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An Insight into Genetic Diversity and Risk Factors of Ovine and Caprine Babesiosis in Erbil Governorate, Northern of Iraq

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A B S T R A C T

Ovine and caprine babesiosis is a significant tick-borne disease affecting small ruminants, causing economic losses and health challenges in endemic regions such as northern Iraq. This study aimed to determine the prevalence, molecular characteristics, and associated risk factors of *Babesia* spp. infections in small ruminants in Erbil Province, Iraq. A total of 235 animals (125 sheep and 110 goats) were clinically examined and sampled between October 2024 and March 2025. Blood smears were screened microscopically, and DNA was extracted from the blood sample collected for molecular detection. PCR targeting the 18S rRNA gene of *Babesia* spp., *B. ovis*, and *B. motasi* was carried out using the extracted DNA from the blood samples. Microscopic examination results revealed infection rates to be 16.8% in sheep and 8.2% in goats, while PCR-based detection showed notably higher prevalence, 28.8% and 12.7%, respectively. Sequencing and phylogenetic analysis of *B. ovis* isolates confirmed strong genetic similarity with regional strains from Turkey, Iran, and Iraq. Additionally, the presence of *B. ovis* sequences clustering with those from non-ruminant hosts (e.g., rabbits and horses) was observed. Notably, *Babesia motasi* was not detected in any of the examined samples. Risk factor analysis demonstrated significant associations between infection and tick infestation, lack of acaricide use, and prior exposure to ticks. Specifically, tick-infested animals exhibited markedly higher infection rates, with odds ratios of 9.93 for sheep and 4.16 for goats. However, no statistically significant differences were observed concerning sex, age, or grazing system. These findings underscore the continued threat of Babesia infections among small ruminants in northern Iraq and highlight the need for improved tick control strategies to mitigate disease transmission.

Keywords: risk factors; molecular; babesiosis; sheep, goats

INTRODUCTION

Tick-borne protozoal diseases, particularly those are caused by *Babesia* species, are recognized for their substantial economic losses on small ruminant farming. These losses stem from both direct effects, such as morbidity and mortality in sheep and goats, and indirect consequences, including reduced productivity and increased veterinary expenditures, especially in tropical and subtropical regions (**1, 2**). In Iraq, microscopic examinations have identified several *Babesia* species in goats, including *B. ovis*, *B. motasi*, *B. foliata*, and *B. taylori*, particularly in Mosul and Sulaimani provinces. However, data on the presence and distribution of *Babesia* spp. in Erbil Province remain scarce and largely unverified by molecular methods (**3, 4**).

The epidemiology of babesiosis is intrinsically linked to the ecology and distribution of its tick vectors. Notable tick species implicated in the transmission of *Babesia* include *Rhipicephalus bursa*, *R. turanicus*, *Hyalomma anatolicum* excavatum, and potentially *R. evertsi evertsi* (**5, 6**). Clinical manifestations in infected small ruminants commonly

include anorexia, pallor of mucous membranes, fever, jaundice, weight loss, nasal discharge, recumbency, hemoglobinuria, and in severe cases, death (**7, 8**).

Traditionally, microscopic examination of Giemsa-stained blood smears has been the standard method for detecting *Babesia* spp. (**9**). However, molecular diagnostics, particularly polymerase chain reaction (PCR) have gained prominence in recent years due to their superior sensitivity and specificity. PCR not only enables detection at low parasitemia levels but also facilitates species-level identification and the recognition of mixed infections in endemic settings (**2, 10, 11**).

Despite Erbil Province's significance as a major livestock-producing region in Iraq, research on *Babesia* spp. infections in sheep and goats had remained scarce. To address this critical gap, the present study employed both microscopic and molecular diagnostic techniques to detect and identify Babesia species infecting small ruminants across the province. It further investigated the prevalence of infection and examined associations with host-related factors such as age and sex, as well as seasonal patterns and the distribution of tick vectors. By offering novel insights into the molecular identification and associated risk factors of *Babesia* spp., the findings aimed to guide the development of more effective control and management strategies, ultimately leading to improved animal health and increased productivity in the region's livestock sector.

MATERIALS AND METHODS

Ethical Approval

All procedures and methodologies employed in this study were conducted in accordance with the ethical guidelines of the Scientific Ethical Committee on Animal Experimentation, College of Veterinary Medicine, University of Duhok (Approval No. CVM2024/011UoD).

Sampling and Microscopic Examination

A total of 235 clinically examined domestic small ruminants, comprising 125 sheep and 110 goats of various ages and both sexes, were randomly selected from multiple farms across Erbil Province, Iraq, between Oct 2024 and March 2025. The sample size was determined according to Thrusfield (**12**). Blood samples were aseptically collected from the jugular vein using EDTA-coated vacutainers to prevent coagulation. Thin blood smears were prepared from each sample, air-dried, fixed with 99% methanol for 5 min, and stained using a 10% Giemsa solution (Atom Scientific Ltd., Cheshire, UK) for 30 min. The stained smears were examined under a light microscope at 1000× magnification using an oil immersion lens to identify *Babesia* spp. based on morphological characteristics (**13**). The remaining blood samples were stored at −20°C for subsequent molecular analysis.

Data Collection

Structured questionnaires were employed to collect data at both the herd and individual animal levels during sampling. Detailed clinical examinations were conducted to assess the health status of each animal, with recorded variables including sex, age, and observed clinical symptoms. Information on potential risk factors such as tick infestation levels, presence of ticks within the housing environment including (presence of ticks in animal housing, bedding materials, proximity to vegetation harboring ticks), acaricide usage, and general management practices were also gathered. All data were compiled for subsequent statistical analysis to determine associations with the prevalence and distribution of *Babesia* infection.

Genomic DNA Isolation and PCR-Based Amplification

Genomic DNA was extracted from 200 µL of EDTA-preserved whole blood using the Primary Prep™ Genomic DNA Extraction Kit (addbio, Korea), following the manufacturer's instructions. To detect and differentiate *Babesia* species, PCR was conducted targeting a conserved region of the 18S rRNA gene. Three sets of primers were used to amplify fragments specific to *Babesia* spp., *B. ovis*, and *B. motasi* (**Table 1**).

Table 1. PCR primers targeting the 18S rRNA genes of *Babesia* spp

Gene	Sequences 5'-3'	Temperature (°C)	Size (bp)	Ref
Babesia spp.	GTGAAACTGCGAATGGCTCA CCATGCTGAAGTATTCAAGAC	53	650	14
B. ovis	TGGGCAGGACCTTGGTTCTTCT CCGCGTAGCGCCGGCTAAATA	63	549	15
B. motasi	TTTGCGATGTTCCATTCA CACCTACGGAAACCTTGT	52	1489	16

Each PCR reaction was prepared in a 25 µL total volume, comprising 12.5 µL of 2× PCR Master Mix, 1 µL each of forward and reverse primers (20 µM), 3 µL of DNA template (50ng/µL), and 7.5 µL of nuclease-free water. Amplification was carried out in a G-Storm GS2 Thermal Cycler (Canada) under the following cycling conditions: initial denaturation at 95°C for 5 min; 40 cycles of denaturation at 94°C for 1 min, annealing at 53°C (*Babesia* spp.), 63°C (*B. ovis*), or 52°C (*B. motasi*) for 1 min, and extension at 72°C for 40 sec (*Babesia* spp. and *B. ovis*) and 90 sec (*B. motasi*); followed by a final extension step at 72°C for 5 min. PCR products were held at 4°C until further processing. Amplicons were resolved by electrophoresis on 1.5% agarose gels and visualized using a gel documentation system to confirm the presence and size of specific target bands.

Sequence and Phylogenetic Analysis

To confirm the molecular identity of *Babesia ovis*, two representative PCR amplicons were purified and subjected to unidirectional Sanger sequencing by Macrogen Inc. (Seoul, South Korea). Sequence analysis confirmed the presence of *B. ovis* in both samples. The obtained sequences were then queried against the GenBank nucleotide database using the NCBI BLAST algorithm for comparative validation.

Multiple sequence alignments were performed in MEGA 7 (July 2016; http://www.megasoftware.net) using the MUSCLE algorithm to ensure precise positional homology

with reference sequences (**17**). The reference sequences used in the alignment included sheep isolates (accession numbers PV488628.1 and PV488640.1) and goat isolates (accession numbers PV488616.1 and PV488627.1). Phylogenetic trees were constructed using the Neighbor-Joining method, and the robustness of tree topology was evaluated through 1000 bootstrap replicates (**18**).

Statistical Analysis of Epidemiological Data

Statistical analyses were conducted using GenStat 12th Edition to evaluate the association between management-related variables and *Babesia* infection prevalence. Odds ratios (ORs) with corresponding 95% confidence intervals (CIs) were calculated to estimate the relative risk of infection across different groups. The Chi squared test (χ^2) and Fisher's exact test were used to evaluate differences in prevalence rates. A *P*-value of less than 0.05 was considered statistically significant (**19**).

RESULTS

Microscopic examination of Giemsa-stained blood smears revealed the presence of *Babesia* spp. in 16.8% (21/125) of sheep and 8.2% (9/110) of goats. Morphological identification was based on characteristic forms of intraerythrocytic merozoites, which included single spherical, paired spherical, and triple spherical configurations (**Figure 1A**). A particularly notable morphological hallmark was the presence of the classic double pear-shaped form (**Figure 1B**), a distinguishing feature of *Babesia* spp.

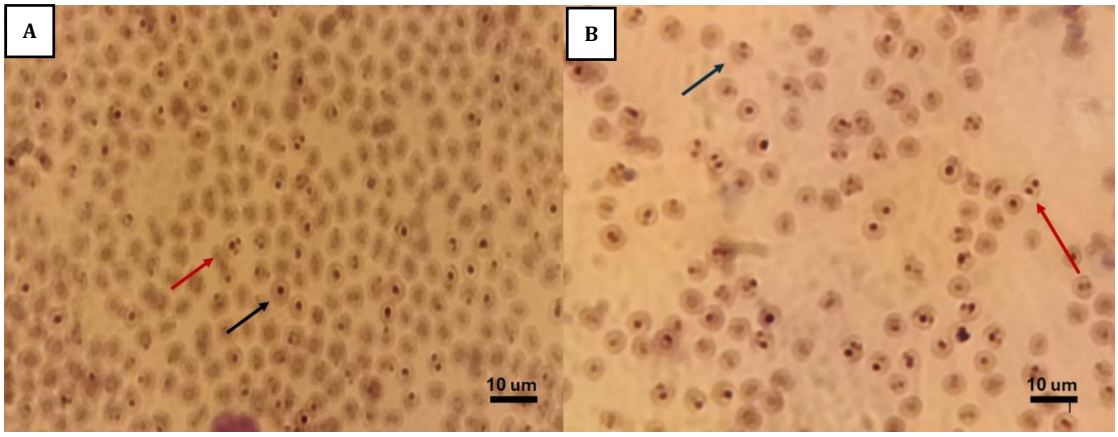

Figure 1. Morphological forms of *Babesia* spp. within infected erythrocytes stained with Giemsa and examined under an oil immersion lens (100×). **(A)** Single round-shaped merozoite (black arrow); two round-shaped merozoites (red arrow). **(B)** Two pear-shaped merozoites (red arrow); two round-shaped merozoites (black arrow)

Molecular detection via conventional PCR confirmed and expanded upon these findings, revealing a higher prevalence of *Babesia* infection: 28.8% (36/125) in sheep and 12.7% (14/110) in goats (**Table 2**). Amplification using genus-specific primers produced a ~650 bp fragment, while species-specific primers targeting *B. ovis* generated distinct bands at approximately 549 bp, consistent with expected amplicon sizes (**Figure 2 A, B**). However, no amplification was observed with *B. motasi*-specific primers in any of the samples, indicating a negative result for this species.

Table 2. Prevalence of *Babesia* spp. in sheep and goats detected by light microscopy and PCR

Animal	Total samples	Total Positive Samples (%)	
		Microscopy	c-PCR
Sheep	125	21 (16.8)	36 (28.8)
Goats	110	9 (8.2)	14 (12.7)

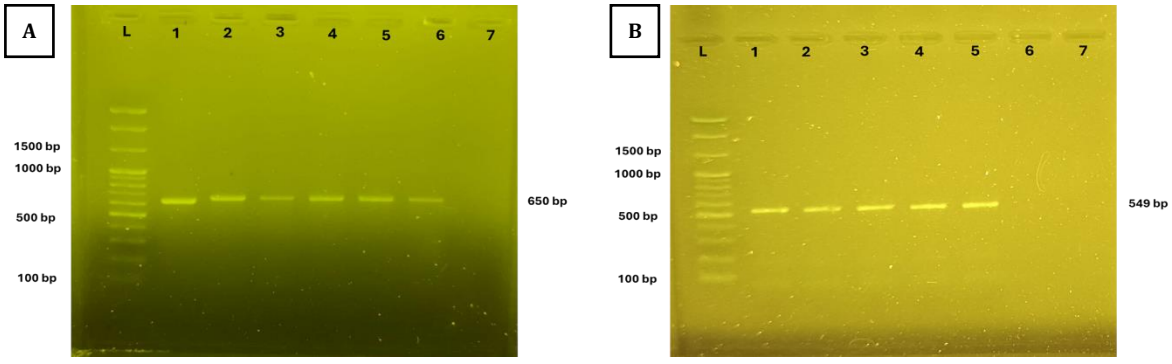

Figure 2. Agarose Gel Electrophoresis of *Babesia*-Specific PCR Amplicons: **(A)** Lanes 1–6 display amplification products (~650 bp) corresponding to *Babesia* spp., confirmed via universal primers. **(B)** Lanes 1–6 exhibit B. ovis-specific bands (~549 bp) generated using species-discriminative primers. Lane L contains a 100 bp DNA ladder (reference ladder indicated at left

Risk Factors Associated with *Babesia* spp. Infection

As shown in **Table 3**, molecular detection of *Babesia* spp. revealed no significant differences in prevalence based on gender or age in either sheep or goats. In sheep, infection rates were 20.8% (33/107) in females and 16.7% (3/18) in males. Similarly, in goats, females showed a prevalence of 13.8% (12/87) versus 8.6% (2/23) in males. Although animals aged 1–2 years had higher odds of infection 1.83 in sheep, and 2.25 in goats compared to other age groups, these differences were not statistically significant.

Table 4 presents the influence of management factors on the prevalence of Babesia spp. Tick infestation was identified as a major risk factor, with visibly infested sheep and goats showing significantly higher infection rates (65.6% and 43.15%, respectively) compared to their non-infested counterparts (16.1% in sheep and 12% in goats). The corresponding ORs were 9.93 (95% CI: 3.63–27.52; P = 0.0001) for sheep and 4.2 (95% CI: 1.25–17.77; P = 0.0007) for goats. Lack of regular acaricide utilization also correlated with increased infection rate. Non-treated sheep and goats showed prevalence rates of 50% and 56.4%, respectively, compared to 17.4% and 37.7% in regularly treated animals. Corresponding ORs were 3.79 (95% CI: 1.50–9.53; P = 0.002) for sheep and 2.53 (95% CI: 1.05–6.11; P = 0.018) for goats. Animals with a history of tick infestation were significantly more likely to be tested positive as compared with those without history of ticks' infestation. The prevalence was up to 45.9% in sheep and 65.1% in goats with prior exposure, compared to 12.5% and 26.9% in those without exposure. ORs were 5.94 (95% CI: 2.27–16.68; P = 0.0001) and 5.08 (95% CI: 2.06–12.66; P = 0.0001), respectively. Although animals in communal grazing systems had higher infection rates (31.4% in sheep, 43.8% in goats) than those under restricted grazing (23.1% in sheep, 33.3% in goats), the difference was not statistically significant (P > 0.05).

Table 3. Sex and age score -wise prevalence of babesiosis by PCR

	Sheep				Goat			
Factor	**No. of sheep tested**	**N. (%)**	**OR (95%CI)**	***P*-value**	**No. of goat tested**	**N. (%)**	**OR (95%CI)**	***P*-value**
Sex								
Female	107	33 (20.8)	2.23 (0.57 to 12.8)	0.173	87	12 (13.8)	1.68 (0.33 to 16.6)	0.402
Male	18	3.0 (16.7)	0.45 (0.08 to 1.75)		23	2.0 (8.6)	0.6 (0.06 to 3.02)	
Age (year)								
<1	20	3.0 (15)	0.39 (0.07 to 1.48)		27	2.0 (7.4)	0.47 (0.05 to 2.37)	
1-2	37	14 (37.8)	1.83 (0.73 to 4.46)	0.109	24	5.0 (20.8)	2.25 (0.53 to 8.50)	0.186
>2	68	19 (27.9)	0.91 (0.39 to 2.14)		59	7.0 (11.9)	0.85 (0.23 to 3.07)	
Total	125	36 (28.8)			110	14 (12.7)		

N=Number of positive samples, CI=Confidence interval, OR=Odd ratio, *P*-value ≤ 0.05

Table 4. Prevalence of *Babesia* spp. in relation to tick infestation and management practices as determined by PCR

	Sheep				Goat			
Factor	**No. of sheep tested**	**N. (%)**	**OR (95%CI)**	***P*-value**	**No. of goat tested**	**N. (%)**	**OR (95%CI)**	***P*-value**
Tick infestation								
Present	32	21 (65.6)	9.93 (3.63 to 27.5)	0.0001	95	41 (43.2)	4.20 (1.25 to 17.8)	0.0007
Absent	93	15 (16.1)	0.10 (0.04 to 0.28)		25	3 (12)	0.24 (0.06 to 0.80)	
Acaricides application								
No	34	17 (50)	3.79 (1.50 to 9.53)		39	22 (56.4)	2.53 (1.05 to 6.11)	
Regular	22	7 (31.8)	1.19 (0.37 to 3.50)	0.002	18	4 (22.2)	0.34 (0.08 to 1.20)	0.018
Irregular	69	12 (17.4)	0.28 (0.11 to 0.68)		53	20 (37.7)	0.72 (0.31 to 1.66)	
Previous tick history								
Yes	61	28 (45.9)	5.94 (2.27 to 16.7)	0.0001	43	28 (65.1)	5.08 (2.06 to 12.7)	0.0001
No	64	8 (12.5)	0.17 (0.06 to 0.44)		67	18 (26.9)	0.20 (0.08 to 0.49)	
Grazing system								
Communal	86	27 (31.4)	1.53 (0.60 to 4.16)	0.232	89	39 (43.8)	1.56 (0.53 to 5.01)	0.266
Restricted	39	9 (23.1)	0.66 (0.24 to 1.67)		21	7 (33.3)	0.64 (0.20 to 1.90)	
Total	125	36 (28.8)			110	14 (12.7)		

N=Number of positive samples, CI=Confidence interval, OR=Odd ratio, *P*-value ≤ 0.05

Phylogenetic Analysis of *Babesia ovis*

The *Babesia ovis* 18S rRNA gene sequences generated in this study were submitted to NCBI GenBank under accession numbers PV488628 and PV488640 (sheep isolates) and PV488616 and PV488627 (goat isolates). Phylogenetic construction using the neighbor-joining method (**Figure 3**) revealed that all isolates clustered within a highly supported clade (bootstrap values: 99.60%–100%). The tree was rooted with *Toxoplasma gondii* (KX270370) to establish evolutionary context. Collectively, these results confirm that the *B. ovis* isolates from this study are closely related to regional strains, with minimal intraspecific divergence.

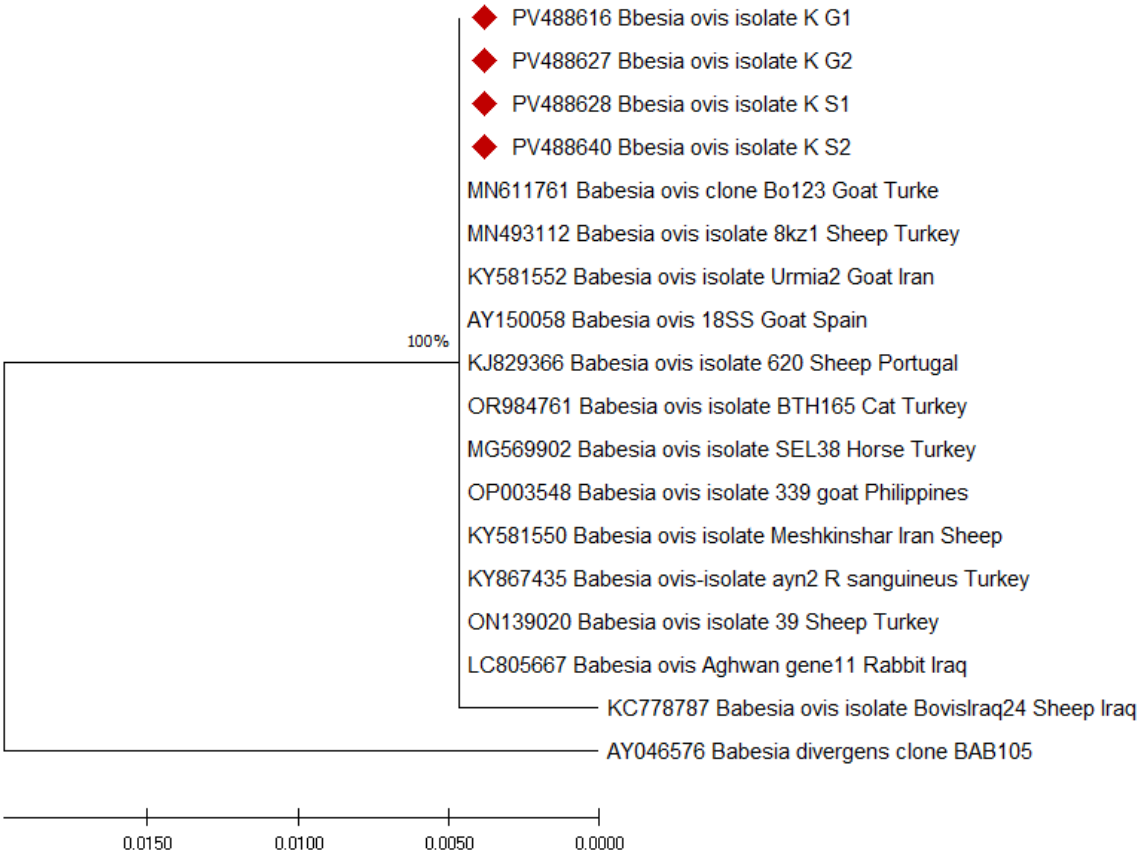

Figure 3. Phylogenetic tree of *Babesia ovis* isolates based on partial 18S rRNA gene sequences. The red diamond denotes *B. ovis* sequences obtained in the present study. Bootstrap values were calculated based on 1000 replicates. The analysis was performed using the Neighbor-joining method in MEGA 7 software. *Babesia divergens* (GenBank: AY046576) was used as an outgroup

DISCUSSION

Ovine and caprine babesiosis is a serious tick-borne protozoal disease affecting sheep and goats worldwide, caused by various *Babesia* species. In Iraq, studies on the prevalence of babesiosis in small ruminants remain limited, with most relying on Giemsa-stained blood smears (**20, 21**) and a few employing molecular diagnostics tools such as PCR (**21, 22**). The current study is the first to investigate the presence of *Babesia* in sheep and goats in Erbil Province, Northern Iraq, using both microscopy and PCR. Additionally, this study contributes to the genetic characterization of local *Babesia* isolates. Microscopic examination identified *Babesia* spp. in 16.8% of sheep (21/125) and 8.2% of goats (9/110). In contrast, PCR revealed higher prevalence rates—28.8% in sheep and 12.7% in goats. These results aligned with prior studies from other parts of Iraq. For instance, microscopy-based studies reported prevalence rates of 15.55% in Baghdad (**19**), 57.5% in Sulaymaniyah (**3**), and 15.42% and 43.07% in Mosul (**7, 20**) respectively. Molecular investigations reported varying prevalence rates, such as 1.5% in the Kurdistan Region (**22**), 25.78% in Sulaymaniyah, and 27.83% in Diyala (**24, 25**). 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 (**2, 26**).

Regionally, prevalence in neighboring countries also varies. In Iran, studies reported rates of 23.5% (**25**), 86.4% (27), and 18% (**28**). In Turkey, Bozan et al. (**29**) and Ulucesme et al. (**30**) found infection rates of 1.9% and 32.3%, respectively. In more distant countries, prevalence was reported as 12.7% in China (**15**), 37% in Pakistan (**31**), and 14% in Egypt (**32**). These discrepancies are likely attributable to differences in diagnostic methods, sampling criteria, environmental factors, and the degree of exposure to tick vectors. Climatic and ecological changes significantly influence the prevalence and transmission of *Babesia*. The hot climate in Kurdistan likely increases tick activity,

facilitating transmission (**9, 33**). Similarly, the Middle East climate characterized by mild winters and warm summers supports year-round tick activity, thus enabling continuous *Babesia* transmission (**34**). Although our study period falls within the low-temperature months (October 2024, with an average of 22.7°C, to March 2025, with 12.5°C), recent climate shifts due to global warming have altered tick ecology and the dynamics of tick-borne diseases in the region. In recent years, persistently warm autumns, along with mild winters, have promoted extend tick activity and allowed survival of piroplasm infections beyond, the traditional peak vector periods. Similar trends have been observed in other regions, where climate changes have increased winter temperatures and humidity, thereby expanding the active season for ticks and facilitating the spread of vector-borne diseases (**35**).

Our study found no statistically significant differences in *Babesia* prevalence by sex or age group. Although the odds of infection were higher in females 2.23 (0.57–12.75) in sheep and 1.68 (0.33–16.56) in goats and in animals aged 1–2 years 1.83 (0.73–4.46) in sheep and 2.25 (0.53–8.50) in goats these differences were not significant. This suggests a relatively uniform exposure risk across demographic groups, likely due to similar husbandry practices, environmental exposure and sample size. However, the wide confidence intervals reflect underlying variability and indicate that the observed differences may have been influenced by random chance. These findings mirror those of previous studies indicating a homogeneous distribution of tick-borne infections under similar conditions (**2, 20, 36, 37**).

Tick infestation was strongly associated with *Babesia* infection, this underscores the critical role of ticks particularly *Hyalomma* spp. as vectors, corroborating earlier research (**38-40**). The association between tick burden and *Babesia* infection was statistically significant, with a high odds ratio, indicating nearly six-fold increased risk among previously infested animals. Findings also affirm the protective role of acaricide use. Animals regularly treated with acaricides had significantly lower infection rates in sheep and in goats among untreated groups versus markedly lower proportions in treated ones. These results are consistent with studies emphasizing tick control as essential for reducing piroplasmosis prevalence (**41**). Additionally, improved sanitation and covered housing, especially for sheep, may have contributed to lower infection rates, as reported by Naveed et al. (**42**). Communal grazing further increases exposure risk, as supported by previous research (**43-45**). These findings highlight the need for comprehensive tick management, including consistent acaricide application and improved husbandry, to effectively mitigate *Babesia* transmission in small ruminants (**2, 9, 34, 45**).

Finally, the study presents the first genetic characterization of *Babesia ovis* in the Kurdistan Region using 18S rRNA gene sequencing. The two sequences obtained demonstrated high identity (99.64–100%) with strains from sheep and goats in Iraq and Iran, and even from rabbits and horses in the same region (e.g., KC778787, LC805667, MN611761, MN493112, MG569902). Lower identity (95.81%) was found with strains from Iran, Portugal, and Bangladesh. These results indicate a high degree of conservation in the 18S rRNA gene across hosts and geographic regions, supporting previous findings of limited intraspecific variation. The use of *Babesia* divergens as an outgroup also provides a distinct root for the tree and reinforced the distinction between *Babesia* and the non-piroplasmid apicomplexans, affirming the monophyletic status of *B. ovis* (**46**).

The presence of *B. ovis* sequences clustering with those from non-ruminant hosts (e.g., rabbits and horses) suggests potential cross-species transmission or the involvement of shared tick vectors, such as Rhipicephalus spp. These findings underscore the need for continued molecular surveillance and broader genomic analyses to explore emerging variants, transmission pathways, and host-vector dynamics. Integrating multi-locus genotyping with epidemiological studies will enhance our understanding of *Babesia* evolution and ecology in this under-investigated region.

This study confirmed the ongoing endemicity of *Babesia ovis* among sheep and goats in Erbil Province and underscores its close genetic affiliation with regional strains, suggesting localized transmission. *Babesia motasi* was not detected in any of the examined samples, indicating its limited or absent circulation in the study area during the sampling period. The strong correlation between infection and tick presence emphasized the urgent need for routine acaricide application and integrated tick control strategies to mitigate disease impact and associated economic losses in small ruminant herds.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

ARTIFICIAL INTELLIGENT DECLARATION

The authors declare that they are responsible for the accuracy and integrity of all content of the manuscript, including part generated by AI, and it is not used as a co-author.

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نظرة على التنوع الوراثي وعوامل الخطر لمرض البابيزيا في الأغنام والماعز في محافظة أربيل، شمال العراق

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الخلاصة
هدفت هذه الدراسة إلى تحديد معدل انتشار عدوى جنس بابيزيا وتوصيفها الجزيئي وعوامل الخطر المرتبطة بها في المجترات الصغيرة في محافظة أربيل بالعراق. خضع ما مجموعه ٢٣٥ حيوانًا (١٢٥ رأسًا من الأغنام و١١٠ رؤوس من الماعز) للفحص السريري وأخذ العينات بين أكتوبر ٢٠٢٤ ومارس ٢٠٢٥. وفحصت لطاخات الدم مجهريًا، واستُخلص الحمض النووي للكشف الجزيئي باستخدام تفاعل البوليميراز المتسلسل التقليدي (PCR) الذي يستهدف جين S rRNA١٨ لأنواع بابيزيا، ovis، وmotasi. كشف الفحص المجهري عن معدلات إصابة بلغت ١٦,٨٪ لدى الأغنام و٨,٢٪ لدى الماعز، بينما أظهر الكشف القائم على تفاعل البوليميراز المتسلسل (PCR) معدل انتشار أعلى بشكل ملحوظ بلغ ٢٨,٨٪ و١٢,٧٪ على التوالي. وأكد تحليل التسلسل والتطور الجيني لعزلات بابيزيا ovis وجود تشابه وراثي قوي مع السلالات الإقليمية من تركيا وإيران والعراق. أظهر تحليل عوامل الخطر ارتباطًا وثيقًا بين الإصابة بالعدوى وانتشار القراد، وعدم استخدام مبيدات القراد، والتعرض السابق للقراد. وتحديدًا، أظهرت الحيوانات المصابة بالقراد معدلات إصابة أعلى بشكل ملحوظ، حيث بلغت نسبة الأرجحية ٩,٩٣ للأغنام و٤,١٦ للماعز. ومع ذلك، لم تُلاحظ أي فروق ذات دلالة إحصائية فيما يتعلق بالجنس أو العمر أو نظام الرعي. وتؤكد هذه النتائج استمرار خطر الإصابة بداء البابيزيا بين المجترات الصغيرة في شمال العراق، وتُبرز الحاجة إلى تحسين استراتيجيات مكافحة القراد للحد من انتقال المرض.
الكلمات المفاحية: الأغنام والماعز، البابيزيا، المجهرية، الجزيئية، عوامل الخطر