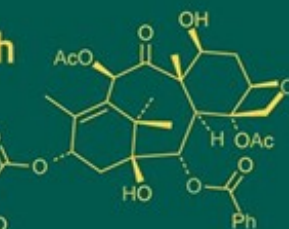
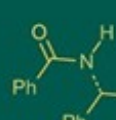
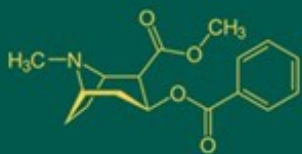


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## Characterization of gene encoding 24 kDa excretory-secretory (E/S) protein of *Haemonchus contortus* isolated from goats

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### ABSTRACT

Gastrointestinal parasite *Haemonchus contortus* produces excretory-secretory (E/S) proteins, which are crucial for tissue penetration/host protein degradation, inside the host (survival). 24 kDa E/S protein, have most important biological and immunogenic functions. Molecular characterization of gene encoding 24kDa E/S protein was done to explore it as potential vaccine candidate. Total RNA of *Haemonchus contortus* was isolated and cDNA was produced. Amplified product of 24kDa E/S gene was obtained by PCR. Sequencing of 24kDa E/S gene was done and the result was compared with published sequences of other species available, and submission in NCBI GenBank. Amplification of 24kDa E/S gene revealed that it consists of 661 base pairs (bp) with maximum frequency of A (Adenine) nucleotide and NCBI BLAST report confirmed that it was a sequence of 24kDa E/S gene of *Haemonchus contortus* (*HcESPs*). The phylogenetic analysis revealed that the sequence found in current investigation was in same clad of *Haemonchus contortus* 24 kDa E/S gene of other global available sequences. The mRNA sequence of 24kDa E/S protein was translated, analyzed and was consists of 219 amino acids with maximum frequency of Asparagine and lowest frequency of Histidine. By further application of r-DNA technology, 24kDa E/S antigenic proteins can be considered potential vaccine candidates upon determining their chemical as well as functional nature, against haemonchosis which causes severe anaemia in small ruminants.

**Keywords:** Excretory-secretory (E/S) protein, *Haemonchus contortus*, Molecular characterization, Phylogenetic study, Goats

### Introduction

India has a goat population of 148.88 million, accounting for about 27.74% of total livestock population (Livestock census, 2019) [1]. In developing nations like India, goats hold tremendous potential to strengthen the economy and serve as a major income source for marginal farmers as well as landless laborers. However, goats are highly susceptible to numerous parasitic diseases that significantly reduce productivity and lead to increased morbidity and mortality (Singh *et al.*, 2015) [2].

*Haemonchus contortus* is a blood-feeding nematode of small ruminants, particularly sheep and goats, and is considered both highly pathogenic and economically significant (Arunkumar, 2012) [3]. The parasite penetrates the abomasal mucosa, consuming the host's blood, which causes anemia and a decline in total plasma protein levels (Gadahi *et al.*, 2016a) [4]. In goats, *H. contortus* infections are associated with hypoproteinaemia, hypoalbuminemia, decreased glucose levels, and elevated cholesterol. Increased concentrations of alanine aminotransferase and aspartate aminotransferase in goats with higher worm loads further suggest its damaging effect on the liver (Bandhaiya *et al.*, 2019) [5]. The FAMACHA® chart scoring method allows farmers for identifying anemic goats, especially in cases of haemonchosis. Treatment is advised for goats with an Egg per Gram (EPG) count of 400–600 or higher (Bandhaiya *et al.*, 2020) [6]. Control measures such as pasture management, along with intensive anthelmintic treatment as well as prophylaxis, have proven effective in decreasing “meat and wool losses in sheep and goats. However, emergence of multiple drug-resistant *H. contortus* strains has compelled farmers and veterinarians” to seek alternative preventive and therapeutic methods (Tak *et al.*, 2015) [7].

Purified excretory and secretory products (ESPs) of *H. contortus* have proven to be of adequate antigenicity in order to be used in serodiagnosis (Tomar *et al.*, 2019) [8]. ESPs secrete several proteins and glycoproteins, which repress host immunity and regulate immune system of the host at an early stage of infection so that parasites can survive. A good number of proteins in excretory and secretory products (*HcESPs*) have ability to penetrate tissues and degrade host proteins (Gadahi *et al.*, 2016a) [4]. The proteins have the ability to attach

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“to goat peripheral blood mononuclear cells (PBMCs) and affect secretion of cytokines, cell migration, proliferation, and nitric oxide production (Gadahi *et al.*, 2016b; Ehsan *et al.*, 2020a; Ehsan *et al.*, 2020b) [9, 10, 11]. *HcESPs* are also able to attenuate upregulation of pro-inflammatory mediators in PBMCs induced by LPS by blocking TLR4/NF- $\kappa$ B/MAPKs/NLRP3 pathway” (Wen *et al.*, 2022) [12].

The immune response of the host is difficult to analyze due to complex antigenic profiles of helminths. The excretory-secretory (E/S) products of helminths have been found to be of significance in determination of specific antigens as they usually have simpler antigenic composition compared to the whole-worm antigens (Arunkumar, 2012) [3]. The interaction between Th9 cells and *HcESPs* was a proteomics based study that demonstrated a new strategy to the detection of immunostimulatory antigens present in *HcESPs* and identified possible candidates that would provide immunity based prevention against *H. contortus* infection (Liang *et al.*, 2022; Memon *et al.*, 2024) [13, 14]. NPs with recombinant excretory/secretory-24 protein (HcES-24) were found to provide effective protection against *H. contortus* and this led to possibility of developing commercial vaccines against it (Hasan *et al.*, 2024) [15]. In a recent study, existing knowledge regarding “host immune responses to *H. contortus* and difficulties in development of protective, long-lasting vaccine” were summarized. It also highlighted the achievements and failure of previous

studies in the field of vaccine development and this gave a guide of how further research can be done to find a vaccine candidate that will control and prevent *H. contortus* infections (Ehsan *et al.*, 2020c) [16].

## Materials and methods

For molecular characterization of 24kDa E/S gene, *Haemonchus contortus* was extracted using total RNA. This extracted RNA was used to create cDNA and 24 kDa E/S gene specific primers were designed based on earlier published primer sequences (Li *et al.*, 2007) [17] to be used in the amplification. All substances that were applied in the process of RNA isolation were first subjected to overnight treatment of 0.01% DEPC so as to make them RNase-free and then dried by placing in a hot air oven that had been set to 60 °C. After drying, the tips and tubes were autoclaved at 15 lbs pressure and 121 °C for 20min for inactivating DEPC. Total RNA extraction was carried out using the Trizol method (Sambrook *et al.*, 2001) [18]. Concentration of the isolated RNA was examined using Nanodrop ND-2000 spectrophotometer.

### cDNA synthesis

cDNA was generated from 11 $\mu$ l of total RNA by employing “RevertAid™ first strand cDNA synthesis kit (Fermentas) following manufacturer’s protocol. Required reagents were placed in a sterile, nuclease-free tube on ice as outlined in Table” 1.

**Table 1.** Components for cDNA synthesis

|                                                                                                                                     |                             |
|-------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|
| <b>Total RNA template</b>                                                                                                           | <b>11 <math>\mu</math>l</b> |
| Oligo (dT) primer                                                                                                                   | 1 $\mu$ l                   |
| <b>Total volume</b>                                                                                                                 | <b>12 <math>\mu</math>l</b> |
| The above reagents were mixed gently, centrifuged briefly and incubated at 65 °C for 5 min and the following components were added. |                             |
| 5X reaction buffer                                                                                                                  | 4 $\mu$ l                   |
| RiboLock™ RNase inhibitor (20 U/ $\mu$ l)                                                                                           | 1 $\mu$ l                   |
| 10mM dNTP mixture                                                                                                                   | 2 $\mu$ l                   |
| RevertAid™ M-MuLV reverse transcriptase (200 unit/ $\mu$ l)                                                                         | 1 $\mu$ l                   |
| <b>Total volume</b>                                                                                                                 | <b>20 <math>\mu</math>l</b> |

The reaction components were mixed gently and centrifuged briefly.

### Reaction protocol for cDNA synthesis

| Parameter   | Step- I | Step-II | Step-III |
|-------------|---------|---------|----------|
| Temperature | 42°C    | 70°C    | 4°C      |
| Time        | 60 min  | 5 min   | $\infty$ |

### Amplification of 24 kDa E/S gene from cDNA

#### Dilution of primer

The published primer was synthesized from Integrated DNA technology. Primers were dissolved in nuclease free sigma water and were further reconstituted in nuclease free water (Sigma-Aldrich, USA) to attain final concentration of 10pmol/ $\mu$ l.

| Name of Primer | Sequence(5' to 3')          |
|----------------|-----------------------------|
| Hc Forward     | TAGGATCCGCTTTTAAGCACATCTGGT |
| Hc Reverse     | GCGAAGCTTGAAGGTTTATTGTCAGTG |

### PCR Amplification of 24kDa E/S gene

1. The above synthesized cDNA was employed as template for amplification of 24kDa E/S gene.

2. After thawing, all “PCR reagents were gently vortexed and briefly spun down.
3. Thin-walled PCR tube was kept on ice, and reagents were added as listed in Table 2.

**Table 2.** Composition of reaction mixture used in PCR for amplification of 24 kDa excretory secretory (E/S) gene

|                      |                               |
|----------------------|-------------------------------|
| <b>cDNA template</b> | <b>2 <math>\mu</math>l</b>    |
| PCR master mix       | 12.5 $\mu$ l                  |
| Nuclease-free water  | 8.5 $\mu$ l                   |
| Forward HC primer    | 1 $\mu$ l (10 pmol/ $\mu$ l)  |
| Reverse HC primer    | 1 $\mu$ l (10 pmol / $\mu$ l) |
| <b>Total volume</b>  | <b>25 <math>\mu</math>l</b>   |

(continued on next page)

PCR was carried out in a thermal cycler equipped with a heated lid following the steps outlined below.

| Steps                 | Temperature (°C) | Time  | Number of cycles |
|-----------------------|------------------|-------|------------------|
| “Initial denaturation | 94               | 3 min | 1                |
| Denaturation          | 94               | 45 s  | 35               |
| Annealing             | 56               | 45 s  |                  |
| Extension             | 72               | 45 s” |                  |

A mixture of 10 µl of PCR-amplified product “and 2 µl of 6X loading dye was prepared and loaded onto a 2% agarose gel along with 100bp DNA ladder. Agarose gel electrophoresis was conducted in 1X TAE buffer at a constant voltage of 5-8V/cm for” 50-60min. After ethidium bromide staining, a clear band of approximately 650bp corresponding to 24kDa fragment was observed. Gel was photographed by employing Gel Doc System for documentation.

#### Sequencing of amplified PCR product of 24 kDa E/S gene

For sequencing the amplified PCR product was send to Chromous Biotech Pvt. Ltd, India. The result was compared with published sequences of other species available on National Centre for Biotechnology Information (NCBI) for molecular characterization.

## Results and discussion

### Quantification of RNA

Concentration of “extracted total RNA was measured using Nanodrop ND-2000 spectrophotometer”. A sample with an A260/A280 ratio of 2.01 was selected for conversion into cDNA using the cDNA synthesis kit (Fermentas).

### Amplification of 24 kDa E/S gene from cDNA

The 24kDa E/S gene was amplified from the synthesized cDNA using previously published primers via PCR, resulting in a single amplified product of approximately 650bp (Fig. 1).

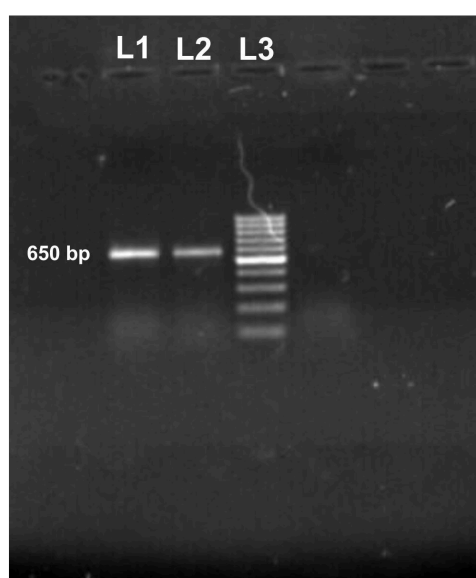


**Figure 1.** Amplification of *Haemonchus contortus* 24 kDa E/S gene

Lane 1 and Lane 2: PCR amplified product

Lane 3: DNA molecular marker (100 bp)

The findings of this work agree with those of Li *et al.* (2007) [17] who used RNA extraction kit (Novagen) to extract total RNA of *Haemonchus contortus*. RNA obtained was subsequently utilized as a template in RT-PCR in which open reading frame (ORF) of 24kDa E/S gene (*ES*<sub>24</sub>) was successfully amplified by employing specific primers, which produced a single band of approximately 650bp, expected length of ORF.

Results also partially confirm the research by Gadahi *et al.* (2016c) [19] who extracted total RNA of adult *Haemonchus contortus* collected in abomasum of goats. Reverse transcription kit was used to synthesize cDNA and full ORF of protein coding 24kDa E/S protein (HcES-24) was amplified by RT-PCR with specific primers. In their study, they were able to get a 609bp fragment that represents HcES-24 gene by using their cDNA.

### Sequence and phylogenetic analysis of gene encoding 24 kDa E/S protein of *Haemonchus contortus*

#### Sequence analysis of 24 kDa E/S gene of *Haemonchus contortus*

The amplified PCR product was send to Chromus Biotech, India for sequencing. The sequence obtained from Chromus Biotech was annotated by DNASTar software and submitted to NCBI GenBank

(GenBank accession number: MN396756.1) and it consists of 661 base pairs with the maximum frequency of A nucleotide (Table 3) and BLAST on NCBI website for sequence similarity.

**Table 3.** Nucleotide composition of 24 kDa excretory-secretory (E/S) gene sequence of *Haemonchus contortus*

| Nucleotide | Frequency (%) |
|------------|---------------|
| T(U)       | 24.7          |
| C          | 20.1          |
| A          | 30.7          |
| G          | 24.5          |

NCBI BLAST results verified that the sequence corresponded to 24kDa E/S gene of *Haemonchus contortus*. Similar sequences were retrieved from NCBI BLAST, aligned using ClustalW method, and “phylogenetic tree was constructed via Neighbor-Joining (NJ) method in MEGA 6.0 software” (Fig. 2). Phylogenetic evaluation demonstrated that sequence identified in this study clustered within the same clade as other globally reported 24kDa E/S gene sequences of *Haemonchus contortus*. Similarly, Toaleb *et al.* (2021) [20] demonstrated that the glucose (Gluc) fraction, containing proteins of 83, 66,

and 24kDa, effectively detected *H. contortus*-specific IgG in naturally infected sheep using indirect ELISA.

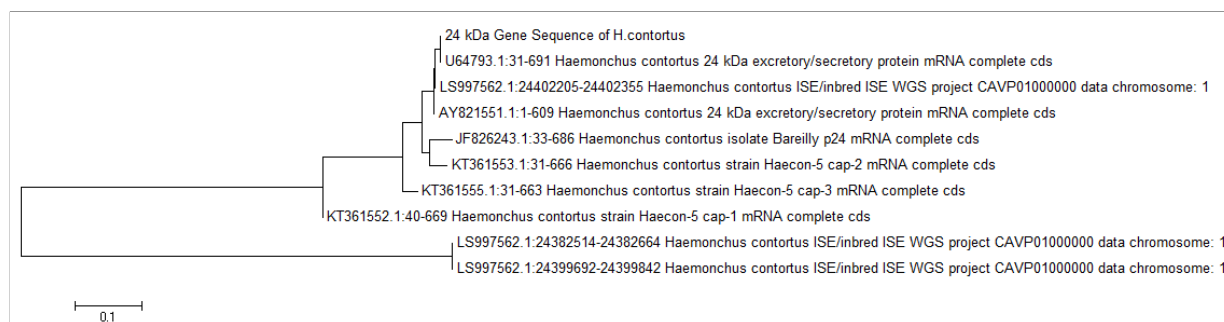


**Figure 2.** Phylogenetic tree of 24 kDa excretory-secretory (E/S) mRNA sequence of *Haemonchus Contortus*

The mRNA sequence was translated and analyzed by MEGA 6.0 software, the translated protein sequence was found of 219 amino acids with maximum frequency of Asparagine and lowest frequency of Histidine (Table 4).

**Table 4.** Amino acid composition and frequency of 24 KDa excretory-secretory (E/S) protein sequence translated by MEGA 6.0 software

| Amino Acids         | Frequencies (%) |
|---------------------|-----------------|
| Alanine (Ala)       | 9.589041096     |
| Cysteine (Cys)      | 5.479452055     |
| Aspartic acid (Asp) | 4.566210046     |
| Glutamic acid (Glu) | 5.936073059     |
| Phenylalanine (Phe) | 2.739726027     |
| Glycine (Gly)       | 5.936073059     |
| Histidine (His)     | 1.826484018     |
| Isoleucine (Ile)    | 3.196347032     |
| Lysine (Lys)        | 5.02283105      |
| Leucine (Leu)       | 5.02283105      |
| Methionine (Met)    | 4.566210046     |
| Asparagine (Asn)    | 10.0456621      |
| Proline (Pro)       | 2.739726027     |
| Glutamine (Gln)     | 3.652968037     |
| Arginine (Arg)      | 2.283105023     |
| Serine (Ser)        | 5.936073059     |
| Threonine (Thr)     | 6.849315068     |
| Valine (Val)        | 7.762557078     |
| Tryptophan (Trp)    | 2.283105023     |
| Tyrosine (Tyr)      | 4.566210046     |
| <b>Total</b>        | <b>219</b>      |

24 kDa gene sequence of *Haemonchus contortus*

ACGCTTTTAAAGCACATCTGGTCATGCATCCATGTGTCCA  
GACACCAATGGTATGTCAGATGAAGTAAGAC  
AGACCTTCGTCAACAAACACAACGCGTATCGAACACTCG  
TTGCCAAAGGAGAAGCGAAAAATGCCAAAGA  
GATTGGTGGTTACGCTCCTAAGGCAGCCAGGATGTTGAA  
AGTGACGTACGATTGCGCCATTGAAGAAAAC  
ACGATGAATTTTCGTAAGAAGTGTGATTTGCGCATAAC  
TCATATCTGAGAGTAACAATTGGGGACAGA  
ACCTTTATATGACATCCATTTTGAACCAAAATAAGACAGT  
AGCCGCAGCCGAGAGTGTTCGATCTTTGGTT  
CGATGAACATAACAGAATGGTGTTCCTTATGATAACGT  
CATGACCATGGCGGTTTTCAATCGTGGCGTT  
GGTCATTATACCCAGGTGGTCTGGCAGTGGAGCAACAA  
GATCGGATGCGCAGTAGAGTGGTGTAGTGACA  
TGACCTTCGTGGCATGCGAGTATGATTGACAGGAACT  
ATATGGGAATGCCTATTTATGAAGTTGGCAA  
CCCGTGACGAATAACGAGGACTGCAAATGTACAAATTG  
TGTTTGTAGCAGAGATGAAGCTCTCTGTATT  
GCCCCATAACAAGCACTGACAATAAACCTTC

24 kDa E/S protein sequences of *Haemonchus contortus* translated by MEGA 6.0 software

TLLSTSGHASMCPDTNGMSDEVQRQTFVNKHNAVRTLVAKG  
EAKNAKEIGGYAPKAARMLKVTYDCAIEENTMNFACKCV  
FAHNSYSESNNWQONLYMTSILNQNKTVAAAESVDLWFDE  
LQQNGVPYDVMMAVFNRGVGHYTVQVWQWSNKGCA  
VEWCSDMTFVACEYDSAGNYMGMPIYEVGNPCTNNEDCK  
CTNCVCSRDEALCIAP\*QALTINL

The current observations partially align with “those reported by Li *et al.* (2007) [17] and Gadahi *et al.* (2016c) [19]. In the earlier study Li *et al.* (2007) [17], a single 650 bp band was obtained through RT-PCR, which matched the predicted ORF of *ES*<sub>24</sub> gene. Sequencing results revealed that cloned *ES*<sub>24</sub> gene comprised 609 nucleotides and encoded a protein of 203 amino acids, with an estimated molecular mass of 22.7kDa. In another earlier study Gadahi *et al.* (2016c) [19], amplicon of HcES-24 gene was amplified by PCR with use of specific primers against cDNA of *Haemonchus contortus*. The sequences performed by amplification were validated as HcES-24 gene by using BLASTx and ORF had 609bp which code 202 amino acids proteins. Also, Lu *et al.* (2021) [21] suggested that recombinant *H. contortus* alpha/beta-hydrolase domain protein (HcABHD) was potentially useful in field applications for protection of goats against *H. contortus*. Comprehensive immunological approach of ES antigen identification, screening as well as characterization may offer good avenues to come up with recombinant subunit vaccines towards management of *H. contortus* infections.

In this work, antigenic proteins that are associated with excretory-secretory (E/S) parts of *Haemonchus contortus* are explored in detail, and research objective is to assess their suitability as potential vaccine targets and the development of simple diagnostic assays of haemonchosis in goats, e.g., ELISA. The gene coding 24 kDa E/S protein of *H. contortus* was analyzed at the molecular level to show that it contains 661bp, coding into 219 amino acids of protein.

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## Ethical approval

Study was performed after taking clearance of Institutional Animal Ethical Committee, Nanaji Deshmukh Veterinary Science University, College of Veterinary Science and Animal Husbandry, Mhow, Madhya Pradesh, and conducted as per the laid down ethical guidelines.

## Conflict of interest

None

## References

1. Livestock census, 2019. 20th All India Livestock Census, Department of Animal Husbandry and Dairying Ministry of Agriculture, Government of India. 2019.
2. Singh AK, Das G, Roy B, Nath S, Naresh R, Kumar S. Prevalence of gastrointestinal parasitic infections in goat of Madhya Pradesh, India. *J Parasit Dis*. 2015;39(4):716-719.
3. Arunkumar S. Immunoprotection in sheep against *Haemonchus contortus* using its thiol-purified excretory/secretory proteins. *Vet Res Forum*. 2012;3(4):239-244.
4. Gadahi JA, Wang S, Bo G, Ehsan M, Yan R, Song X, Xu L, Li X. Proteomic analysis of the excretory and secretory proteins of *Haemonchus contortus* (HcESPs) binding to goat PBMCs in vivo revealed stage-specific binding profiles. *PLoS One*. 2016;11(7):e0159796.
5. Bandhaiya D, Aich R, Sharda R, Agrawal V. Biochemical parameters assessment in goats naturally infected with *Haemonchus contortus*. *J Entomol Zool Stud*. 2019;7(5):1316-1320.
6. Bandhaiya D, Aich R, Sharda R, Agrawal V. Haematological parameters and its relationship with faecal egg count and FAMACHA© score in *Haemonchus contortus* naturally infected goats. *J Anim Res*. 2020;10(4):659-665.
7. Tak I, Chishti MZ, Ahmad F. Protein profiling of *Haemonchus contortus* found in sheep of Kashmir valley. *J Parasit Dis*. 2015;39(4):639-644.
8. Tomar A, Aich R, Chhabra D, Agrawal V, Singh AP. Immuno-biochemical characterization of excretory secretory proteins of *Haemonchus contortus* isolated from goats. *J Entomol Zool Stud*. 2019;7(5):432-436.
9. Ehsan M, Gadahi JA, Hasan MW, Haseeb M, Ali H, Yan R, Xu L, Song X, Zhu X, Li X. Characterization of *Haemonchus contortus* excretory/secretory antigen (ES-15) and its modulatory functions on goat immune cells in vitro. *Pathogens*. 2020;9(162).
10. Ehsan M, Haseeb M, Hu R, Ali H, Memon MA, Yan R, Xu L, Song X, Zhu X, Li X. Tropomyosin: An excretory/secretory protein from *Haemonchus contortus* mediates the immunosuppressive potential of goat peripheral mononuclear cells in vitro. *Vaccines*. 2020;8(109).
11. Gadahi JA, Yongqian B, Ehsan M, Zhang Z, Wang S, Yan R, Song X, Xu L, Li X. *Haemonchus contortus* excretory and secretory proteins (HcESPs) suppress functions of goat PBMCs in vitro. *Oncotarget*. 2016;7(24):35670-35679.
12. Wen Z, Zhang Y, Feng J, Aimulajiang K, Aleem MT, Lu M, Xu L, Song X, Li X, Yan R. Excretory/secretory proteins inhibit host immune responses by downregulating the TLR4/NF- $\kappa$ B/MAPKs signaling pathway: A possible mechanism of immune evasion in parasitic nematode *Haemonchus contortus*. *Front Immunol*. 2022;13:1013159.
13. Liang M, Lu M, Aleem MT, Zhang Y, Wang M, Wen Z, Song X, Xu L, Li X, Yan R. Identification of excretory and secretory proteins from *Haemonchus contortus* inducing a Th9 immune response in goats. *Vet Res*. 2022;53:36.
14. Memon MA, Tunio S, Abro SM, Lu M, Song X, Xu L, Yan R. A comprehensive review on *Haemonchus contortus* excretory and secretory proteins (HcESPs): TH-9 stimulated ESPs as a potential candidate for vaccine development and diagnostic antigen. *Acta Trop*. 2024;107462.
15. Hasan MW, Haseeb M, Gadahi JA, Ehsan M, Wang Q, Lakho SA, Haider A, Aleem MT, Aimulajiang K, Lu M, Xu L, Song X, Li X, Yan R. Nanoparticle containing recombinant excretory/secretory-24 protein of *Haemonchus contortus* enhanced the cellular immune responses in mice. *Front Vet Sci*. 2024;11:1470084.
16. Ehsan M, Hu R, Liang Q, Hou J, Song X, Yan R, Zhu X, Li X. Advances in the development of anti-*Haemonchus contortus* vaccines: challenges, opportunities and perspectives. *Vaccines*. 2020;8(555).
17. Li X, Du A, Cai W, Hou Y, Pang L, Gao X. Evaluation of a recombinant excretory secretory *Haemonchus contortus* protein for use in a diagnostic enzyme-linked immunosorbent assay. *Exp Parasitol*. 2007;115:242-246.
18. Sambrook J, Russel DW. Molecular cloning. 3rd edn. Cold Spring Harbor: Cold Spring Harbor Laboratory Press; 2001.
19. Gadahi JA, Li B, Ehsan M, Wang S, Zhang Z, Wang Y, Hasan MW, Yan R, Song X, Xu L, Li X. Recombinant *Haemonchus contortus* 24 kDa excretory/secretory protein (rHcES-24) modulate the immune functions of goat PBMCs in vitro. *Oncotarget*. 2016;7(51):83926-83937.
20. Toaleb NI, Abdel-Rahman EH. Potentials of glycoprotein fraction in successful diagnosis of sheep haemonchosis. *Adv Anim Vet Sci*. 2021;9(3):335-343.
21. Lu M, Tian X, Zhang Y, Wang W, Tian A, Aimulajiang K, Liu L, Li C, Yan R, Xu L, Song X, Li X. Protection studies of an excretory-secretory protein HcABHD against *Haemonchus contortus* infection. *Vet Res*. 2021;52:3.

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