

RESEARCH ARTICLE

First molecular detection of *Ehrlichia* spp. and *Theileria* spp. closely related to *Theileria parva* in *Hyalomma dromedarii* ticks infesting camels in the United Arab Emirates



Mohamad Taha Al Masri , Amgd Sayed Ali, Sabir Bin Muzaffar and Mohammad Ali Al-Deeb

Department of Biology, College of Science, United Arab Emirates University, P.O. Box 15551, Al Ain, United Arab Emirates.

ABSTRACT

Background and Aim: Tick-borne pathogens pose a growing threat to animal health and livestock production, particularly in arid regions where *Hyalomma* ticks are abundant. *Hyalomma dromedarii*, the predominant camel tick in the Middle East and North Africa, has been implicated in the transmission of several bacterial and protozoal pathogens. Despite the economic importance of camels in the United Arab Emirates (UAE), comprehensive surveillance of tick-borne microorganisms in *H. dromedarii* across the country remains limited. This study investigated the occurrence of *Anaplasma*, *Rickettsia*, *Ehrlichia*, *Theileria*, and *Babesia* in *H. dromedarii* collected from camels in the UAE and characterized the detected pathogens using molecular and phylogenetic analyses.

Materials and Methods: A total of 804 camels from 182 farms in Abu Dhabi, Dubai, Sharjah, and Umm Al Quwain were examined between June 2022 and October 2023. One semi-engorged female *H. dromedarii* tick was selected from each camel whenever available, yielding 671 ticks for molecular analysis. Genomic DNA was extracted and screened using polymerase chain reaction (PCR) assays targeting *Anaplasma*, *Rickettsia*, *Ehrlichia*, *Theileria*, and *Babesia*. Positive amplicons were confirmed by Sanger sequencing, and phylogenetic analyses were performed to determine their genetic relationships with previously reported isolates.

Results: No evidence of *Anaplasma*, *Rickettsia*, or *Babesia* DNA was detected in the analyzed ticks. In contrast, *Theileria* and *Ehrlichia* DNA were detected in 0.60% (4/671) and 0.30% (2/671) of samples, respectively. The detected *Ehrlichia* represents the first molecular record of this genus in *H. dromedarii* from the UAE. One *Theileria* sequence exhibited 98.96% nucleotide similarity to *Theileria parva*; however, species-specific PCR failed to confirm *T. parva*, indicating that the detected organism was a closely related *Theileria* species rather than confirmed *T. parva*. Phylogenetic analyses showed that the detected *Ehrlichia* and *Theileria* sequences clustered with corresponding reference sequences reported previously from other geographical regions.

Conclusion: This study provides the first molecular evidence of *Ehrlichia* in *H. dromedarii* ticks in the UAE and identifies a *Theileria* isolate closely related to *T. parva*. Although pathogen prevalence was low, these findings expand current knowledge of tick-borne microorganisms associated with camel ticks in the UAE and highlight the need for continued molecular surveillance to clarify the epidemiological significance, host-pathogen interactions, and potential veterinary and One Health implications of these microorganisms in the region.

Keywords: camel, *Ehrlichia*, *Hyalomma dromedarii*, molecular epidemiology, One Health, polymerase chain reaction, *Theileria*, United Arab Emirates.

INTRODUCTION

Ticks are obligate blood feeding arthropods [1] that transmit a wide range of tick-borne pathogens, including viruses, bacteria, and protozoa [2]. The incidence and geographic distribution of tick-borne diseases have increased in several regions [3]. The genus *Hyalomma* comprises hard ticks adapted to hot and humid climates [4] and includes important vectors of viral and bacterial pathogens [5]. Camels are a major livestock species in the United Arab Emirates (UAE) [6] and contribute to transportation, tourism, and milk and meat production [7]. The previous detection of *Anaplasma*, *Ehrlichia*, *Francisella*, *Rickettsia*, *Babesia*, and *Theileria* in regions where camels and *Hyalomma* ticks occur [8–12] underscores the importance of investigating tick-borne microorganisms

Corresponding Author: Mohammad Ali Al-Deeb

E-mail: m_aldeeb@uaeu.ac.ae

Received: 13-04-2026, **Accepted:** 18-09-2026, **Published online:** 22-10-2026

Co-authors: MTA: 202190173@uaeu.ac.ae; ASA: amgd.s@uaeu.ac.ae; SBM: s_muzaffar@uaeu.ac.ae

How to cite: Al Masri MT, Ali AS, Muzaffar SB, Al-Deeb MA. First molecular detection of *Ehrlichia* spp. and *Theileria* spp. closely related to *Theileria parva* in *Hyalomma dromedarii* ticks infesting camels in the United Arab Emirates. Vet World. 2026;19(10):4657–4668.

Copyright: Al Masri et al. This article is an open access article distributed under the terms of the Creative Commons Attribution 4.0 International License (<https://creativecommons.org/licenses/by/4.0/>).

associated with camel ticks in the UAE.

Ticks transmit several bacterial pathogens of veterinary and public health importance. *Anaplasma*, a tick-borne bacterial genus within the order Rickettsiales, includes the causative agents of anaplasmosis [13, 14]. In northern Finland, 1.1% of *Ixodes* ticks collected from cats and dogs tested positive for *Anaplasma phagocytophilum* [15]. Similarly, 5.8% of *Hyalomma* and *Rhipicephalus* ticks collected from cattle in the Kingdom of Saudi Arabia tested positive for *Anaplasma ovis* [16]. In *Hyalomma dromedarii*, *Anaplasma marginale* was detected in 9.81% of sampled ticks in Egypt [8]. Likewise, *Ehrlichia*, which includes causative agents of ehrlichiosis [17], has been reported in 14.2% of *Hyalomma aegyptium* ticks collected from the tortoise *Testudo graeca* in Qatar [11] and in 6.3% of *Hyalomma asiaticum* and *Hyalomma turanicum* ticks collected from goats and sheep in Pakistan [18]. Although *Ehrlichia* spp. was detected in 54.8% of tested dromedary camels (*Camelus dromedarius*) in Somalia [9], no previous record of *Ehrlichia* in *H. dromedarii* from the UAE has been reported.

Tick-borne protozoa have also been documented in several tick species, including *Babesia* spp. [19], *Hepatozoon*, and *Theileria* [20, 21]. Several *Theileria* species have been detected in *Hyalomma* ticks. *Theileria annulata* and *Theileria ovis* were detected in 4.55% and 10%, respectively, of *Hyalomma anatolicum* ticks collected in the UAE [12]. In *H. dromedarii*, *Theileria* spp. has been reported in Egypt at a frequency of 0.4% [8]. However, no previous record of *Theileria parva* in *H. dromedarii* has been reported. *T. parva*, the causative agent of East Coast fever, causes substantial losses in livestock [22], and *Rhipicephalus appendiculatus* is its typical vector [23]. *T. parva* has also been detected in *Rhipicephalus praetextatus*, *Rhipicephalus pravus*, *Rhipicephalus turanicus*, and *Rhipicephalus* sp. collected from African buffalo (*Syncerus caffer*) in Kenya at frequencies of 17%, 40%, 100%, and 15%, respectively [24]. Polymerase chain reaction (PCR) has been successfully used for genus- and species-specific molecular detection of tick-borne microorganisms [25, 26].

Despite previous reports of *Rickettsia* in *H. anatolicum* [12] and *Theileria* in *H. dromedarii* [27] from Abu Dhabi Emirate, information on the occurrence and genetic characteristics of tick-borne microorganisms associated with *H. dromedarii* across the UAE remains limited. Previous sampling for pathogen detection has been geographically restricted and has not provided broader molecular surveillance across multiple Emirates. In particular, evidence regarding *Ehrlichia* associated with *H. dromedarii* in the UAE is lacking, and the occurrence and genetic relationships of *Theileria* organisms potentially related to *T. parva* in camel ticks remain poorly characterized. These gaps are relevant because camel trade within the UAE and the wider Arabian Peninsula [7], together with the close proximity of camels to humans in the UAE [28], may create interfaces at which ticks, hosts, and tick-borne microorganisms interact. Molecular surveillance across a broader geographic area is therefore needed to characterize these microorganisms and provide baseline evidence for understanding their potential veterinary and One Health significance.

This study aimed to investigate the occurrence of *Anaplasma*, *Ehrlichia*, *Rickettsia*, *Babesia*, and *Theileria* in *H. dromedarii* ticks collected from camels across multiple Emirates of the UAE. Molecular screening was combined with sequencing and phylogenetic analyses to characterize detected microorganisms and assess their genetic relationships with previously reported sequences. Particular attention was given to characterizing *Ehrlichia* detected in *H. dromedarii* and to determining the genetic relationship of detected *Theileria* sequences to *T. parva*. This approach was intended to broaden current knowledge of tick-borne microorganisms associated with camel ticks in the UAE and provide molecular evidence relevant to future epidemiological surveillance.

MATERIALS AND METHODS

Ethical approval

The experimental protocol was approved by the Research Office of United Arab Emirates University (UAEU), and all sampling procedures were conducted in accordance with the recommendations of the Animal Research Ethics Committee (A-REC) of UAEU (ethical approval no. ERA_2022_1629, dated 22/10/2022). Ticks were removed from camels by trained personnel using routine manual collection procedures designed to minimize handling time and animal distress. All animal-associated sampling procedures were performed in accordance with the approved institutional animal research ethics protocol.

Study period and location

The study was conducted from June 2022 to October 2023 across four Emirates of the UAE: Abu Dhabi, Dubai, Sharjah, and Umm Al Quwain. Tick samples were collected from 182 farms and 804 camels, comprising 333 camels from Abu Dhabi, 261 from Dubai, 172 from Sharjah, and 38 from Umm Al Quwain (Figure 1). Collected

ticks were transported in a portable cooler to the Entomology Laboratory, College of Science, UAEU, and stored at -80°C until further processing.

Study design

This study used a field-based molecular surveillance design to investigate selected tick-borne microorganisms in *Hyalomma dromedarii* collected from camels. At each location five farms were selected from those that were accessible and whose owners granted permission for sampling. Five camels per farm were sampled, depending on availability, and 10 ticks were randomly selected from each camel. This sampling strategy aimed to maximize geographic coverage while reducing redundancy in sample collection. From the 804 sampled camels, one semi-engorged female *H. dromedarii* per camel was randomly selected, when available, for molecular analysis. Semi-engorged females were available from 671 camels, resulting in 671 individual ticks for subsequent processing. The study combined morphological and molecular tick identification, pooled molecular screening, individual retesting of positive pools, Sanger sequencing, and phylogenetic analysis.

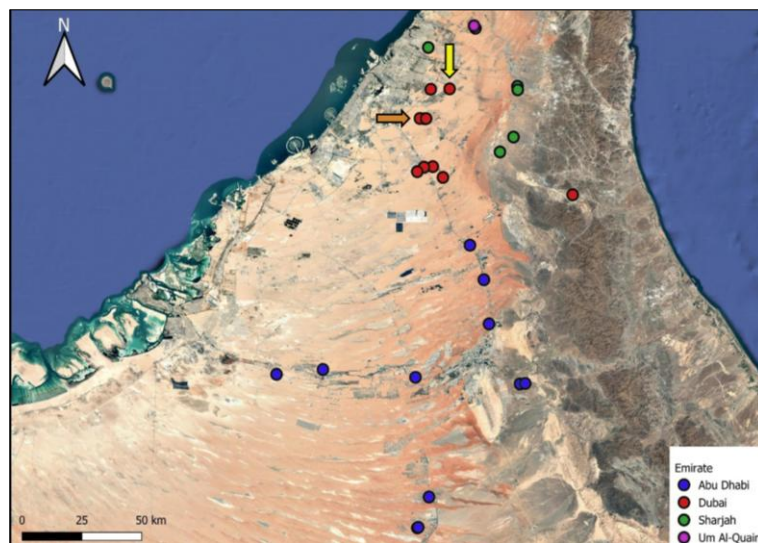


Figure 1: Sampling sites across the United Arab Emirates. The map was generated using QGIS Desktop version 3.36.2 (Zurich) and basemap imagery from Esri, Maxar, and Earthstar Geographics. The yellow arrow indicates Al Owair, and the orange arrow indicates Al Khawaneej.

Morphological identification of ticks

Collected ticks were identified under a stereomicroscope using available morphological identification keys [29, 30], and only *H. dromedarii* ticks were included in the study. This species is characterized by pale rings on the legs, and females have narrow, posterior V-shaped lips on the genital pore. To select ticks that had already fed on their hosts and thereby represent the sampled host–tick association, one semi-engorged female was selected per camel whenever available. Of the 804 sampled camels, semi-engorged females were obtained from 671. All 671 morphologically identified semi-engorged females were retained for DNA extraction and subsequent molecular analyses.

DNA extraction and quality assessment

All 671 semi-engorged female ticks were rinsed with water and 70% ethanol to reduce potential surface contamination. Each tick was placed individually in a 1.5-mL centrifuge tube, cut into pieces using sterile scissors, and homogenized. DNA was extracted using the QIAamp Tissue Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. The quality of the extracted DNA was assessed using a NanoDrop ND-2000 spectrophotometer (Thermo Scientific, Waltham, USA).

Molecular identification of ticks

Morphological identification of the ticks was molecularly verified by amplification of the cytochrome c oxidase subunit I (COI) gene. Amplification was performed using the Fish1F forward primer 5'-TCAACCAACCACAAAGACATTGGCAC-3' and Fish1R reverse primer 5'-TAGACTTCTGGGTGGCCAAAGAATCA-3'. The reported thermal conditions comprised an initial denaturation step at 95°C for 2 min, followed by 30 cycles of denaturation at 94°C for 1 min, annealing at 54°C for 1 min, and an extension at 72°C for 90 s followed by a final extension step at 72°C for 10 min [31].

Pooling and PCR amplification

The 671 extracted DNA samples were randomly combined into pools of five, resulting in 135 pools, from which 134 were complete five-samples pool and one is a single-sample pool. Individual tick samples were handled separately before pooling using sterile consumables, and instruments were cleaned between samples. DNA extraction and PCR setup were performed in a clean pre-PCR area physically separated from the post-PCR analysis area. Aerosol-resistant filter tips and sterile nuclease-free consumables were used, gloves were changed frequently, and work surfaces and equipment were routinely decontaminated. A no-template negative control containing nuclease-free water was included in each PCR run to monitor potential contamination.

Initial screening for *Anaplasma*, *Ehrlichia*, and *Rickettsia* was performed using the AccuPower® Rickettsiales 3-Plex PCR Kit (Bioneer, South Korea), whereas *Babesia* and *Theileria* were initially screened using the AccuPower® Babesia & Theileria PCR Kit (Bioneer, South Korea). Because the primers incorporated in these commercial kits were proprietary, positive samples were subsequently retested using previously published primers (Table 1) [32–36] to permit further characterization.

The PCR reaction volume was 25 µL including 12.5 µL of master mix, 7.5 µL of nuclease-free water, 1 µL of forward primer, 1 µL of reverse primer and 3 µL of template DNA. PCR assays targeting *Ehrlichia*, *Rickettsia*, *Anaplasma*, and the piroplasms *Theileria* and *Babesia* were performed using the following thermal cycling conditions: initial activation at 95°C for 15 min; 10 cycles of denaturation at 94°C for 20 s, step-down annealing for 25 s from 63.5°C to 53.5°C with a decrease of 1°C per cycle, and extension at 72°C for 30 s; followed by 25 cycles of denaturation at 94°C for 25 s, annealing at 50°C for 20 s, and extension at 72°C for 30 s; and a final extension at 72°C for 7 min [37].

Table 1: Primers used for molecular detection of the tested microorganisms.

Pathogen	Target gene	Primer	Sequence (5'-3')	Amplicon size (bp)	Reference
<i>Anaplasma</i>	16S rRNA	AnaplasmaJVF	CGGTGGAGCATGTGGTTTAATTC	300	[32]
		AnaplasmaJVR	CGRCGTTGCAACCTATTGTAGTC		
<i>Ehrlichia</i>	16S rRNA	Ehrlichia16SF	CGTAAAGGGCACGTAGGTGGACTA	200	[33]
		Ehrlichia16SR	CACCTCAGTGTCAGTATCGAACCA		
<i>Rickettsia</i>	16S rRNA	Rick-F	GAACGCTATCGGTATGCTTAACACA	364	[34]
		Rick-R	CATCACTCACTCGGTATTGCTGGA		
<i>Rickettsia</i>	ompB	120–2788	AAACAATAATCAAGGTACTGT	812	[35]
		120–3599	TACTTCCGGTTACAGCAAAGT		
<i>Babesia</i> , <i>Theileria</i>	18S rRNA	RLB F	GAGGTAGTGACAAGAAATAACAATA	460–520	[36]
		RLB R	TCTTCGATCCCCTAACTTC		

Gel electrophoresis and sequencing

PCR products were separated by electrophoresis on 1.5% agarose gels stained with ethidium bromide and visualized using a gel documentation system (Major Science, Taipei, Taiwan). Pools yielding positive amplification were identified, and their constituent individual tick samples were subsequently retested to identify the positive specimens. PCR products from positive individual samples were submitted to Macrogen Inc. (Seoul, South Korea) for Sanger sequencing. The resulting sequences were deposited in GenBank.

Phylogenetic analysis and detection frequencies

Phylogenetic trees were constructed using Geneious Prime version 2024.1 (Biomatters Ltd., Auckland, New Zealand) according to published guidelines [38]. MEGA X was used to determine the most appropriate distance model, which was identified as the Jukes–Cantor model. Sequences were subsequently aligned using MUSCLE, and neighbor-joining consensus trees were constructed using the Jukes–Cantor distance model with 1000 bootstrap replicates.

For phylogenetic analysis of *Theileria parva*, *Babesia bovis* was selected as the outgroup, and the available *T. parva* sequences in GenBank were included in the analysis. For the *Ehrlichia* phylogenetic analysis, *Anaplasma phagocytophilum* was used as the outgroup, and tick-borne *Ehrlichia* isolates showing ≥99% sequence similarity to the isolate detected in the present study were included.

Detection frequencies were calculated by dividing the number of positive ticks by the total number of ticks tested at each location and across the study as a whole.

Multi-tiered approach

The study used a multi-tiered approach comprising morphological and molecular identification of ticks, initial

screening with commercial PCR assays, retesting with conventional published primers, Sanger sequencing of positive amplification products, and phylogenetic analysis of the resulting sequences.

RESULTS

Of the 671 *H. dromedarii* ticks analyzed, two microorganisms were detected: *Ehrlichia* spp. and *Theileria* spp. No co-infections were detected. *Anaplasma*, *Rickettsia*, and *Babesia* were not detected in any of the analyzed ticks (Tables 2 and 3). Pools yielding positive amplification were subsequently retested individually to identify the positive ticks.

Table 2: Frequency of detected microorganisms across all sampling sites.

Date	Location	Camels sampled	Semi-engorged females tested	Microorganism detected	Positive, n/N
27/08/2022	Al Fou'ah	15	15	—	0/15
27/08/2022	Al Jeeah	18	13	—	0/13
27/08/2022	Al Jabeeb	24	24	—	0/24
17/09/2022	Al Khawaneej	22	22	—	0/22
04/09/2022	Al Lisaili	24	21	—	0/21
18/09/2022	Al Marmoom	22	18	—	0/18
05/10/2022	Al Madam	36	34	—	0/34
17/09/2022	Al Owair	23	18	<i>Theileria</i> spp.	4/18
05/10/2022	Al Ruwayyah	5	5	<i>Ehrlichia</i> spp.	2/5
27/07/2022	Al Saa	25	20	—	0/20
04/08/2022	Al Zaabah	12	3	—	0/3
20/07/2022	Al Zalah	27	25	—	0/25
11/09/2022	Dhaid	25	20	—	0/20
04/09/2022	Al Nawasi	17	14	—	0/14
04/08/2022	Emran	11	7	—	0/7
18/09/2022	Grayteesah	21	21	—	0/21
17/12/2022	Jebel Mileina	24	24	—	0/24
03/08/2022	Al Khatim	11	7	—	0/7
03/08/2022	Al Khaznah	10	9	—	0/9
05/10/2022	Lahbab	15	13	—	0/13
27/07/2022	Malaqet	10	7	—	0/7
11/12/2022	Maleha	5	5	—	0/5
15/09/2022	Margham	20	19	—	0/19
28/07/2022	Al Salamat	18	15	—	0/15
04/08/2022	Tal Ramil	10	6	—	0/6
11/09/2022	Um Fanain	5	5	—	0/5
19/08/2023	Al Hiyyar	20	20	—	0/20
19/08/2023	Al Khawaneej	25	19	—	0/19
24/07/2023	Al Lebsa	20	11	—	0/11
12/08/2023	Al Lisaili	25	18	—	0/18
12/08/2023	Al Marmoom	24	23	—	0/23
29/10/2023	Al Madam	25	10	—	0/10
28/10/2023	Al Owair	20	19	—	0/19
16/09/2023	Al Saa	35	32	—	0/32
01/08/2023	Hatta	18	15	—	0/15
24/07/2023	Kabir	18	10	—	0/10
14/10/2023	Al Khatim	23	16	—	0/16
07/10/2023	Malaqet	24	24	—	0/24
05/08/2023	Maleha	33	33	—	0/33
19/08/2023	Margham	10	9	—	0/9
07/10/2023	Al Salamat	10	7	—	0/7
21/10/2023	Al Weshah	19	15	—	0/15
Total		804	671	<i>Theileria</i> and <i>Ehrlichia</i>	6/671

Table 3: Frequency of microorganisms detected by location

Location	Camels sampled	Semi-engorged females tested	Microorganism detected	Frequency
Al Owair	43	37	<i>Theileria</i> sp. (GenBank accession no. PQ216298)	4/37
Al Ruwayyah	5	5	<i>Ehrlichia</i> sp. (GenBank accession no. PP348046.1)	2/5

Detection of *Ehrlichia*

Ehrlichia-specific band (Figure 2) was detected in two ticks collected from Al Ruwayyah, corresponding to a

location-specific detection frequency of 40.00% (2/5) and an overall detection frequency of 0.30% (2/671). Sanger sequencing supported the PCR findings, and sequence analysis identified the detected organism as uncultured *Ehrlichia*. The *Ehrlichia* sequence recorded in this study was deposited in GenBank under the accession number PP348046.1. BLAST analysis showed 99.64% sequence identity, 100% query coverage and E-value of 7×10^{-143} to uncultured *Ehrlichia* of accession number PX452793.1. Moreover, the resulting phylogenetic tree showed that the detected *Ehrlichia* sequence clustered with sequences previously obtained from *H. asiaticum* in Pakistan (Figure 3).

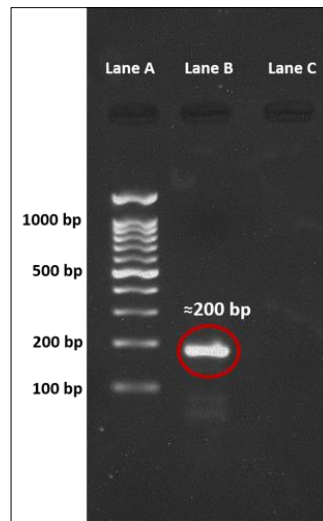


Figure 2: A 1.5% agarose gel showing an *Ehrlichia*-specific amplification product. Lane A: 100-bp deoxyribonucleic acid ladder (Promega, USA); lane B: *Ehrlichia*-specific band; lane C: negative control.

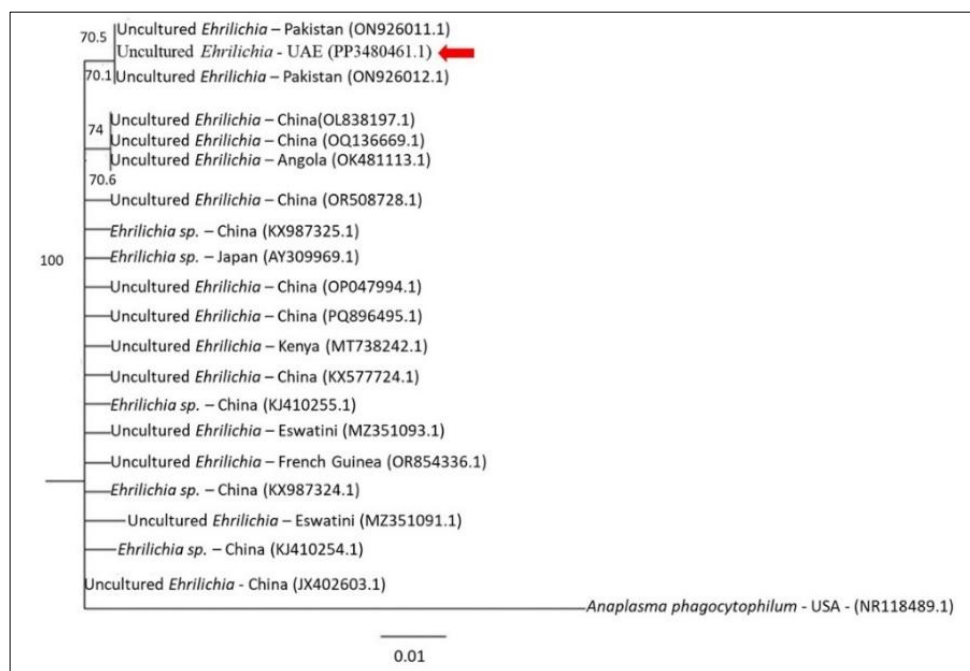


Figure 3: Phylogenetic tree comparing the detected *Ehrlichia* isolate with other GenBank records. The red arrow indicates the isolate detected in the present study. The scale bar represents 0.01 substitutions per site, and *Anaplasma phagocytophilum* was used as the outgroup.

Detection of *Theileria*

Theileria-specific band (Figure 4) was detected in four ticks collected in 2022 from Al Owair with no positive records in 2023, corresponding to a location-specific detection frequency of 10.81% (4/37) and an overall detection frequency of 0.60% (4/671). Sanger sequencing showed that a representative positive sample had 98.96% sequence identity to *T. parva* (GenBank accession no. PQ001545.1; query coverage, 92%; E-value, 0). Phylogenetic analysis further showed clustering of the detected sequence with several *T. parva* sequences available in GenBank (Figure 5).

However, subsequent PCR using the *T. parva*-specific primers L3231 (forward: 5'-ATTTAAGGAACCTGACGT

GACTGC-3') and IL755 (reverse: 5'-TAAGATGCCGACTATTAATGACACC-3') did not produce species-level confirmation. Therefore, the sequence generated in the present study was deposited in GenBank as *Theileria* sp. under accession no. PQ216298.

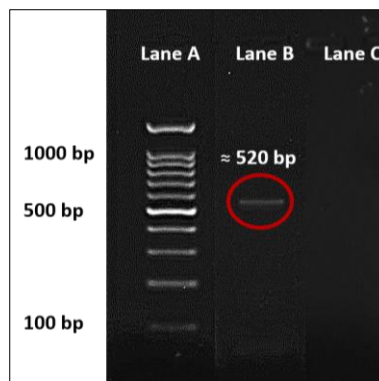


Figure 4: A 1.5% agarose gel showing a *Theileria*-specific amplification product. Lane A: 100-bp deoxyribonucleic acid ladder (Promega, USA); lane B: *Theileria*-specific band; lane C: negative control.

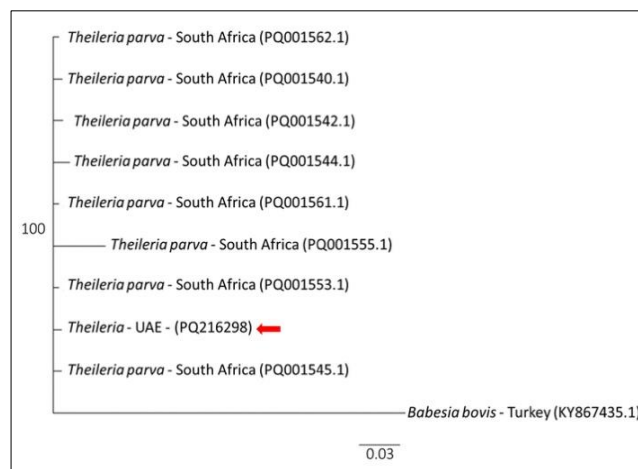


Figure 5: Phylogenetic tree comparing the detected *Theileria* isolate with other GenBank records. The red arrow indicates the isolate detected in the present study. The scale bar represents 0.03 substitutions per site, and *Babesia bovis* was used as the outgroup.

DISCUSSION

Detection and potential significance of *Ehrlichia*

Ticks are vectors of pathogens affecting humans and other animals [39]. The genus *Hyalomma* is among the major tick genera in the Middle East and North Africa (MENA) and parasitizes a wide range of hosts [5]. *H. dromedarii* is a major camel-infesting tick species [40], and an increasing number of tick-borne microorganisms and potential pathogens have been reported in this species [21]. The present study provides the first molecular detection of *Ehrlichia* in *H. dromedarii* in the UAE. The increasing trade of camels within MENA [7] provides a possible route for the movement of infected hosts and their associated ticks. The King Fahd Causeway, which connects Saudi Arabia and Bahrain, has facilitated terrestrial connectivity within the Arabian Peninsula [41]. However, the present study did not investigate the geographic origin or movement of infected camels; therefore, any relationship between camel trade and the introduction of *Ehrlichia* remains hypothetical.

The detection of *Ehrlichia* in camel-associated ticks may have veterinary and public health relevance because members of this genus include pathogens of animals and humans [42]. Ehrlichiosis can be associated with clinical manifestations including headache, fever, hematological and neurological abnormalities, hepatomegaly, and musculoskeletal pain [43]. The lack of an available vaccine against the microorganism detected in this study may further emphasize the importance of surveillance [44]. Nevertheless, the pathogenicity and zoonotic potential of the *Ehrlichia* detected in the present study were not established and should not be inferred solely from genus-level molecular identification.

The present findings can be considered alongside the previous detection of *Ehrlichia canis* in 0.58% of *Hyalomma*-infested camels in Saudi Arabia [10]. In addition, *Ehrlichia ewingii* was reported in 68.1% of *H.*

dromedarii ticks sampled at the Iranian–Pakistani border [45]. The *Ehrlichia* sequence obtained in the present study showed >99% similarity to previously reported sequences and clustered phylogenetically with sequences reported from Pakistan (Figure 3). This genetic relatedness indicates similarity among the compared sequences; however, the available data are insufficient to establish regional circulation, transmission pathways, or a common source.

Detection and molecular characterization of *Theileria*

The present study also detected a *Theileria* sequence showing >98% similarity to *T. parva*. *Theileria* species have previously been reported in *Hyalomma* ticks. *T. annulata* and *T. ovis* were detected at frequencies ranging from 4.55% to 10% in *H. anatolicum* collected from cattle, goats, and sheep in the UAE [21, 31]. Previous investigations of *H. dromedarii* have also reported *Theileria camelensis* in Egypt [46] and *T. annulata* in the UAE [31].

In the present study, amplification of a fragment of the 18S rRNA gene yielded PCR products from four samples. Sanger sequencing followed by similarity searches using the National Center for Biotechnology Information Basic Local Alignment Search Tool (NCBI BLAST) showed >98% sequence similarity to *T. parva*. However, a search of the published literature did not identify confirmed reports of *T. parva* in *H. dromedarii* or other *Hyalomma* species [47]. Furthermore, *R. appendiculatus* is the established vector of *T. parva* [48], and confirmed detection of this pathogen in *Hyalomma* ticks has not been established in the cited literature.

To further evaluate the initial sequence-based finding, PCR assays using *T. parva*-specific primers were performed; however, the expected amplification products were not obtained. Sequence variation at primer-binding sites has been reported as a potential cause of false-negative amplification with species-specific assays [48]. Nevertheless, because the *T. parva*-specific PCR assays were negative, the present findings do not provide sufficient evidence to identify the detected organism as *T. parva*. Accordingly, the sequence was conservatively classified as *Theileria* sp.

The sequenced fragment represents part of the 18S rRNA gene, a highly conserved locus that may provide insufficient discriminatory resolution for definitive species-level identification among closely related *Theileria* species. Therefore, additional molecular characterization using alternative species-specific markers or multiple genetic loci is required to establish the taxonomic identity of the detected *Theileria*. These findings should consequently be interpreted as evidence of a *Theileria* organism genetically related to *T. parva*, rather than evidence of *T. parva* infection or vector spillover into *Hyalomma*.

The possible occurrence of *T. parva*-related organisms in camel-associated ticks warrants further investigation because *T. parva*, the causative agent of East Coast fever, is an important livestock pathogen for which vaccine deployment remains limited [49]. Cattle and camels are abundant in the UAE [6], and individual hosts may be exposed to both *Hyalomma* and *Rhipicephalus* ticks [50]. However, the present study did not demonstrate transmission of *T. parva* by *Hyalomma*, host co-infection, or movement of the organism between tick genera. Such epidemiological relationships therefore require direct investigation.

Epidemiological and One Health implications

The adaptation of *Hyalomma* ticks to arid environments [4], together with evidence that elevated temperatures can influence their reproductive biology [51], may affect their ecology and geographic distribution. The abundance of camels in the UAE [6], the diversity of microorganisms associated with camel ticks [5], and close interactions between humans and camels or camel farms [28, 52] further support continued surveillance of camel-associated tick-borne microorganisms.

From a One Health perspective, surveillance integrating ticks, animal hosts, environmental conditions, and relevant human–animal interfaces may improve understanding of the epidemiology of these microorganisms. However, the present findings are based on molecular detection in ticks and do not demonstrate pathogen transmission to camels or humans, clinical disease, or zoonotic transmission. The One Health relevance of the detected organisms should therefore be interpreted as a rationale for further investigation rather than evidence of established public health risk.

Strengths and limitations

A strength of this study was the relatively large molecular survey of 671 *H. dromedarii* ticks collected from camels across four Emirates of the UAE. The investigation simultaneously screened for five groups of tick-borne microorganisms and combined morphological and molecular tick identification with PCR screening, Sanger sequencing, and phylogenetic analysis. This multi-tiered approach provided molecular evidence of *Ehrlichia* and

Theileria in the sampled camel ticks.

Several limitations should be considered when interpreting the findings. Sampling was conducted predominantly during warmer periods because tick populations decline during colder periods, which may limit assessment of seasonal variation. Molecular characterization relied principally on the 16S rRNA and 18S rRNA genes, which are relatively conserved and may provide insufficient resolution for definitive species-level identification of closely related organisms. This limitation was particularly relevant to the *Theileria* sequence showing high similarity to *T. parva*. Experimentally determined limits of detection were also unavailable for the molecular assays. In addition, the low detection frequencies of *Ehrlichia* (0.30%) and *Theileria* (0.60%) limit broader epidemiological inference and indicate the need for expanded sampling and additional molecular characterization.

CONCLUSION

This study provides molecular evidence of *Ehrlichia* and *Theileria* in *H. dromedarii* ticks collected from camels across four Emirates of the UAE. Among the 671 ticks analyzed, *Ehrlichia* was detected in two samples (0.30%), whereas *Theileria* was detected in four samples (0.60%); *Anaplasma*, *Rickettsia*, and *Babesia* were not detected. The study provides the first molecular detection of *Ehrlichia* in *H. dromedarii* from the UAE. The detected *Theileria* sequence showed 98.96% identity to *T. parva* and clustered with *T. parva* reference sequences; however, species-specific PCR did not confirm *T. parva*. Therefore, the detected organism is appropriately interpreted as *Theileria* sp. genetically related to *T. parva*, rather than confirmed *T. parva*.

The detection of these microorganisms in camel-associated ticks expands current knowledge of the microorganisms associated with *H. dromedarii* in the UAE. Although the detection frequencies were low, the findings support continued molecular surveillance of camel ticks, particularly at interfaces involving camel movement, livestock populations, and human–animal contact. Such surveillance may facilitate the early recognition and molecular characterization of potentially important tick-borne microorganisms without assuming that their detection in ticks demonstrates transmission or disease in animal or human hosts.

Future studies should expand geographic and seasonal sampling and include larger numbers of ticks, camels, and, where relevant, other sympatric livestock hosts. Molecular characterization using additional species-specific markers, multiple genetic loci, or higher-resolution genomic approaches is required to establish the taxonomic identity of the detected organisms, particularly the *Theileria* sequence related to *T. parva*. Parallel investigation of ticks and their vertebrate hosts would help clarify host–tick–microorganism associations. Further studies should also investigate vector competence and transmission dynamics before assigning a vector role to *H. dromedarii* for newly detected microorganisms.

The detection of *Ehrlichia* and *Theileria* in *H. dromedarii* adds to the documented diversity of microorganisms associated with camel ticks in the UAE. Of particular importance, the study documents *Ehrlichia* in *H. dromedarii* in the UAE and identifies a *Theileria* sequence genetically related to *T. parva* but not confirmed as *T. parva* by species-specific PCR. These findings provide baseline molecular evidence for further epidemiological investigation and support continued surveillance of camel-associated ticks within a One Health framework.

DATA AVAILABILITY

Data are available on GenBank for both *Ehrlichia* (GenBank accession code: PP348046.1) and *Theileria* (GenBank accession number: PQ216298).

GENERATIVE AI DECLARATION

The authors declare that generative artificial intelligence (AI) tools were used solely to improve language, grammar, and readability during manuscript preparation. All scientific content, data analysis, interpretation of results, and conclusions were developed and verified by the authors. The authors take full responsibility for the accuracy, integrity, and originality of the work presented, and no AI tool was listed as an author.

AUTHORS' CONTRIBUTIONS

MAA: Conceptualization. MAA and SBM: Methodology. MTA and ASA: Investigation. MTA, MAA, and ASA: Formal analysis. MTA: Visualization. MAA: Supervision and project administration. MTA (lead) and MAA: Writing-original draft. MAA, MTA, and SBM: Writing-review and editing. All authors have read and approved the final version of the manuscript.

ACKNOWLEDGMENTS

The authors are thankful to Salwa Sultan for administrative assistance. In addition, we thank the UAE University Transportation Department for providing vehicles for field work. The funding for this study was provided by the UAE University through UPAR Grant no. G00003718.

COMPETING INTERESTS

The authors declare that they have no competing interests.

PUBLISHER'S NOTE

Veterinary World remains neutral with regard to jurisdictional claims in the published institutional affiliations.

REFERENCES

1. Neelakanta G, Sultana H. Tick saliva and salivary glands: what do we know so far on their role in arthropod blood feeding and pathogen transmission. *Front Cell Infect Microbiol.* 2022;12:816547.
2. Tahir D, Meyer L, Fourie J, Jongejan F, Mather T, Choumet V, *et al.* Interrupted blood feeding in ticks: causes and consequences. *Microorganisms.* 2020;8(6):910.
3. Estrada-Peña A, De La Fuente J. The ecology of ticks and epidemiology of tick-borne viral diseases. *Antiviral Res.* 2014;108:104–128.
4. Sajid MS, Kausar A, Iqbal A, Abbas H, Iqbal Z, Jones MK. An insight into the ecobiology, vector significance and control of *Hyalomma* ticks (Acari: Ixodidae): a review. *Acta Trop.* 2018;187:229–239.
5. Perveen N, Muzaffar SB, Al-Deeb MA. Ticks and tick-borne diseases of livestock in the Middle East and North Africa: a review. *Insects.* 2021;12(1):83.
6. FAOSTAT. FAO statistical database. Food and Agriculture Organization of the United Nations [Cited 29 April 2025] Available from: <https://www.fao.org/faostat/en/#data/QA>.
7. Kadim IT, Mahgoub O, Faye B, Farouk MM, editors. Camel meat and meat products. Wallingford: CABI; 2013.
8. Elsayy BSM, Abdel-Ghany SMH, Alzan HF, Abdel-Shafy S, Shahein YE. Molecular screening of piroplasms and Anaplasmatidae agents in *Hyalomma dromedarii* ticks from camels over different seasons in Egypt. *Exp Appl Acarol.* 2024;93:849–868.
9. Osman AM, Hassan-Kadle AA, André MR, Collere FCM, Córdova ASA, Montiani-Ferreira F, *et al.* Ehrlichia species in dromedary camels (*Camelus dromedarius*) and ruminants from Somalia. *Pathogens.* 2025;14(1):65.
10. Alanazi AD, Nguyen VL, Alyousif MS, Manoj RRS, Alouffi AS, Donato R, *et al.* Ticks and associated pathogens in camels (*Camelus dromedarius*) from Riyadh Province, Saudi Arabia. *Parasit Vectors.* 2020;13(1):110.
11. Barradas PF, Lima C, Cardoso L, Amorim I, Gärtner F, Mesquita JR. Molecular evidence of *Hemolivia mauritanica*, *Ehrlichia* spp. and the endosymbiont *Candidatus* Midichloria mitochondrii in *Hyalomma aegyptium* infesting *Testudo graeca* tortoises from Doha, Qatar. *Animals (Basel).* 2021;11(1):30.
12. Moraga-Fernández A, Muñoz-Hernández C, Sánchez-Sánchez M, Fernández de Mera IG, de la Fuente J. Exploring the diversity of tick-borne pathogens: The case of bacteria (*Anaplasma*, *Rickettsia*, *Coxiella* and *Borrelia*), protozoa (*Babesia* and *Theileria*) and viruses (*Orthonairovirus*, tick-borne encephalitis virus and louping ill virus) in the European continent. *Vet Microbiol.* 2023;286:109892.
13. Wang JQ, Yu T, Qiu HY, Ji SW, Xu ZQ, Cui QC, *et al.* Differential impact of spotted fever group *Rickettsia* and anaplasmosis on tick microbial ecology: evidence from multi-species comparative microbiome analysis. *Front Microbiol.* 2025;16:1589263.
14. Algeo L, Lincoln C. A case of anaplasmosis infection with rash and coinfection or antibody cross-reactivity. *J Maine Med Cent.* 2025;7(2):7.
15. Sormunen JJ, Vesterinen EJ, Klemola T. Ticks and tick-borne pathogens encountered by dogs and cats: a North European perspective. *Transbound Emerg Dis.* 2025;2025(1):5574554.
16. Alanazi AD, Alouffi AS, Alshahrani MY, Alyousif MS, Abdullah HHAM, Allam AM, *et al.* A report on tick burden and molecular detection of tick-borne pathogens in cattle blood samples collected from four regions in Saudi Arabia. *Ticks Tick Borne Dis.* 2021;12(3):101652.
17. Alvi MA, Javaid T, Yameen AB, Asghar F, Ali A, Zaheer I, *et al.* Molecular detection and genetic diversity of *Anaplasma* and *Ehrlichia* species in livestock and dogs in Pakistan. *Acta Trop.* 2025:107700.
18. Ullah Z, Liaqat I, Khan M, Alouffi A, Almutairi MM, Apanaskevich DA, *et al.* Investigation of *Hyalomma*

turanicum and *Hyalomma asiaticum* in Pakistan, with notes on the detection of tick-borne Rickettsiales. Front Vet Sci. 2024;11:1500930.

19. Alvez R, Félix ML, Santodomingo A, Parodi P, Thomas R, Muñoz-Leal S, *et al.* A survey for piroplasmids in questing *Ixodes fuscipes* ticks reveals undescribed *Babesia* lineages in Uruguay. Parasit Vectors. 2025;18(1):225.
20. Dini FM, Zordan A, Facile V, Balboni A, Magliocca M, Battilani M, *et al.* Tick-borne protozoa in dogs: combined diagnostic approaches reveal unnoticed carriers of *Hepatozoon canis* and *Theileria orientalis* among owned dogs in northern Italy. Res Vet Sci. 2025;193:105765.
21. Perveen N, Muzaffar SB, Al-Deeb MA. Four tick-borne microorganisms and their prevalence in *Hyalomma* ticks collected from livestock in the United Arab Emirates. Pathogens. 2021;10(8):1005.
22. Ngetich W, Gitau GK, Okumu TA, Aboge GO, Muasya D. Morbidity, mortality, and risk factors associated with seropositivity in a longitudinal calf study, Narok, Kenya. Vet Anim Sci. 2025;29:100456.
23. De la Fuente J, Sobrino I, Villar M. Design and evaluation of vaccines for the control of the etiological agent of East Coast fever. Parasit Vectors. 2024;17(1):517.
24. McFarland D, Fredericks LP, Hedlund T, Jones S, Keesing F, Mutinda M, *et al.* A suite of pathogens detected in ticks sampled from wildlife hosts in Central Kenya. Afr J Ecol. 2024;62(3):e13317.
25. Dreghiciu IC, Hoffman D, Florea T, Oprescu I, Dumitru S, Imre M, *et al.* A systematic review on the occurrence of *Babesia* spp. and *Anaplasma* spp. in ticks and wild boar from Europe: a 15-year retrospective study. Pathogens. 2025;14(7):612.
26. Mongkolphan C, Saechin A, Chamsai T, Sedwisai P, Boonyarittichai R, Tangsudjai S. *Ehrlichia canis* and *Hepatozoon* spp. in captive tigers in Thailand. Int J Parasitol Parasites Wildl. 2025;27:101105.
27. Tigani-Asil ETA, Blanda V, Abdelwahab GE, Al Hammadi ZM, Habeeba S, Khalafalla AI, *et al.* Molecular investigation on tick-borne hemoparasites and *Coxiella burnetii* in dromedary camels (*Camelus dromedarius*) in Al Dhafra region of Abu Dhabi, UAE. Animals (Basel). 2021;11(3):666.
28. Al-Deeb MA, Muzaffar SB. Prevalence, distribution on host's body, and chemical control of camel ticks *Hyalomma dromedarii* in the United Arab Emirates. Vet World. 2020;13(1):114–120.
29. Walker AR. Ticks of domestic animals in Africa: a guide to identification of species. Edinburgh: Bioscience Reports; 2003.
30. Apanaskevich DA, Schuster AL, Horak IG. The genus *Hyalomma*: VII. Redescription of all parasitic stages of *Hyalomma* (*Euhyalomma*) *dromedarii* and *Hyalomma* (*Euhyalomma*) *schulzei* (Acari: Ixodidae). J Med Entomol. 2008;45(5):817–831.
31. Al-Deeb MA, Muzaffar SB, Abu-Zeid A, Enan MR, Karim S. First record of a spotted fever group *Rickettsia* sp. and *Theileria annulata* in *Hyalomma dromedarii* (Acari: Ixodidae) ticks in the United Arab Emirates. Fla Entomol. 2015;98(1):135–139.
32. Mwamuye MM, Kariuki E, Omondi D, Kabii J, Odongo D, Masiga D, *et al.* Novel *Rickettsia* and emergent tick-borne pathogens: a molecular survey of ticks and tick-borne pathogens in Shimba Hills National Reserve, Kenya. Ticks Tick Borne Dis. 2017;8(2):208–218.
33. Tokarz R, Kapoor V, Samuel JE, Bouyer DH, Briese T, Lipkin WI. Detection of tick-borne pathogens by MassTag polymerase chain reaction. Vector Borne Zoonotic Dis. 2009;9(2):147–151.
34. Nijhof AM, Bodaan C, Postigo M, Nieuwenhuijs H, Opsteegh M, Franssen L, *et al.* Ticks and associated pathogens collected from domestic animals in the Netherlands. Vector Borne Zoonotic Dis. 2007;7(4):585–595.
35. Roux V, Raoult D. Phylogenetic analysis of members of the genus *Rickettsia* using the gene encoding the outer membrane protein rOmpB (*ompB*). Int J Syst Evol Microbiol. 2000;50(Pt 4):1449–1455.
36. Gubbels JM, De Vos AP, Van Der Weide M, Viseras J, Schouls LM, De Vries E, *et al.* Simultaneous detection of bovine *Theileria* and *Babesia* species by reverse line blot hybridization. J Clin Microbiol. 1999;37(6):1782–1789.
37. Getange D, Bargul JL, Kanduma E, Collins M, Bodha B, Denge D, *et al.* Ticks and tick-borne pathogens associated with dromedary camels (*Camelus dromedarius*) in northern Kenya. Microorganisms. 2021;9(7):1414.
38. Ugo UA, Hamzat MO, Aisida SO, Udoh I, Saha GC, Airenobuwa NA, *et al.* Phylogenetic analysis of 16S rRNA of *Pseudomonas* species isolated from clinical specimens in Nigeria and other regions. Open Access Res J Biol Pharm. 2024;11(1):13–30.

39. Narasimhan S, Fikrig E. Tick microbiome: the force within. *Trends Parasitol.* 2015;31(7):315–323.
40. Guglielmone AA, Robbins RG, Apanaskevich DA, Petney TN, Estrada-Peña A, Horak IG. The hard ticks of the world (Acari: Ixodida: Ixodidae). Dordrecht: Springer; 2014.
41. Gazder U, Ratrout NT. Determining factors affecting cross-border transport on King Fahd Causeway and comparison with urban travel. *Case Stud Transp Policy.* 2018;6(4):737–742.
42. Briggs C, Smith E, Vansandt J, Carr B, Loftin K, McDermott EG. Prevalence of *Ehrlichia* and *Anaplasma* spp. in ticks collected from cattle and deer in Arkansas, USA. *J Parasitol.* 2023;109(5):530–536.
43. Andrić B. Diagnostic evaluation of *Ehrlichia canis* human infections. *Open J Med Microbiol.* 2014;4(2):132–139.
44. Ismail N, McBride JW. Tick-borne emerging infections: ehrlichiosis and anaplasmosis. *Clin Lab Med.* 2017;37(2):317–340.
45. Choubdar N, Karimian F, Koosha M, Nejati J, Oshaghi MA. *Hyalomma* spp. ticks and associated *Anaplasma* spp. and *Ehrlichia* spp. on the Iran-Pakistan border. *Parasit Vectors.* 2021;14(1):576.
46. Hamed MI, Zaitoun AMA, El-Allawy TA, Mourad MI. Investigation of *Theileria camelensis* in camels infested by *Hyalomma dromedarii* ticks in Upper Egypt. *J Adv Vet Res.* 2011;1:4–7.
47. Silatsa BA, Simo G, Githaka N, Kamga R, Oumarou F, Keambou Tiambo C, *et al.* First detection of *Theileria parva* in cattle from Cameroon in the absence of the main tick vector *Rhipicephalus appendiculatus*. *Transbound Emerg Dis.* 2020;67(S1):68–78.
48. Stadhouders R, Pas SD, Anber J, Voermans J, Mes THM, Schutten M. The effect of primer-template mismatches on the detection and quantification of nucleic acids using the 5' nuclease assay. *J Mol Diagn.* 2010;12(1):109–117.
49. Nene V, Morrison WI. Approaches to vaccination against *Theileria parva* and *Theileria annulata*. *Parasite Immunol.* 2016;38(12):724–734.
50. Monakale KS, Smith RM, Gaorekwe RM, Ledwaba MB, Malatji DP. Phenotypic and genotypic characterization of ticks and tick-borne pathogens from cattle in selected villages of Greater Letaba Municipality in Limpopo Province, South Africa. *Parasitol Res.* 2024;123(8):317.
51. ElGhali A, Hassan SM. Life cycle of the camel tick *Hyalomma dromedarii* (Acari: Ixodidae) under field conditions in Northern Sudan. *Vet Parasitol.* 2010;174(3–4):305–312.
52. Yusof MF, Eltahir YM, Serhan WS, Hashem FM, Elsayed EA, Marzoug BA, *et al.* Prevalence of Middle East respiratory syndrome coronavirus (MERS-CoV) in dromedary camels in Abu Dhabi Emirate, United Arab Emirates. *Virus Genes.* 2015;50(3):509–513.
