (Chartier and Paraud, 2012). *Toxocara* spp. infections in cattle are uncommon; however, the ingestion of embryonated *Toxocara* eggs from contaminated environments leads to larval migration within the tissues of livestock animals (Ziegler and Macpherson, 2019). Among *Toxocara* spp., *Toxocara vitulorum* is a pathogenic GI nematode that infects cattle and buffalo in tropical and subtropical regions, where calves raised in contaminated environments are at increased risk of infection. Heavy infections in young calves may cause intestinal obstruction and, in severe cases, death, making this parasite clinically and economically important (Rast *et al.*, 2013).

Regarding statistical analyses, GI infections appeared to be higher in older cattle, suggesting either prolonged exposure or different immune responses among the groups (Jittapalapong *et al.*, 2011; Sirbu *et al.*, 2020). Similar to our findings, a higher prevalence of GI parasitic infection in adult cattle has been reported by Income *et al.* (2021), while Raza *et al.* (2007) found younger cattle were more prone to intestinal helminth infections. The influence of sex on GI parasite infections in ruminants appears to be multifactorial and context-dependent. Although female ruminants may be more susceptible due to physiological stressors (Paul *et al.*, 2020), the behaviors and management practices of male ruminants can also increase the risk of GI infections (Mpofu *et al.*, 2020). However, no significant sex-related differences in GI parasitic infections have been reported (Income *et al.*, 2021). Similar to Sayeed *et al.* (2024), indigenous cattle were significantly more infected with GI parasites than crossbred cattle in the present study. This could be due to the grazing habitat of all indigenous cattle in small-scale farming systems due to the limited pasture area in Myanmar, whereas crossbred dairy cattle are kept in a semi-intensive grazing system, which reduces prolonged exposure to parasitic infection in grazing pasture. Supporting this fact, sharing grazing pasture has been reported as a potential risk of parasitic infection in ruminants (Chuenpreecha *et al.*, 2014). The lack of regular deworming practice was significantly associated with parasitic infection in the present study. GI parasitic infections were linked to farm management and deworming intervals. Most cattle in intensive farms followed a 6-month deworming schedule using either ivermectin, albendazole, or fenbendazole, a routine that was generally inadequate (Income *et al.*, 2021). These anthelmintics are ineffective against protozoa parasites such as *Eimeria* spp. (Foreyt, 2013). Therefore, lesser deworming intervals with suitable drug usage, along with farmer training, routine surveillance, and prompt treatment after proper diagnosis, are recommended to reduce parasite transmission.

In addition, the molecular identification of strongyles was conducted in five samples which showed single-

species (four with *H. contortus* and one with *T. colubriformis*) infection. Previously, *T. colubriformis* and *H. contortus* had been reported to be widely distributed in different parts of Lao PDR, Thailand, Indonesia, and Pakistan (Sato *et al.*, 2014; Purwati *et al.*, 2017; Income *et al.*, 2021; Ahmad *et al.*, 2024). Therefore, our study revealed common findings of dominant strongyle species similar to the above-mentioned studies. These two species are supposed to be widely distributed and probably the most dominant GI parasites in Myanmar. Consequently, the capabilities of the cattle on local transmission of these parasitic infections should be contemplated. *Haemonchus contortus* spp. pose a significant challenge to ruminant production because of their high egg production, with females producing thousands of eggs daily (Biffa *et al.*, 2006). *Trichostrongylus colubriformis* can cause villous atrophy, increased intestinal permeability, and protein loss, leading to diarrhea and reduced weight gain, which later result in poor feed conversion efficiency in infected animals (Greer *et al.*, 2009). Therefore, we highlight the significant role of cattle as reservoirs of GI parasites in Myanmar, but also, it should be taken into account that other zoonotic parasites could be co-infecting these animals, even when we have not identified them (probably because of the limitations of the diagnostic techniques employed, such as the low sensitivity of the fecal microscopy and the low number of samples analyzed by molecular methods). To sum up, the high prevalence of GI parasitic infection in cattle in Myanmar highlights the importance of continuous surveillance and effective control measures and the need for collaboration between the veterinary and public health sectors. Since a cross-sectional study in specific areas may not represent the intensity and persistence of the infection overtime, a further longitudinal approach would be beneficial to evaluate the infection dynamics more accurately.

Conclusion

Overall, our study provides updated knowledge on the most abundant GI parasitic infection in cattle in the Ayeyarwaddy Division, Myanmar. In this study, the only GI parasites identified were strongyles, *Eimeria* spp., and *Toxocara* spp., *H. contortus,* and *T. colubriformis* were identified through molecular detection, and phylogenetic analysis revealed their genetic relationship to previously reported sequences in neighboring countries. Our findings highlight the importance of continuous surveillance and the development of effective control strategies for GI parasites in livestock. The high prevalence of parasitic infections in cattle underscores the need for further investigations across different regions of Myanmar, particularly to address the gaps in diagnostic techniques and enhance the understanding of parasite dynamics. Collaboration between the veterinary and public health sectors is essential for improving control measures and mitigating the impact of these infections.

Acknowledgments

We appreciate the farm owners' permission to collect samples from their animals.

Conflict of interest

The authors declare that they have no conflicts of interest.

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Authors contributions

B.K.S. conceptualized the idea of the study and designed the experiments. B.K.S., K.S.H., and T.W.N. collected the samples. B.K.S., K.S.H., and W.M. underwent laboratory investigations. B.K.S., A.A., and A.H.L. analyzed the data. B.K.S. wrote the original manuscript. B.K.S., A.H.L., and A.A. revised the manuscript. All authors have read and approved the final version of the manuscript.

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