

# PREVALENCE OF *Theileria annulata* AND THE FIRST REPORT OF *Theileria sinensis* IN CATTLE FROM ERBIL PROVINCE, IRAQ

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## ABSTRACT

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Bovine theileriosis is a significant tick-borne protozoan disease of cattle, primarily caused by species of the genus *Theileria*. This study investigated the prevalence of bovine theileriosis in cattle using both microscopic examination and conventional PCR (c-PCR). Microscopic analysis of Giemsa-stained blood smears identified an infection rate of 51/236 (21.6%), while c-PCR revealed a significantly higher prevalence of 106/236 (44.9%). *Theileria* species were characterized morphologically and confirmed via molecular methods. PCR analysis identified *Theileria annulata* and *Theileria sinensis* as the causative agents, with *T. annulata* showing the highest rate of single infections 89/106 (84%) compared to *T. sinensis* 17/106 (16%). Mixed infections were detected in 13/106 (12.3%) of cases. Age, sex, breed, housing conditions, acaricide use, and tick infestation were identified as key risk factors influencing infection rates. Management and tick-related factors significantly influenced *Theileria* prevalence, with higher infection rates observed in cattle with tick infestation 54/102 (52.9%), irregular or no acaricide use 58/115 (50.4%) and 27/47 (58.7%) respectively, non-cemented floors 72/125 (57.6%), and tick presence in barns 64/127 (50.4%). Phylogenetic analysis demonstrated genetic similarities between the identified *T. annulata* and *T. sinensis* sequences and strains reported from other geographical regions. Notably, this study provides the first report of *T. sinensis* in Iraq, highlighting its emergence and underscoring the need for enhanced surveillance and control measures against *Theileria* infections in the country. The high prevalence of the disease underscores the urgent need for enhanced surveillance, effective tick control measures, and the implementation of integrated strategies to mitigate the impact of bovine theileriosis on cattle health and productivity.

**KEYWORDS:** Molecular; Epidemiology, *Theileria annulata*; *Theileria sinensis*; Cattle.

## 1. INTRODUCTION

Bovine theileriosis is a tick-borne haemoprotozoan disease of cattle, classified under the kingdom Protista. It is transmitted by hard ticks of the genera *Hyalomma*, *Rhipicephalus*, and *Haemaphysalis* and leads to major economic losses in the cattle industry. The tropics and subtropical regions are where the disease is most prevalent (Ismael & Omer, 2021; Larcombe *et al.*, 2022; Shahedi *et al.*, 2022).

Bovine theileriosis is globally distributed, and it poses a serious risk to livestock production. *Theileria annulata*, *T. orientalis*, *T. velifera*, *T. sergenti*, *T. mutans*, and *T. sinensis* are major species, the latter of which is very closely related phylogenetically to *T. orientalis*, and has recently been discovered as a causative agent of bovine theileriosis in China and Malaysia (Kamani *et al.*, 2023; Liu *et al.*, 2010; Qin *et al.*, 2016). The host's immune

status, particularly its acquired immunity, along with the *Theileria* species, determined the virulence and impact of infections. *Theileria orientalis* and *Theileria sinensis* have been reported to be associated with non-symptomatic or benign infections (Liu *et al.*, 2010; McFadden *et al.*, 2011). While varying degrees of pathogenicity and eliciting serious clinical signs in cattle, such as anemia, and jaundice, are found in *T. orientalis* genotypes such as Ikeda, Chitose, and Buffeli infections (Oakes *et al.*, 2019; Schnittger *et al.*, 2022; Lakew *et al.*, 2023). Highly pathogenic tropical theileriosis was recorded in *T. annulata* infection (McFadden *et al.*, 2011; Ota *et al.*, 2009). The availability of susceptible hosts and environmental parasite vectors is factored as an important factor in the prevalence, intensity, and transmission of theileriosis. Chronic carriers typically serve as reservoirs for the disease. Additionally, the prevalence of *Theileria*

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infections is also found to be determined by biological factors like sex, breed, management systems, habitat type, and tick infestation (Riaz & Tasawar, 2017; Larcombe *et al.*, 2022).

In warm or temperate climates, ixodid ticks serve as vectors for the transmission of *Theileria* species by injecting the pathogen into bovine blood (Payne *et al.*, 2009; Zangana and Naqid, 2011). *Hyalomma anatolicum*, the three-host tick, plays a significant role in *Theileria* spp. since it possesses the capability of transstadial transmission. Likewise, *H. dentritum*, *H. marginatum*, *H. asiaticum*, and *Rhipicephalus turanicus* are crucial vectors for *Theileria* spp. Due to their transstadial transmission capability (Zangana *et al.*, 2013). Apart from the cattle breed and the pathogen, additional determinants of risk, such as intensity of tick infestation and age of animal, influence the severity of the illness (Al-Saeed & AL-Badrani, 2014; Li *et al.*, 2020; Gharbi *et al.*, 2020; Kozhabaev *et al.*, 2023; Norouzi *et al.*, 2023).

The most common symptoms of tropical theileriosis include fever, extensive ocular and nasal discharge, hypersalivation, swelling of superficial lymph nodes, respiratory distress, icterus, and, in severe cases, death due to asphyxiation (Omer *et al.*, 2003). The most common lesions in infected cattle are pulmonary emphysema, lymph node enlargement, splenomegaly, and subcutaneous and intramuscular hemorrhages. Hepatomegaly is also extremely common, followed by pleural and pericardial fluid excessive accumulation (Ma *et al.*, 2020).

Traditional diagnosis of theileriosis is based on microscopy and clinical presentation, wherein lymph node smears are stained to see the schizont stage and blood smears are stained to see piroplasm's (Aulakh & Singla, 2006). Parasites cannot be seen by these traditional methods during subclinical and chronic phases of disease due to extremely low parasitemia (Tuli *et al.*, 2015). Thus, genetic and serological tests have been considered to be more sensitive methods for diagnosis of tropical theileriosis (TP) (Aktas *et al.*, 2006; Liu *et al.*, 2008; Tuli *et al.*, 2015).

Given the limited data on the prevalence of bovine theileriosis in Erbil Province, the present study aims to investigate the presence of *Theileria* species in cattle using both microscopic and molecular diagnostic techniques. Additionally, the study seeks to identify potential risk factors and management practices associated with the prevalence of disease, and to characterize the molecular epidemiology of *Theileria* in the region.

## 2. MATERIAL AND METHODS

### Sample Collection and Study Design:

This cross-sectional study was conducted in Erbil city, north Iraq, between June and October 2024. In total,

236 (97 from males and 139 from females) blood samples were collected randomly from the coccygeal vein of cattle. Clinical signs such as raised body temperature, weakness, lymph node swelling, rapid respiration, and nasal discharge were observed at the time of sampling. Diagnosis was achieved by clinical examination and laboratory confirmation through Giemsa staining of blood smears. Besides sample collection, a previously designed questionnaire was used to acquire information on the farms and animals, including location, sex, age, breed, and risk factors such as acaricide use, floor types, tick presence in barns, and tick infestation. Multivariable analysis was performed to assess the association between these risk factors and *Theileria* infection rates.

### Examination of Blood Stain:

Aseptically, blood samples were collected from the coccygeal vein of every animal and placed in EDTA tubes. Then, thin and thick blood smears were prepared, air-dried, fixed with 70% methanol for 5 minutes, and stained with 10% of Giemsa stain for 30–40 minutes. The smears were then examined using a microscope at 100X oil immersion magnification to identify and examine the morphological characteristics of *Theileria* species and the estimation of parasitemia according to the protocol described by Zajac *et al.* (2021). The remaining blood samples were stored at  $-20^{\circ}\text{C}$  for molecular work.

### DNA Extraction and PCR Amplification:

DNA was extracted from the blood samples using a commercial DNA isolation kit (AddBio, South Korea), as indicated by the manufacturer. Genomic DNA concentration ( $\text{ng}/\mu\text{L}$ ) was measured using a NanoDrop spectrophotometer (IMPLEN, Germany). The extracted genomic DNA was stored at  $-20^{\circ}\text{C}$  until polymerase chain reaction (PCR) analysis. The *Theileria annulata* merozoite surface antigen 1 (Tams1) and 18S rRNA genes were amplified by species-specific PCR using primers specific to *T. annulata* and *T. sinensis*, respectively (Table 1). PCR amplification was performed with a gradient thermal cycler (BioRad, Canada) as described by (Albakri *et al.*, 2024). The cycling conditions for *Theileria* spp., *T. annulata* and *T. sinensis* are begin with DNA denaturation at  $95^{\circ}\text{C}$  for five minutes. Following this, DNA from all species was denatured for one minute at  $94^{\circ}\text{C}$ . Next, the primer annealing occurs at  $55^{\circ}\text{C}$  for 45 seconds for *Theileria* spp.,  $60^{\circ}\text{C}$  for *T. annulata*, and  $56^{\circ}\text{C}$  for 1 minute for *T. sinensis*. The extension step was performed for one minute at  $72^{\circ}\text{C}$  for all species. To amplify the DNA, steps 3 through 5 are repeated 35 times. Finally, a 7-minute extension was carried out at  $72^{\circ}\text{C}$ , after which the samples were stored at  $4^{\circ}\text{C}$  until removed. After amplification, the PCR products were run on a 1.5% agarose gel and visualized using a gel documentation system.

**Table 1:** Primers used to amplify the 18S rRNA and Tams genes of *Theileria* spp.

Amplified gene	Sequences 5'-3'	Binding Temperature	Product size (bp)	References
989F	5'- AGTTTCTGACCTATCAG -3'	55°C.	1098	d'Oliveira <i>et al.</i> , 1995
990R	5'- TTGCCTTAAACTTCCTTG -3'			
Tams1F	5'- ATGCTGCAAATGAGGAT -3'	60°C	785	Kirvar <i>et al.</i> , 2000
Tspms1R	5'- GGACTGATGAGAAGACGATGAG -3'			
Tsin-F	5'- CACTGCTATGTTGTCCAAGAGATATT -3'	56°C	887	Liu <i>et al.</i> , 2010
Tsin-R	5'- AATGCGCCTAAAGATAGTAGAAAAC -3'			

989F: *Theileria* spp. Universal forwards primers, 990R: *Theileria* spp. Universal reverse primers, Tams1F: *T. annulata* - targeted forward primer, Tspms1R: *T. annulata* - targeted reverse primer, Tsin-F: *T. sinensis* - targeted forward primer, Tsin-R: *T. sinensis* - targeted reverse primer.

### DNA Sequencing and phylogenetic Analysis:

In the present study, three sets of PCR primers targeting universal *Theileria* spp., *T. annulata*, and *T. sinensis* that yielded positive amplification via conventional PCR were submitted to a commercial sequencing facility (Macrogen Inc., South Korea) for purification and Sanger dideoxy sequencing. The resulting sequences were compared against existing entries in the GenBank database using the BLAST algorithm. Multiple sequence alignments were conducted with MEGA X software (<http://www.megasoftware.net>, July 2016), employing the MUSCLE algorithm to align sequences alongside reference entries from NCBI GenBank (Edgar, 2004). A phylogenetic tree was subsequently constructed using the Neighbor-Joining method, and the robustness of the branching patterns was assessed through 1,000 bootstrap replicates (Tamura *et al.*, 2021).

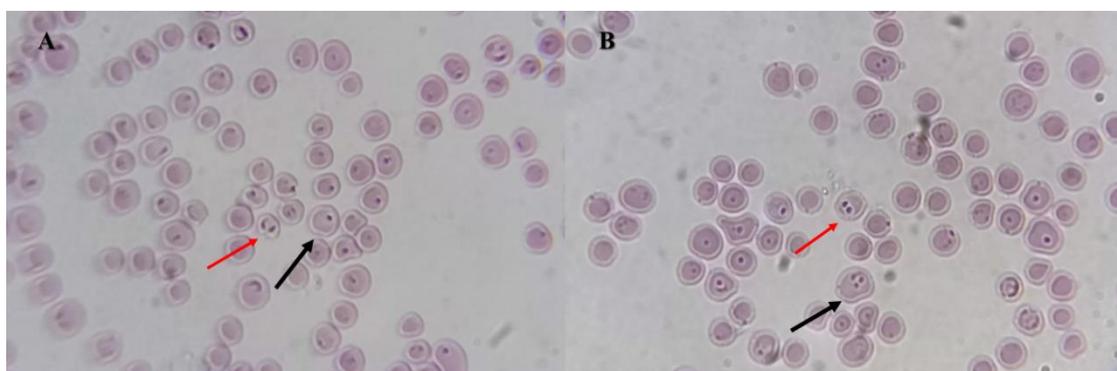
### Statistical Analysis:

To assess differences in prevalence rates among the studied groups, Chi-square and Fisher's exact tests were

applied. Furthermore, binomial logistic regression was performed using GenStat, 12<sup>th</sup> Edition, to estimate the odds ratios along with their corresponding 95% confidence intervals. A p-value of less than 0.05 was regarded as the threshold for statistical significance (Payne *et al.*, 2009).

### 3. RESULTS

Giemsa-stained blood smears were employed to determine the prevalence of bovine theileriosis, revealing an infection rate of 21.6% (51/236). *Theileria* sp, were identified based on the physical characteristics of merozoites observed in infected red blood cells (RBCs). The parasites predominantly appeared as small, double pyriform structures with acute or obtuse angles. Additionally, as illustrated in Figure 1, they exhibited diverse morphological forms, including oval, spherical, and the distinctive double pear shape. The infection rate was 21.6% (51/236) by microscopic examination and 44.9% (106/236) by molecular analysis, as summarized in Table 2.



**Figure 1:** Morphological forms of *Theileria* spp. Within infected erythrocytes stained with Giemsa, examined under oil immersion lens (100X); A) Two pear-shaped merozoites (red arrowhead), One round-shaped merozoite (black arrowhead); B) Two round-shaped merozoites (red arrowhead), three round -shaped merozoites (black arrowhead).

**Table (2):** Prevalence rates of *Theileria* spp. in cattle by microscopic and c-PCR examination.

Status	Total Tested Sample	Total Positive Samples	%	P value
Microscopy	236	51	21.6	0.001
c-PCR		106	44.9	

The prevalence of *Theileria* species infection in cattle is presented in Table 3. Out of the total of 106 positive samples, 89 (84%) were found to be infected with *Theileria annulata*, while 17 (16%) were infected with

*Theileria sinensis*. A mixed infection was observed in 13 (12.3%) cattle. Statistical analysis revealed a significant association between *T. annulata* infection and the total prevalence ( $p < 0.001$ ).

**Table (3):** Prevalence rates of *Theileria* sp. infection in Cattle

<i>Theileria</i> Species	Cattle	
	No. (%)	*p-value
<b>Single infection</b>		
<i>T. annulata</i>	89 (84)	0.001
<i>T. sinensis</i>	17 (16)	
<b>Mixed infection</b>	13 (12.3)	
<b>Total</b>	106	

\* p-value is determined using ( $p\text{-value} \leq 0.05$ )

**Multivariable Analysis of Molecular Prevalence of *Theileria* spp:**

Table 4 revealed the prevalence of *Theileria* spp. Based on sex, age, breed, and the purpose of keeping cattle. In the current research, the prevalence rates of *Theileria* spp. in female cattle was higher (49.6%) compared to males (38.1%). The odds of infection were 1.6 times higher in females than in males (CI: 0.91–2.81), with a significant difference ( $p < 0.05$ ). Cattle aged 2–4 years had a prevalence rate of 53.8%, with odds of infection 1.8 times greater than cattle of other age groups

(CI: 1.02–3.17), showing a significant difference ( $p < 0.001$ ). In contrast, cattle older than 4 years had the lowest prevalence (23.2%), while those under 2 years of age showed a prevalence of 49.4%. Imported breeds exhibited a higher prevalence of infection (49.2%) compared to local breeds (28.6%). The odds of infection were 2.42 times higher in imported breeds compared to local breeds (CI: 0.19–0.85), with a significant difference ( $p < 0.007$ ). However, no significant differences in the prevalence of *Theileria* spp. were observed between cattle kept for dairy production (49.3%) and those raised for beef production (38.8%).

**Table (4):** Sex, age, breed and purpose of keeping score -wise prevalence of *Theileria* sp. by c-PCR.

Factor	No. of examined cattle	c-PCR			
		No. of positive sample	Percentage (%)	OR (95%CI)	P value
<b>Gender</b>					
Female	139	69	49.6	1.6 (0.91 to 2.81)	0.05
Male	97	37	38.1	0.63 (0.36 to 1.10)	
<b>Age group</b>					
<2	89	44	49.4	1.34 (0.76 to 2.35)	0.001
2-4	91	49	53.8	1.8 (1.02 to 3.17)	

>4	56	13	23.2	0.28 (0.13 to 0.58)	
<b>Breeds</b>					
Local	49	14	28.6	0.41 (0.19 to 0.85)	0.007
Imported	187	92	49.2	2.42 (1.17 to 5.19)	
<b>Purpose of keeping</b>					
Dairy	138	68	49.3	1.53 (0.88 to 2.69)	0.071
Beef	98	38	38.8	0.65 (0.37 to 1.14)	
<b>Total</b>	236	106	44.9		

N=Number of positive samples, CI=Confidence interval, OR=Odd ratio

**Association of Molecular Prevalence of *Theileria* spp with Management and Tick Vector Factors:**

The current research showed that the prevalence of *Theileria* spp. was not statistically significant between cattle kept alone (45.2%) and those mixed with other animal species in stables (43.9%). Similarly, while grazing style did not show a statistically significant difference, cattle that grazed had a higher prevalence of infection (51.6%) compared to those kept in barns (42.4%), as presented in Table 5. Cattle with tick infestations had a prevalence rate of 52.9% and were 1.77 times more likely to be infected compared to those without tick infestations (CI: 1.02–3.09), with statistically significant differences

( $p < 0.021$ ). Additionally, cattle that did not receive acaricide treatment showed the highest prevalence (58.7%), with significantly increased odds of infection compared to those treated regularly (28%) or irregularly (50.4%) (CI: 0.99–4.08;  $P < 0.001$ ). Cattle housed on non-cemented floors had three times higher odds of infection compared to those housed on cemented floors (CI: 1.74–5.46), with significant differences ( $P < 0.001$ ). The prevalence was 57.6% in cattle housed on non-cemented floors, compared to 30.6% of those on cemented floors. Moreover, barns with ticks present exhibited a higher prevalence (50.4%) compared to barns without ticks (39.6%). The odds of infection were 1.65 times higher in barns with ticks (CI: 0.93–2.82;  $p = 0.045$ ) (Table 5).

**Table (5):** Management and Tick Vector Factor Scores and Prevalence rates of *Theileria* spp. by c-PCR.

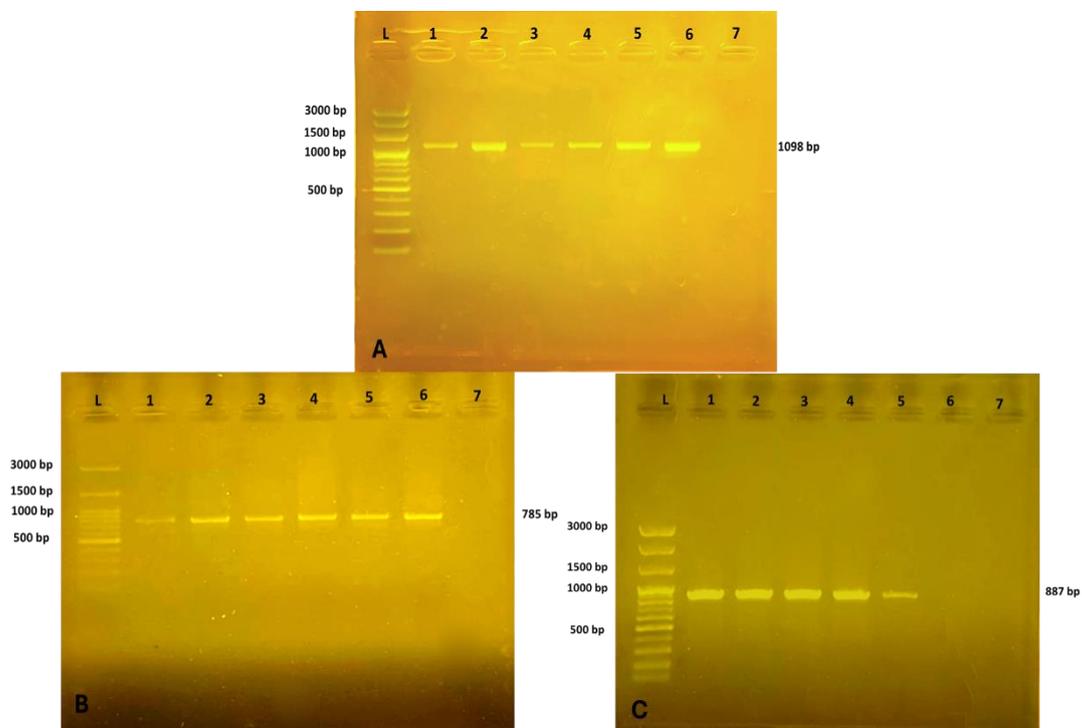
Factor	No. of examined cattle	c-PCR			p
		No. of positive sample	Percentage (%)	OR (95%CI)	
<b>Animals in stable</b>					
Only cattle	197	89	45.2	1.07 (0.51 to 2.28)	0.499
Mixed with other animals	39	17	43.9	0.94 (0.44 to 1.98)	
<b>Management</b>					
In grazing	64	33	51.6	1.44 (0.78 to 2.68)	0.135
In barn	172	73	42.4	0.69 (0.37 to 1.28)	
<b>Tick infestation</b>					
Present	102	54	52.9	1.77 (1.02 to 3.09)	0.021
Absent	134	52	38.8	0.56 (0.32 to 0.98)	
<b>Acaricides application</b>					

No	46	27	58.7	2.0 (0.99 to 4.08)	
Regular	75	21	28	0.35 (0.18 to 0.65)	0.001
Irregular	115	58	50.4	1.55 (0.89 to 2.68)	
<b>Floor</b>					
<b>Cemented</b>	111	34	30.6	0.33 (0.18 to 0.58)	
<b>Non cemented</b>	125	72	57.6	3.08 (1.74 to 5.46)	0.001
<b>Tick existence in barn</b>					
<b>Yes</b>	127	64	50.4	1.65 (0.93 to 2.82)	
<b>No</b>	109	42	39.6	0.62 (0.35 to 1.07)	0.045
<b>Total</b>	236	106	44.9		

N=Number of positive samples, CI=Confidence interval, OR=Odd ratio

The results of the amplified (PCR) product using general or universal primers (Macrogen Inc., South Korea) revealed that the DNA band size for the initial reaction was 1098 bp, indicating a positive presence of *Theileria* spp.

(Figure 2A). In contrast, the second reaction using specific primers for *T. annulata* displayed a DNA band size of 785 bp while specific primers for *T. sinensis* displayed a DNA band size of 887 bp (Figure 2C).



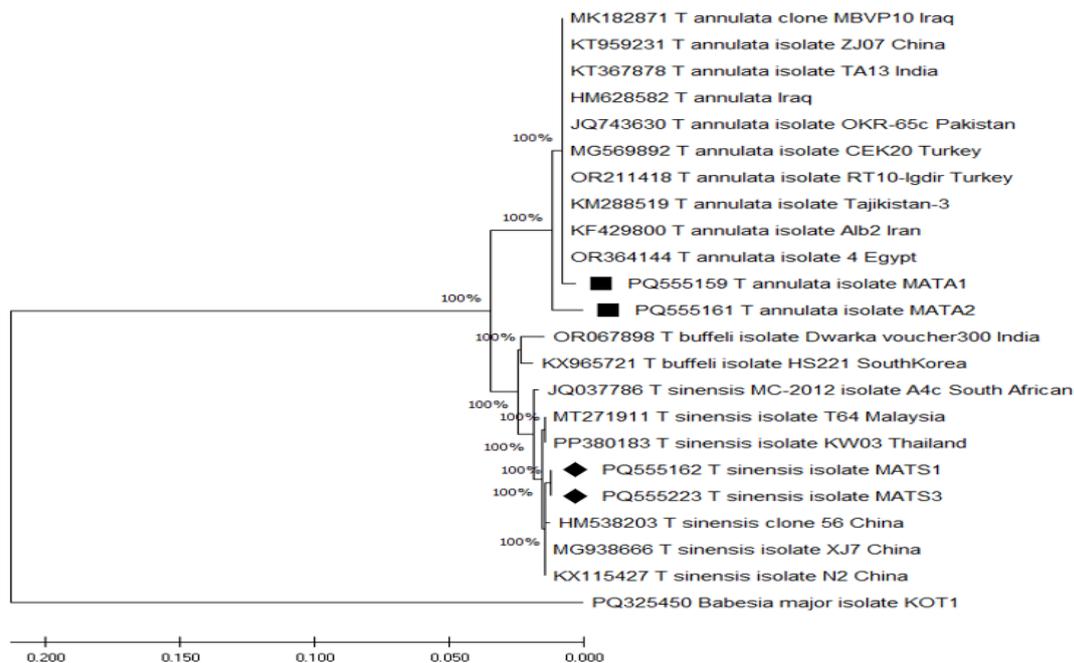
**Figure 2:** PCR gel electrophoresis results for *Theileria* detection. Lane M shows the 100 bp DNA ladder. (A) Lanes 1–6 show clear bands at approximately 1098 bp, indicating positive samples for *Theileria* spp.; lane 7 was used as a negative control. (B) Lanes 1–6 display bands at approximately 785 bp, confirming *T. annulata*; lane 7 was used as a negative control. (C) Lanes 1–5 show bands at approximately 887 bp, indicating positive results for *T. sinensis*; lane 7 was used as a negative control.

The sequences of the DNA of the 18S rRNA gene have been made available at NCBI GenBank under the accession numbers: *T. annulata*: (PQ555159 and PQ555161); *T. sinensis*: (PQ555162 and PQ555223).

Phylogenetic trees of 18S rRNA sequence analyses based on a neighbor-joining program showed that *Theileria* spp. have a relation to *T. annulata* and *T. sinensis*. The two sequences blasted with previous GenBank registration and found that PQ555159 and PQ555161 showed 99.03% identity with HM628582/Iraq,

MG569892/Turkey, KF429800/Iran, KT367878/ India, KT182871/China and OR364144/Egypt to those sequences previously reported *T. annulata* in NCBI GenBank (Figure 3).

A phylogenetic tree of *T. sinensis* showed that the two sequence isolates (PQ555162 and PQ555223) observed in the present study clustered with HM538203/China, PP380183/ Thailand, MT271911/Malaysia and JQ037786/South Africa (Figure 3).



**Figure 3:** Phylogenetic tree showing *Thieleria* spp. some partial 18S sequences of the isolates. The sequences in this study are marked with a black square for *T. annulata* and black diamond for *T. sinensis*. The clade supports were indicated by the bootstrap values (from 1000 replicates) at each node. MEGA X software was employed to conduct the analysis and *Babesia major* (PQ325450) was the outgroup.

**4. DISCUSSION**

This study represents the first comprehensive investigation into the management practices and risk factors influencing bovine theileriosis in Erbil, Iraq. As one of the foremost tick-borne diseases, bovine theileriosis represents a serious threat to the health and productivity of cattle, especially in tropical and subtropical areas (Valente *et al.*, 2022). Study results showed a 21.6% prevalence based on examination of microscopically and 44.9% with PCR testing, indicating the advantage of sensitivity with molecular testing for sub-clinical infections. The findings are in line with earlier research, including that conducted by Aktas *et al.* (2006) in Turkey. PCR is more sensitive and specific than blood smear examination, allowing for the detection of low-level or subclinical Babesia infections

that are often missed under microscopy due to low parasitemia or observer limitations (Almería *et al.* 2001).

The study found that several risk factors are associated with theileriosis prevalence. Age emerged as a significant determinant, with the highest prevalence of the disease observed in cattle aged 2–4 years. This could be due to greater exposure to tick infestation, exacerbated by physiological stressors of first lactation and reproductive cycles (Tuli *et al.*, 2015). Younger calves were less at risk of infection as they had less exposure to pastures and tick infestation. These findings are analogous to those conducted by Bishop *et al.* (2008) that link grazing behavior to vector contact. Differences were also noted among the genders, where the prevalence of the disease was higher in females than males, even though the differences were not statistically significant. This

increased susceptibility in females could be attributed to endocrine changes during pregnancy and lactation, along with prolonged physiological stress (Almería *et al.* (2001). More studies are needed to clarify the differences in the adaptive and innate immune response between genders in terms of *Theileria* infection.

Cattle breed was identified as the second risk factor in this study, which was more common in exotic and crossbred cattle than in native breeds. These differences could be due to the long-term adaptation of the local breed to local conditions, which provides an enzootic, stable habitat and tick resistance. These findings are in line with Zeb *et al.* (2020), who found that the local breed's resistance to disease stressors. The higher percentage of disease was among those with Tick infestation. Earlier studies, as shown by Aziz & Al-Barwary (2019) Highlighting the interaction between tick infestation and infection, it highlights the importance of effective tick control in controlling disease. Grazing practices also found to play a role in the prevalence of the disease; free-roaming cattle in tick-infested grazing fields had a higher risk of contracting the disease than cattle kept in barns, where exposure to tick vectors was decreased (Tuli *et al.*, 2015).

Living conditions also proved a vital determinant, with cattle raised on non-cemented floors exhibiting far higher prevalence rates than those raised on cemented floors. Poor drainage and sanitation in non-cemented floors predispose the survival and proliferation of ticks, promoting infection. The same has been reported by Simuunza *et al.* (2011), crediting the contribution of environmental conditions towards the transmission of disease. Another of the critical factors that were determined was application of acaricides, with nonuniform or none acaricide application leading to significantly greater infection. This underlines the significance of frequent acaricide application as a pillar of disease avoidance, as also indicated by Selim *et al.* (2022). All these findings point towards the worth of integrated management measures in reducing disease prevalence. Molecular characterization provided additional data on genetic diversity of *Theileria* sp. in the region. Phylogenetic analysis revealed high genetic identity among *T. annulata* and *T. sinensis* strains from the region and neighboring countries such as Turkey, Iran, and China, suggesting regional patterns of transmission. The first detection of *T. sinensis* in Iraq adds valuable epidemiological information. The main strength of this study is its combined microscopic and molecular approach, enhancing diagnostic accuracy. However, its limitation is the restricted sampling to one governorate and a short time frame, which may not represent the entire country. Future studies across more regions and seasons are recommended.

## CONCLUSION

The study emphasizes how host, environmental, and management factors interact to affect the epidemiology of bovine theileriosis. Age, breed, management status, tick infestation, and acaricide therapy were identified as significant risk factors for infection. The phylogenetic relatedness and genetic diversity of *Theileria* species necessitate integrated control programs. To minimize the effects of bovine theileriosis, a combination of vector control, better housing, extensive acaricide use, and focused observation is essential. Future research should focus on understanding host-pathogen interactions and developing sustainable countermeasures to address the multifaceted problems posed of this disease.

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### Ethics approval:

Ethical Committee Number (CVM2024/1205UoD).

### Author contribution

Both authors contributed equally to the design of the research, the performance of experiments, data analysis, and the writing of the paper.

### Conflict of Interest:

The authors declare no conflicts of interest

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