Original Article

Genetic diversity and morphotypes of *Haemonchus contortus* in sheep in Thailand: A combined morphological and molecular approach

Gunjan Das[1] Mohamed H. Hamad[2,3] Witchuta Junsiri[4,5] Piyanan Taweethavonsawat[4,5*]

Abstract

Haemonchus contortus is a highly pathogenic gastrointestinal nematode of small ruminants, yet molecular information on sheep-derived isolates in Thailand remains limited. This study aimed to characterize *H. contortus* recovered from sheep in Nakhon Pathom Province using integrated morphological and molecular approaches. Adult nematodes collected post-mortem from the abomasum were examined morphologically, and the internal transcribed spacer 2 (ITS2) region of ribosomal DNA was amplified and sequenced. Morphological examination identified males with characteristic copulatory bursae and females exhibiting linguiform, knobbed, and simple vulvar morphotypes. ITS2 sequences showed 95.26–98.11% identity with reference *H. contortus* sequences deposited in GenBank. Molecular and phylogenetic analyses supported the identification of the examined sheep-derived isolates as *H. contortus*. These findings provide baseline morphological and ITS2 sequence data for *H. contortus* in sheep from Nakhon Pathom Province. Broader sampling across farms and geographical regions, together with additional mitochondrial and nuclear markers, would help clarify genetic diversity and population structure in Thai sheep.

Keywords: *Haemonchus contortus*, ITS2, morphological identification, phylogenetic analysis, sheep, Thailand

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Introduction

Haemonchus contortus is one of the most pathogenic gastrointestinal nematodes of sheep and represents an important constraint to small-ruminant production, particularly in tropical and subtropical regions where warm and humid environmental conditions favor the development and transmission of infective larvae (Gasser and Newton, 2000; Hildreth and Harmon, 2013). As a highly hematophagous parasite inhabiting the abomasum, *H. contortus* can cause anemia, hypoproteinemia, weight loss, reduced productivity, and, in severe infections, death (Gasser *et al.,* 2008). Effective management of haemonchosis therefore requires accurate identification and characterization of the parasite populations circulating in susceptible small-ruminant hosts.

Sheep warrant specific investigation because parasite populations recovered from different ruminant hosts may exhibit morphological and genetic variation associated with host-related and geographical factors. Previous studies have demonstrated variation in *H. contortus* populations recovered from sheep and goats in different geographical regions, suggesting that host species, local transmission patterns, and environmental conditions may contribute to parasite population structure (Gharamah *et al.,* 2012; Yin *et al.,* 2013). Morphological variation, particularly polymorphism of the female vulvar flap, has also been documented among *H. contortus* populations from sheep (Rahman and Abd Hamid, 2007).

Molecular characterization provides an important complement to conventional morphological identification of *Haemonchus*. The second internal transcribed spacer (ITS2) of ribosomal DNA is widely used for species identification and phylogenetic characterization because it provides useful interspecific variation while generally showing relatively high intraspecific conservation (Gasser *et al.,* 1998; Heise *et al.,* 1999). Importantly, ITS2 is used in the present study as a taxonomic and phylogenetic marker rather than as a marker of anthelmintic resistance. Although anthelmintic resistance represents an important challenge in the control of *H. contortus*, evaluation of resistance-associated genetic markers is beyond the scope of the present investigation.

In Thailand, *H. contortus* has been reported in small ruminants from several regions (Mangkit *et al.,* 2014; Laosutthipong and Eardmusic, 2019; Vongnady *et al.,* 2020; Pitaksakulrat *et al.,* 2021). However, molecular investigations have predominantly focused on goat-derived populations, including studies of genetic diversity and population structure (Pitaksakulrat *et al.,* 2021). Consequently, information on the morphological characteristics and ITS2-based genetic relationships of *H. contortus* recovered from Thai sheep remains limited. Characterizing *H. contortus* from Thai sheep can strengthen species identification and provide baseline molecular data for future epidemiological studies. Accordingly, the present study aimed to identify and characterize *H. contortus* recovered from sheep in Thailand through integrated morphological examination and ITS2-based molecular analysis, and to assess the genetic diversity and phylogenetic relationships among the sheep-derived isolates.

Materials and Methods

Study area, animal host and parasite collection: Adult worms were collected post-mortem from the abomasum of adult native sheep obtained from a farm in Nakhon Pathom Province and transported to the Faculty of Veterinary Science, Chulalongkorn University (Fig. 1). The animals showed clinical signs including poor body condition, emaciation, and rough or thinning hair coats. Abomasa were processed following the method described by Soulsby (1982). Each abomasum was opened, and the contents were sieved and thoroughly rinsed with tap water. Adult nematodes were carefully isolated and placed in sterile Petri dishes containing 0.85% normal saline. For further analysis, the worms were washed three times with physiological saline, fixed in 70% ethanol, and stored at 4°C.

Morphological study: Individual adult *Haemonchus* spp. worms were randomly selected from infected hosts for morphological examination. Identification was conducted following the criteria described by Soulsby (1982). Adult males were identified by the presence of a copulatory bursa with two lateral lobes and visible spicules. Female worms were categorized based on vulvar morphology, displaying either a linguiform (flapped) or knobbed vulvar structure. A third group, designated as "simple" forms, exhibited clearly distinguishable sex-specific morphological features (Figs. 2A–2D). All specimens were thoroughly washed in phosphate-buffered saline (PBS), preserved in 70% ethanol, and stored in individual tubes at 4 °C until further use for DNA extraction.

DNA extraction and PCR amplification of the Its2 regions: Following morphological identification, adult nematodes stored at 4 °C were washed with 200 µL of ultrapure water (PURELAB® Ultra, ELGA LabWater/VWS Ltd., Marlow, UK) and subsequently minced into small fragments. Genomic DNA was extracted from individual worms, including females with vaginal flaps or nodules, females containing egg-filled uteri, males with copulatory bursae, and morphologically simple forms, using the NucleoSpin® Tissue DNA extraction kit (MACHEREY-NAGEL, Germany), according to the manufacturer's protocol. Extracted DNA was stored at −20 °C until further use.

DNA purity and concentration were assessed using a NanoDrop™ Lite spectrophotometer (Thermo Scientific™, USA) by evaluating absorbance ratios at 260/280 and 260/230 nm. The ITS2 region of *H. contortus* was amplified using the primers NC1F (5′-ACGTCTGGTTCAGGGTTGTT-3′) and NC1R (5′-TTAGTTTCTTTTCCTCCGCT-3′), targeting an expected amplicon of approximately 300 bp (Gasser *et al.,* 1993). Each 25 µL PCR reaction contained 50 ng of DNA template, 0.2 µM of each primer, 1× GoTaq® Green Master Mix (Promega, USA), and nuclease-free water. Reactions were carried out in a thermal cycler (BIOER Technology, China). PCR amplification was performed with an initial denaturation at 95°C for 7

mins, followed by 40 cycles of denaturation at 95°C for 45 sec, annealing at 50°C for 45 sec, and extension at 72°C for 45 sec. A final extension was performed at 72°C for 10 mins.

PCR products were visualized by electrophoresis on 1% agarose gels stained with RedSafe™ Nucleic Acid Staining Solution (INtRON Biotechnology, Korea). Genomic DNA extracted from a previously confirmed *H. contortus* specimen was used as a positive control, while a no-template control containing nuclease-free water instead of DNA was included to monitor contamination. A 100 bp DNA ladder (SibEnzyme®, Russia) was used as a molecular size marker.



Figure 1 Geographical origin of *Haemonchus contortus* recovered from infected sheep in Thailand.

DNA purification and sequencing: Final PCR products were separated on a 1.5% agarose gel prepared in 1× TAE buffer and visualized under UV illumination. Bands corresponding to the expected fragment size were excised and purified using the NucleoSpin® Gel and PCR Clean-up Kit (MACHEREY-NAGEL, Germany) following the manufacturer's protocol. Purified DNA was eluted in nuclease-free water and quantified using either a spectrophotometer or fluorometer to ensure sufficient concentration for sequencing.

Sequencing was performed by a commercial provider (Celemics, Korea) using the Sanger method, which employs fluorescently labeled dideoxynucleotides and capillary electrophoresis. Resulting chromatograms were analyzed using bioinformatics tools to verify sequence quality and confirm the identity of the amplified ITS2 region.

Bioinformatics analysis and constructing phylogenetic tree: The ITS2 sequences were analyzed using the NCBI BLASTN tool (https://www.ncbi.nlm.nih.gov/BLAST/) to identify homologous sequences and assess their similarity. The resulting sequences were submitted to the GenBank database under the accession numbers OR690623, OR690625, OR690624, and OR690626 (sheep isolates), corresponding to the ITS2 gene region. Additional sequence details are provided in Supplementary File S1.

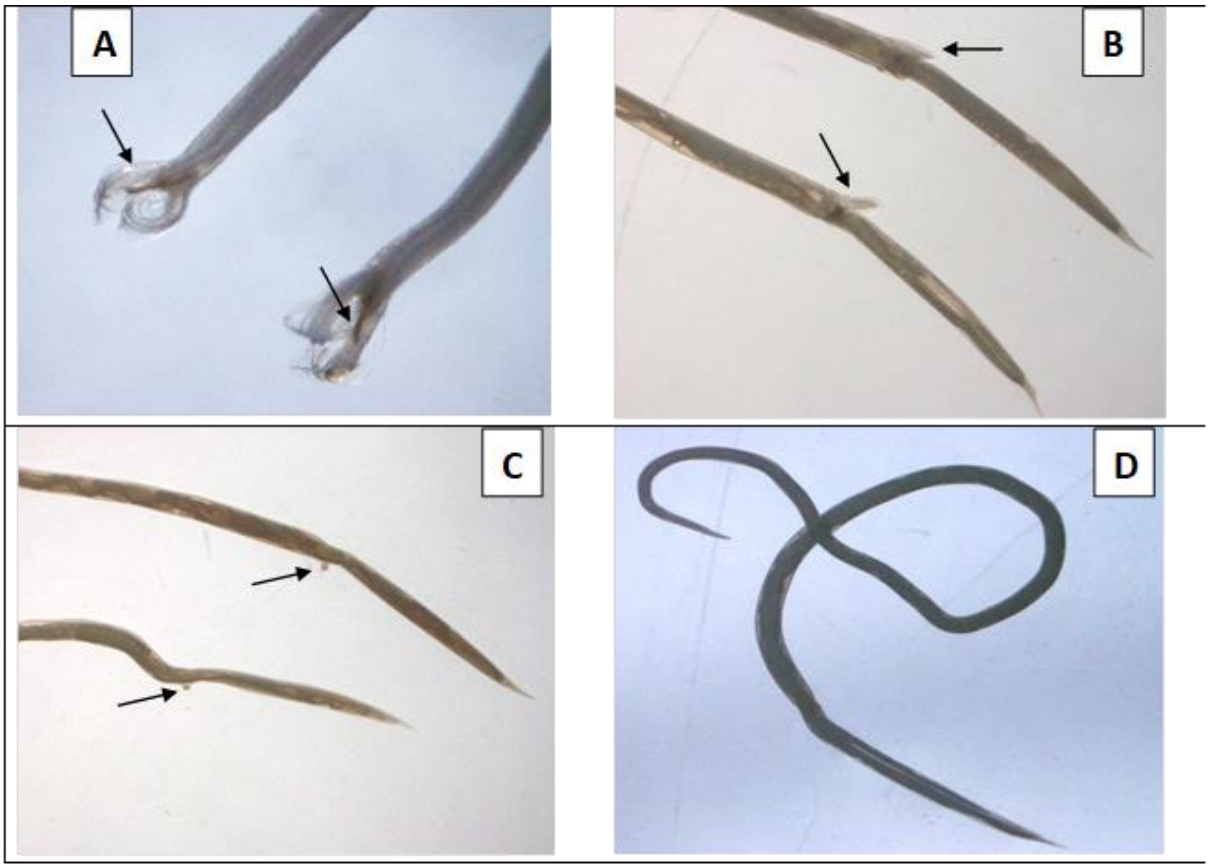


Figure 2 Morphological and microscopic features of *Haemonchus* spp. isolated from the abomasum of sheep, observed under a light microscope. (A) Male specimen showing a copulatory bursa with two distinct lateral lobes (arrow). (B) Female *H. contortus* displaying a linguiform vulva flap, indicating vulva polymorphism (arrow). (C) Female *Haemonchus* spp. with a reduced, knob-like vulva flap (arrow). (D) Female *Haemonchus* spp. with simple vulva.

For phylogenetic reconstruction, homologous ITS2 sequences were retrieved from GenBank based on BLASTN results. Sequences lacking essential metadata (e.g., host or geographic information) or those that were incomplete were excluded, following the methodology outlined by Islam *et al.* (2024). Multiple sequence alignment was carried out using the MAFFT algorithm (Katoh *et al.*, 2002) via NGphylogeny.fr (Lemoine *et al.*, 2019).

The best-fitting nucleotide substitution model was selected using jModelTest v2.1.7 (Posada, 2008). Phylogenetic reconstruction was performed using the maximum-likelihood (ML) method under the general time-reversible model with gamma-distributed rate variation among sites and a proportion of invariant sites (GTR+G+I) (Newman *et al.*, 2016). Branch support was assessed using 1,000 bootstrap replicates. The resulting tree was visualized using the Interactive Tree of Life (iTOL) web platform (https://itol.embl.de/). Phylogenetic relationships were examined to assess the placement of the sheep-derived *H. contortus* isolates relative to reference sequences retrieved from GenBank.

Results

***Morphological structure of the recovered Haemonchus* spp.:** The collected worms were examined both macroscopically and microscopically for morphological characterization. A total of 75 male and 125 female specimens were recovered. In this study, adult *Haemonchus* spp. were predominantly located in the fundus region of the abomasum in infected sheep. Macroscopically, the worms appeared cylindrical and reddish in color, a feature consistent with their hematophagous (blood-feeding) nature. Morphometric analysis revealed that males measured between 12–20 mm in length and 0.3–0.4 mm in width, while females ranged from 16–30 mm in length with a similar width.

***Microscopic appearance of the identified Haemonchus* spp.:** The morphological features of *Haemonchus* nematodes were examined using light microscopy. Male specimens exhibited a well-developed copulatory bursa with two lateral lobes and a single dorsal lobe positioned asymmetrically adjacent to the left lateral lobe (Fig. 2A). In females, the vulva was located 4-6 mm from the posterior end, and three vulvar morphotypes were identified: linguiform, knobbed, and simple. Female specimens were classified into three vulvar morphotypes: linguiform, knobbed, and simple. The linguiform morphotype exhibited a prominent, tongue-like vulvar flap (Fig. 2B), whereas the knobbed morphotype had a reduced, knob-like vulvar process (Fig. 2C). The knobbed morphotype was the most prevalent, accounting for 90 of the 125 females examined (72.0%). The simple morphotype lacked a prominent vulvar process (Fig. 2D).

***PCR amplification of the ITS2 regions*:** The agarose gel electrophoresis results confirmed successful PCR amplification of the ITS-2 gene from *H. contortus* isolates collected in Thailand. Lanes L1–L5 exhibited distinct, single bands at approximately 300 bp, the expected product size, indicating successful amplification (Fig. 3). The absence of non-specific bands reflects the high specificity and efficiency of the primers used, supporting the reliability of these PCR products for subsequent genetic analyses.

***Nucleotide sequence analysis of Its-2 and phylogenetic tree analysis*:** The ITS2 sequences obtained from sheep were analyzed using the NCBI BLASTN program to identify homologous sequences and assess sequence similarity. The BLAST results revealed high sequence identity (ranging from 95.255% to 98.113%) with previously deposited sequences in the GenBank database, indicating strong homology with known ITS2 regions of related species. Detailed alignment statistics, including query coverage, E-values, and percent identity, are provided in Supplementary File S1. Furthermore, the ITS-2 sequences were aligned using MAFFT, as shown in the multiple sequence alignment (Fig. 4). The first four sequences represent our samples, which display high similarity across the alignment region.

Phylogenetic analysis was conducted to elucidate the evolutionary relationships among the ITS2 sequences (Fig. 5). Bootstrap analysis with 1,000 replicates was performed to assess the robustness of the tree topology. The phylogenetic tree revealed a clear clustering of sequences into distinct groups corresponding to their host species (sheep) and geographic origin (Thailand). Additionally, the tree demonstrated close evolutionary ties between the analyzed sequences and reference sequences of *H. contortus* from GenBank, further confirming their taxonomic classification. The results of the sequence analysis and phylogenetic reconstruction provide valuable insights into the genetic diversity and evolutionary relationships of the ITS2 region in the studied populations. The high sequence similarity and well-resolved phylogenetic clades underscore the utility of the ITS2 region as a reliable genetic marker for species identification and phylogenetic studies in this context.

Discussion

Sheep are susceptible to various internal parasites, among which *Haemonchus* spp. are considered some of the most prevalent and pathogenic, affecting goats, sheep, and cattle worldwide (Bishop and Morris 2007; Craig 2009). Multiple studies have demonstrated that sheep and goats are more vulnerable to *Haemonchus* infections compared to cattle (Craig 2009). These hematophagous parasites can cause severe anemia, hypoproteinemia, intermandibular edema, and even death, leading to substantial economic losses in small ruminant production systems. The presence of *H. contortus* poses a major challenge for farmers, significantly limiting the profitability of small ruminant farming, particularly in resource-limited settings (Pal *et al.,* 2014). The present study is the first to combine classical morphological identification with molecular characterization to confirm the presence and genetic identity of *Haemonchus* spp. isolated from the abomasum of sheep in Thailand.

In this study, the adult worms appeared bright red upon gross examination, consistent with their hematophagous nature. Morphometric measurements revealed that males ranged from 12–20 mm in length and 0.3–0.4 mm in width, while females measured 16–30 mm in length with similar width. Morphologically simple forms were comparable in size to females. The knobbed vulvar morphotype predominated among the examined female specimens (72.0%; 90/125), consistent with Das *et al.* (2023), who reported a predominance of the knobbed/button morphotype (76.6%) in *H. contortus* collected from sheep and goats in south Gujarat, India. Microscopic examination further revealed distinct morphological traits. Male *Haemonchus* spp. exhibited a well-developed bursa with two lateral lobes and a single dorsal lobe positioned asymmetrically against the left lateral lobe (Fig. 2A). In females, the vulva was located 4–6 mm from the posterior end and covered by a prominent, thumb-shaped linguiform vulvar flap (Fig. 2B). A subset of specimens displayed a reduced knob-like vulva (Fig. 2C). Additionally, a third category, termed "simple," exhibited female morphological characteristics (Fig. 2D).

These observations are in agreement with previous studies that described the morphological features of *H. contortus* in sheep (Soulsby 1982) (Manfredi *et al.,* 2010). In this study, the knobbed vulvar was the most commonly observed morphotype, aligning with findings from Badawy *et al.* (2015) in both sheep and goats in Egypt. However, other researchers, including Rahman and Abd Hamid (2007) and Gharamah *et al.* (2012) in Malaysia, as well as Abdel-Hafez *et al.* (2013) in Egypt, have reported the predominance of the linguiform vulva flap. Vulva flap polymorphism in female *H. contortus* is of notable taxonomic value and is considered a phenotypic marker for adaptive variation and population diversity.

ITS2 sequence analysis supported the molecular identification of *H. contortus* recovered from sheep in Nakhon Pathom Province and provided information on their relationships with reference sequences. The sheep-derived ITS2 sequences showed 95.26–98.11% identity with reference *H. contortus* sequences in GenBank. These comparisons should be distinguished from genetic variation among the examined isolates and do not establish genetic homogeneity across the regional parasite population.

The phylogenetic placement of the sheep-derived isolates should be interpreted within the limited resolution of a single ribosomal marker. Broader sampling across farms and geographical regions, together with additional mitochondrial and nuclear markers, would help characterize genetic diversity and investigate population structure.

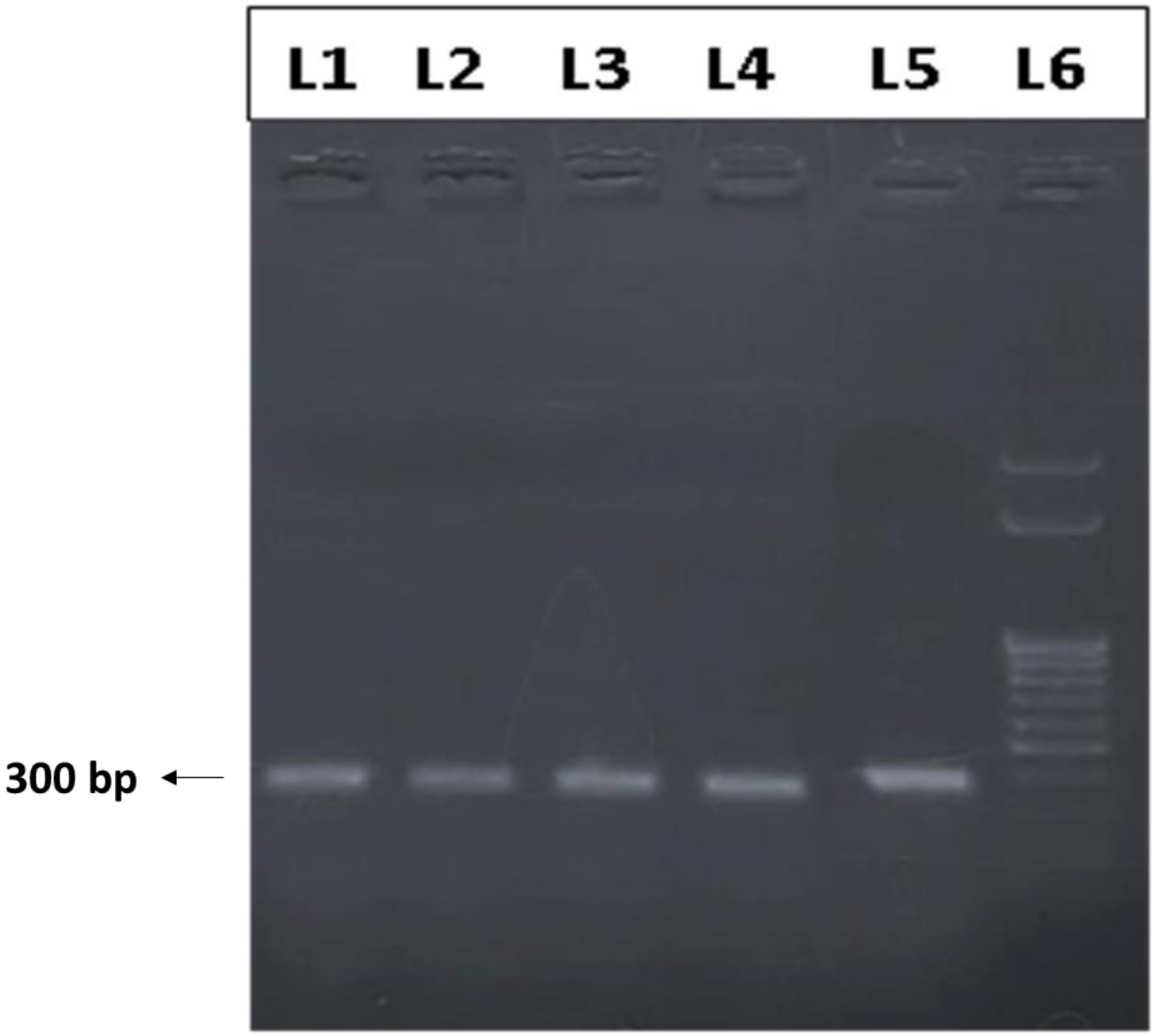


Figure 3 PCR amplification of ITS-2 of 300 bp (Lane 1- Male, Lane 2-Female with Flap, Lane 3- Female with Knob, Lane 4- Simple) genotype sequence of Thailand isolates of *H. contortus*, L5 - +Ve Control and L6-100 bp Ladder.

While this study provides valuable insights into the morphological and genetic characteristics of *H. contortus* in sheep from Thailand, several limitations should be acknowledged. Firstly, the sample size was relatively small and derived from a single geographical location (Nakhon Pathom Province), which may not fully represent the genetic diversity of *H. contortus* populations across Thailand. Secondly, the ITS2 analyses provide information on species identity and genetic relationships among the examined isolates but do not indicate their susceptibility to anthelmintic drugs. Because neither treatment efficacy nor resistance-associated genetic markers were investigated, the anthelmintic resistance status of these isolates remains undetermined. Future studies incorporating fecal egg count reduction testing and validated, drug-specific resistance markers would be required to address this question. Lastly, while ITS2 is a reliable marker for species-level identification, the inclusion of additional genetic markers (e.g., mitochondrial genes) could provide deeper insights into population structure and evolutionary dynamics. Future studies should include sheep from multiple farms and geographical regions and incorporate additional mitochondrial and nuclear markers to better characterize parasite genetic diversity and population structure.

In conclusion, this study confirmed the presence of *Haemonchus contortus* in sheep from Nakhon Pathom Province, Thailand, using integrated morphological examination and ITS2-based molecular identification. Morphological examination documented linguiform, knobbed, and simple female vulvar morphotypes, while molecular analysis provided baseline sequence information for sheep-derived isolates. These findings support species identification and provide a foundation for further investigations of *H. contortus* in Thai sheep. However, sampling from a single locality and reliance on ITS2 limit conclusions about broader genetic diversity and population structure. Future studies should include sheep from multiple farms and geographical regions and incorporate additional mitochondrial and nuclear markers.

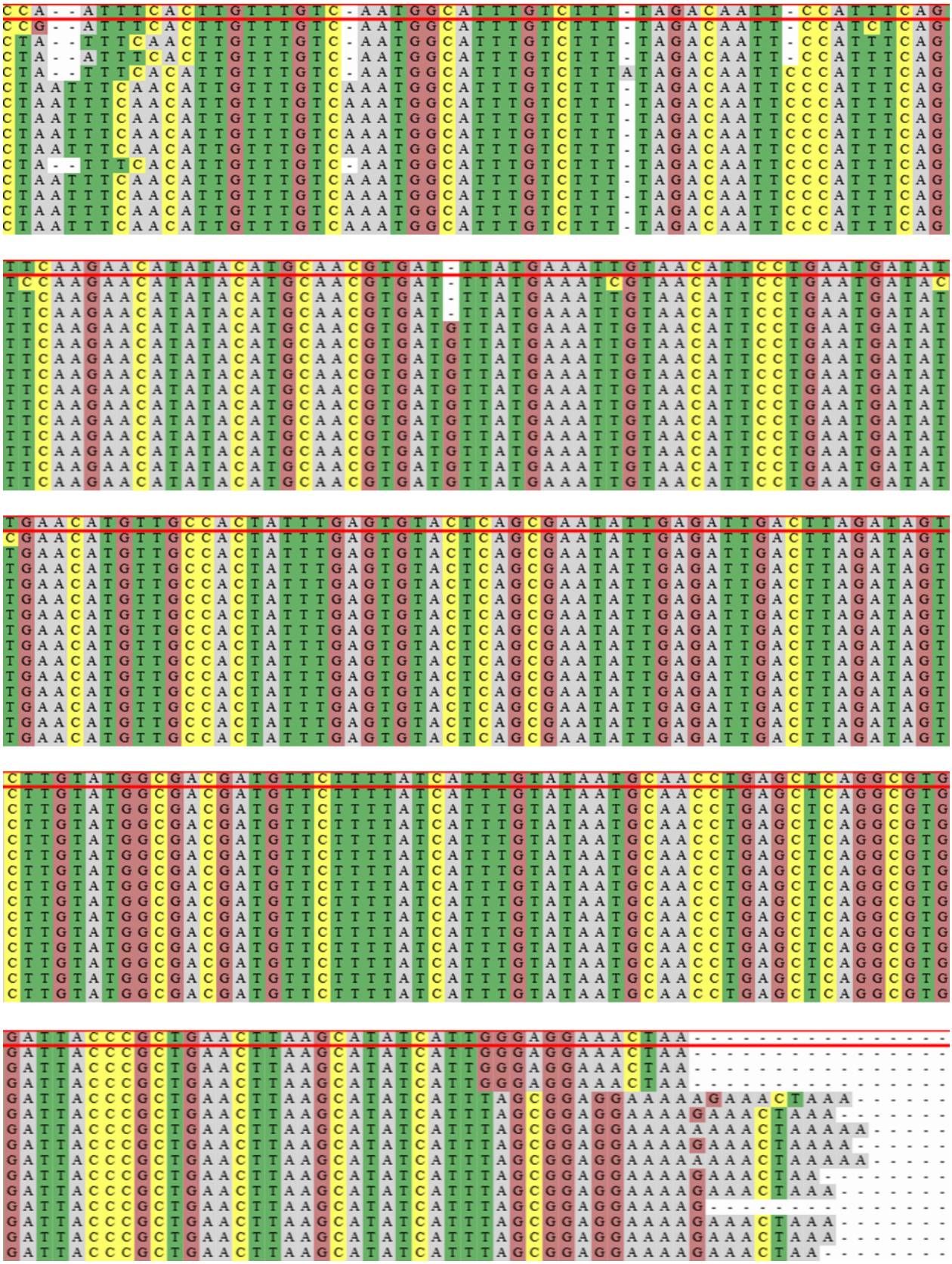


Figure 4 Multiple sequence alignment of ITS-2 gene sequences from *Haemonchus contortus* isolates obtained from sheep using MAFFT. The first four sequences represent field samples, aligned with reference sequences retrieved from NCBI. Conserved regions are highlighted in color.

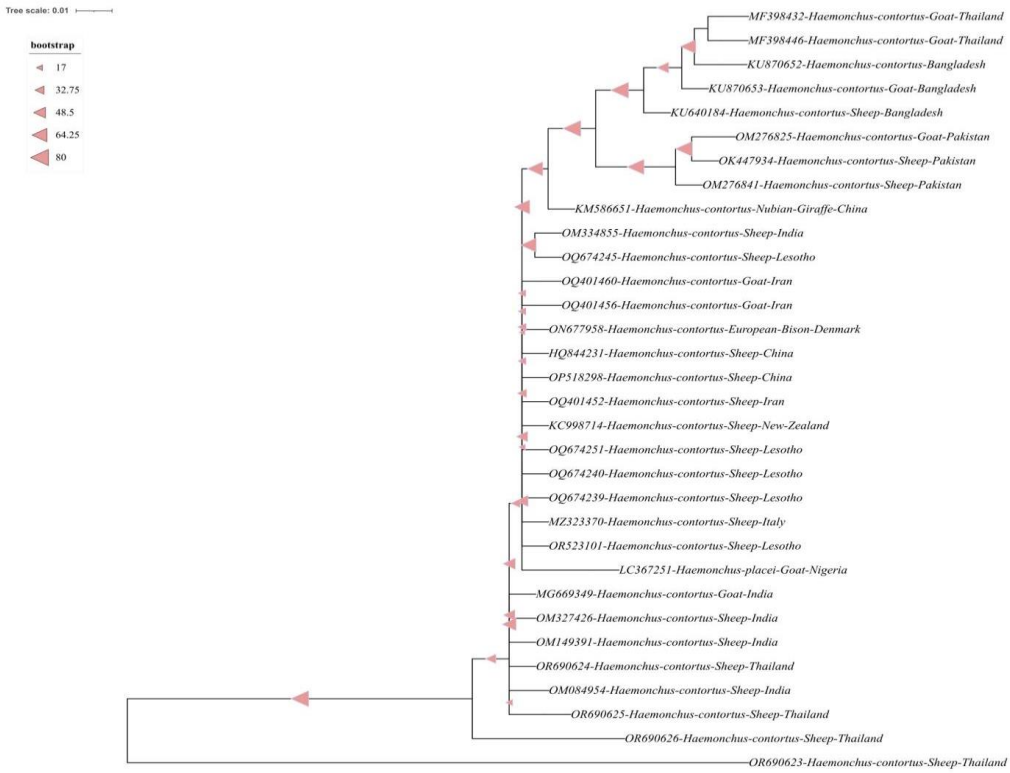


Figure 5 Maximum likelihood phylogenetic tree based on ITS2 sequences of sheep-derived *Haemonchus contortus* isolates and reference sequences retrieved from GenBank. The tree was inferred using the general time-reversible model with gamma-distributed rate variation and a proportion of invariant sites (GTR+G+I). Node support was assessed using 1,000 bootstrap replicates. The scale bar indicates nucleotide substitutions per site.

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***Competing interest statement*:** The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Statement of author contributions: **Gunjan Das:** Conceptualization, Data curation, Formal analysis, Investigation, Writing – original draft. **Mohamed H. Hamad:** Data curation, Formal analysis. **Witchuta Junsiri:** Data curation, Formal analysis. **Piyanan Taweethavonsawat:** Conceptualization, Supervision, Funding acquisition, Writing – original draft, Writing – review & editing. All authors contributed to manuscript revision, read, and approved the submitted version.

Declaration of artificial intelligence use: During the preparation of this manuscript, the authors used ChatGPT to proofread selected sentences. The authors reviewed and edited the output and take full responsibility for the final content.

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Supplement File S1

OR690606	KU870652.1	97.101	276	1	6	3	271	9	284	1.22E-124	459
OR690606	OQ674239.1	96.763	278	1	7	2	271	39	316	4.39E-124	457
OR690606	MG669349.1	96.763	278	1	7	2	271	36	313	4.39E-124	457
OR690606	OQ674251.1	96.763	278	1	7	2	271	40	317	4.39E-124	457
OR690606	OM149391.1	96.763	278	1	7	2	271	36	313	4.39E-124	457
OR690606	OP518298.1	96.763	278	1	7	2	271	599	876	4.39E-124	457
OR690606	MF398446.1	97.091	275	1	6	3	271	8	281	4.39E-124	457
OR690606	KC998714.1	96.763	278	1	7	2	271	167	444	4.39E-124	457
OR690606	MZ323370.1	96.763	278	1	7	2	271	15	292	4.39E-124	457
OR690606	OQ674240.1	96.763	278	1	7	2	271	37	314	4.39E-124	457
OR690606	KM586651.1	96.763	278	1	7	2	271	64	341	4.39E-124	457
OR690606	KU870653.1	97.091	275	1	6	3	271	7	280	4.39E-124	457
OR690606	HQ844231.1	96.763	278	1	7	2	271	599	876	4.39E-124	457
OR690606	OQ401452.1	96.763	278	1	7	2	271	35	312	4.39E-124	457
OR690606	OM327426.1	96.763	278	1	7	2	271	36	313	4.39E-124	457
OR690606	MF398432.1	96.751	277	1	7	2	271	6	281	1.58E-123	455
OR690606	OR523101.1	96.751	277	1	7	2	270	26	302	1.58E-123	455
OR690606	ON677958.1	96.403	278	2	7	2	271	643	920	5.68E-123	453
OR690606	OM276841.1	97.398	269	1	5	9	271	6	274	5.68E-123	453
OR690606	KU640184.1	96.739	276	1	7	3	271	9	283	5.68E-123	453
OR690606	OM084954.1	96.403	278	2	7	2	271	36	313	2.04E-122	451
OR690606	OQ401460.1	96.403	278	2	7	2	271	35	312	2.04E-122	451
OR690606	OQ401456.1	96.403	278	2	7	2	271	35	312	2.04E-122	451
OR690606	OM334855.1	96.403	278	2	7	2	271	36	313	2.04E-122	451
OR690606	OQ674245.1	96.403	278	2	7	2	271	39	316	2.04E-122	451
OR690606	OM276825.1	97.736	265	0	5	13	271	1	265	2.04E-122	451
OR690606	OK447934.1	97.388	268	1	5	10	271	1	268	2.04E-122	451
OR690608	KU870652.1	95.255	274	6	6	5	271	11	284	3.44E-115	427
OR690608	OQ674239.1	95.539	269	4	7	11	271	48	316	4.45E-114	424
OR690608	MG669349.1	95.539	269	4	7	11	271	45	313	4.45E-114	424
OR690608	OQ674251.1	95.539	269	4	7	11	271	49	317	4.45E-114	424
OR690608	OM149391.1	95.539	269	4	7	11	271	45	313	4.45E-114	424
OR690608	OP518298.1	95.539	269	4	7	11	271	608	876	4.45E-114	424
OR690608	MF398446.1	96.255	267	4	5	11	271	15	281	7.40E-117	433
OR690608	KC998714.1	95.539	269	4	7	11	271	176	444	4.45E-114	424
OR690608	MZ323370.1	95.539	269	4	7	11	271	24	292	4.45E-114	424
OR690608	OQ674240.1	95.539	269	4	7	11	271	46	314	4.45E-114	424
OR690608	KM586651.1	95.539	269	4	7	11	271	73	341	4.45E-114	424
OR690608	KU870653.1	96.255	267	4	5	11	271	14	280	7.40E-117	433
OR690608	HQ844231.1	95.539	269	4	7	11	271	608	876	4.45E-114	424
OR690608	OQ401452.1	95.539	269	4	7	11	271	44	312	4.45E-114	424
OR690608	OM327426.1	95.539	269	4	7	11	271	45	313	4.45E-114	424
OR690608	MF398432.1	95.896	268	4	6	11	271	14	281	3.44E-115	427
OR690608	OM276841.1	96.226	265	4	5	13	271	10	274	9.58E-116	429
OR690608	KU640184.1	95.896	268	4	6	11	271	16	283	3.44E-115	427
OR690608	OM084954.1	95.539	269	4	7	11	271	45	313	4.45E-114	424
OR690608	OM334855.1	95.539	269	4	7	11	271	45	313	4.45E-114	424
OR690608	OQ674245.1	95.539	269	4	7	11	271	48	316	4.45E-114	424
OR690608	OM276825.1	96.226	265	4	5	13	271	1	265	9.58E-116	429
OR690608	OK447934.1	96.226	265	4	5	13	271	4	268	9.58E-116	429
OR690605	OQ674239.1	97.122	278	0	7	2	271	39	316	9.44E-126	462
OR690605	MG669349.1	97.122	278	0	7	2	271	36	313	9.44E-126	462
OR690605	OQ674251.1	97.122	278	0	7	2	271	40	317	9.44E-126	462
OR690605	OM149391.1	97.122	278	0	7	2	271	36	313	9.44E-126	462
OR690605	OP518298.1	97.122	278	0	7	2	271	599	876	9.44E-126	462
OR690605	MF398446.1	97.445	274	2	4	3	271	8	281	9.44E-126	462
OR690605	KC998714.1	97.122	278	0	7	2	271	167	444	9.44E-126	462
OR690605	MZ323370.1	97.122	278	0	7	2	271	15	292	9.44E-126	462
OR690605	OQ674240.1	97.122	278	0	7	2	271	37	314	9.44E-126	462
OR690605	KM586651.1	97.122	278	0	7	2	271	64	341	9.44E-126	462
OR690605	KU870653.1	97.445	274	2	4	3	271	7	280	9.44E-126	462
OR690605	HQ844231.1	97.122	278	0	7	2	271	599	876	9.44E-126	462
OR690605	OQ401452.1	97.122	278	0	7	2	271	35	312	9.44E-126	462

OR690605	OM327426.1	97.122	278	0	7	2	271	36	313	9.44E-126	462
OR690605	MF398432.1	97.112	277	2	5	1	271	5	281	9.44E-126	462
OR690605	OR523101.1	97.112	277	0	7	2	270	26	302	3.40E-125	460
OR690605	ON677958.1	96.763	278	1	7	2	271	643	920	1.22E-124	459
OR690605	KU640184.1	97.091	275	2	5	3	271	9	283	1.22E-124	459
OR690605	OM084954.1	96.763	278	1	7	2	271	36	313	4.39E-124	457
OR690605	OQ401460.1	96.763	278	1	7	2	271	35	312	4.39E-124	457
OR690605	OQ401456.1	96.763	278	1	7	2	271	35	312	4.39E-124	457
OR690605	OM334855.1	96.763	278	1	7	2	271	36	313	4.39E-124	457
OR690605	OQ674245.1	96.763	278	1	7	2	271	39	316	4.39E-124	457
OR690605	OM276825.1	98.113	265	0	4	12	271	1	265	4.39E-124	457
OR690607	OQ674239.1	97.122	278	0	7	2	271	39	316	9.44E-126	462
OR690607	MG669349.1	97.122	278	0	7	2	271	36	313	9.44E-126	462
OR690607	OQ674251.1	97.122	278	0	7	2	271	40	317	9.44E-126	462
OR690607	OM149391.1	97.122	278	0	7	2	271	36	313	9.44E-126	462
OR690607	OP518298.1	97.122	278	0	7	2	271	599	876	9.44E-126	462
OR690607	MF398446.1	97.455	275	0	6	3	271	8	281	9.44E-126	462
OR690607	KC998714.1	97.122	278	0	7	2	271	167	444	9.44E-126	462
OR690607	MZ323370.1	97.122	278	0	7	2	271	15	292	9.44E-126	462
OR690607	OQ674240.1	97.122	278	0	7	2	271	37	314	9.44E-126	462
OR690607	KM586651.1	97.122	278	0	7	2	271	64	341	9.44E-126	462
OR690607	KU870653.1	97.455	275	0	6	3	271	7	280	9.44E-126	462
OR690607	HQ844231.1	97.122	278	0	7	2	271	599	876	9.44E-126	462
OR690607	OQ401452.1	97.122	278	0	7	2	271	35	312	9.44E-126	462
OR690607	OM327426.1	97.122	278	0	7	2	271	36	313	9.44E-126	462
OR690607	MF398432.1	97.112	277	0	7	2	271	6	281	3.40E-125	460
OR690607	OR523101.1	97.112	277	0	7	2	270	26	302	3.40E-125	460
OR690607	ON677958.1	96.763	278	1	7	2	271	643	920	1.22E-124	459
OR690607	KU640184.1	97.101	276	0	7	3	271	9	283	1.22E-124	459
OR690607	OM084954.1	96.763	278	1	7	2	271	36	313	4.39E-124	457
OR690607	OQ401460.1	96.763	278	1	7	2	271	35	312	4.39E-124	457
OR690607	OQ401456.1	96.763	278	1	7	2	271	35	312	4.39E-124	457
OR690607	OM334855.1	96.763	278	1	7	2	271	36	313	4.39E-124	457
OR690607	OQ674245.1	96.763	278	1	7	2	271	39	316	4.39E-124	457