



RESEARCH ARTICLE

Molecular screening of *Anaplasma*, *Ehrlichia*, and *Brucella* in ticks (Acari: Ixodidae) infesting farm ruminants in Peninsular Malaysia

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ABSTRACT

Ticks are obligate hematophagous arachnids that parasitize both humans and animals. While considerable research in Malaysia has focused on bacterial detection in ticks, knowledge of tick-borne *Anaplasma*, *Ehrlichia* and *Brucella* in farm ruminants remains limited. In this study, 1,241 ticks comprising of four species (*Rhipicephalus microplus*, *Rhipicephalus haemaphysaloides*, *Haemaphysalis bispinosa*, and *Haemaphysalis wellingtoni*) were collected from 674 farm ruminants across Peninsular Malaysia. The ticks were pooled and molecularly screened for *Anaplasma* and *Ehrlichia* using 16S rRNA gene primers, and *Brucella* using the BSCP31 gene primer. Out of 130 tick pools, five (3.85%) tested positive for *Anaplasma* and two (1.54%) for *Ehrlichia*. No *Brucella* DNA was detected in all four tick species. All positive pools consisted exclusively of *R. microplus*, with no pathogens identified in the other three tick species. BLAST analysis revealed that the *Anaplasma* sequences were identical to *Anaplasma marginale*, *A. platys*, and *Candidatus* “*Anaplasma bovine*”, while the *Ehrlichia* sequences were identical to *Ehrlichia ewingii*. This study represents the first screening for *Anaplasma*, *Ehrlichia*, and *Brucella* in ticks infesting farm ruminants in Peninsular Malaysia.

Keywords: Tick-borne pathogens; veterinary parasitology; ectoparasites; Malaysia.

INTRODUCTION

Ticks are obligate hematophagous ectoparasites that play a significant role in the transmission of a wide range of pathogens, including bacteria, viruses, and protozoa (Service, 2012). Among the bacterial pathogens, *Anaplasma*, *Ehrlichia*, and *Brucella* are of particular importance due to their deteriorative impact on both human and animal health (Foley, 2024). These pathogens are responsible for diseases that range from mild febrile illnesses to severe, life-threatening conditions (CDC, 2024).

In Malaysia, *Anaplasma* and *Ehrlichia* species pose significant health concerns for both animals and potentially humans. A study focusing on stray dogs in Peninsular Malaysia revealed that 39.5% tested seropositive for *Ehrlichia canis*, and 9.3% for *Anaplasma phagocytophilum* (Koh *et al.*, 2016). Molecular analyses further confirmed *E. canis* DNA in 25.5% and *A. phagocytophilum* DNA in 4.3% of the sampled dogs. Additionally, 17 out of 33 *Rhipicephalus sanguineus* ticks (51.5%) collected from these dogs harboured *E. canis*, one (3.0%) positive for *A. phagocytophilum*, and two ticks (6.1%) carrying DNA closely related to *Ehrlichia chaffeensis*. In East Malaysia, research indicated that 47.1% of 104 stray dogs were PCR-positive for *E. canis*, and 38.5% for *Anaplasma platys*, highlighting a substantial prevalence of these pathogens (Mohammed *et al.*,

2017). Beyond canine hosts, a molecular investigation in Peninsular Malaysia detected *Anaplasma marginale* predominantly in cattle and *Anaplasma platys/phagocytophilum* in deer. The study also identified *Anaplasma capra*, *Anaplasma bovis*, and *Candidatus* “*Anaplasma camelii*” in various domestic and wild animals, suggesting a diverse presence of *Anaplasma* species in the region (Koh *et al.*, 2018). Based on these studies, there is a gap of knowledge highlighting the lack of screening of *Anaplasma* and *Ehrlichia* in ticks feeding on farm ruminants in Malaysia.

Brucella remains a significant public health concern in Malaysia, particularly impacting livestock and people in close contact with animals; *Brucella abortus* is common in cattle, while *Brucella melitensis* affects goats and is the main source of human infection (Jama'ayah *et al.*, 2011; Zamri Saad & Kamarudin, 2016). Although a ‘test-and-slaughter’ policy and routine surveillance have reduced prevalence rates in animals to under 5%, eradication remains difficult due to factors like undetected infections and uncontrolled animal movement (Zamri Saad & Kamarudin, 2016). Human cases are relatively low but have occurred, notably during an outbreak linked to unpasteurized goat’s milk that resulted in 79 cases, highlighting the need for ongoing public health education and control measures (Jama'ayah *et al.*, 2011; Leong *et al.*, 2015).

Ticks have been shown to harbour *Brucella* DNA, with a scoping review identifying 16 tick species carrying the pathogen and a pooled prevalence of 33.87%; experimental studies also demonstrated transmission to uninfected animals (i.e., *Bos taurus*, *Cavia porcellus*, and *Ovis aries*) at rates of 45%–80% in controlled settings (Ma *et al.*, 2024). However, human brucellosis cases linked to tick bites remain extremely rare, with only three reported globally in Bulgaria, Turkey, and United Kingdom between 1963 and 2019 (Hutcheson, 1963; Simsek *et al.*, 2011; Popov & Gotseva, 2019). This highlights the need for further research to clarify the epidemiological significance of ticks in *Brucella* transmission and to enhance detection methods (Ma *et al.*, 2024).

To date, knowledge on the presence of *Anaplasma*, *Ehrlichia*, and *Brucella* cattle-infesting ticks remains limited (Kazim *et al.*, 2022). Thus, this study aims to detect the presence of these bacteria in ticks parasitizing farm ruminants (i.e., cattle, buffaloes, goats, and sheep) in the Peninsular Malaysia.

MATERIALS AND METHODS

Animal ethics approval

This study was conducted in accordance with the guidelines for the care and use of animals as approved by the Committee of Animal Research and Ethics at Universiti Teknologi MARA (UiTM CARE; approval number: UiTM CARE 378/2022). Additional approval was obtained from the Research Project Evaluation Committee of the Malaysian Department of Veterinary Services (reference number: JPV.BPI.600-1/7/1 [2021-14]).

Study sites, tick collection, and morphological identification

Ruminant farms across Peninsular Malaysia were visited over a one-year period, from October 2020 to November 2021. Farms were selected from four regions: the central region (Selangor and Kuala Lumpur), southern region (Melaka and Johor), eastern region (Pahang), and northern region (Perak) (Figure 1). Both large ruminants (cattle and buffaloes) and small ruminants (goats and

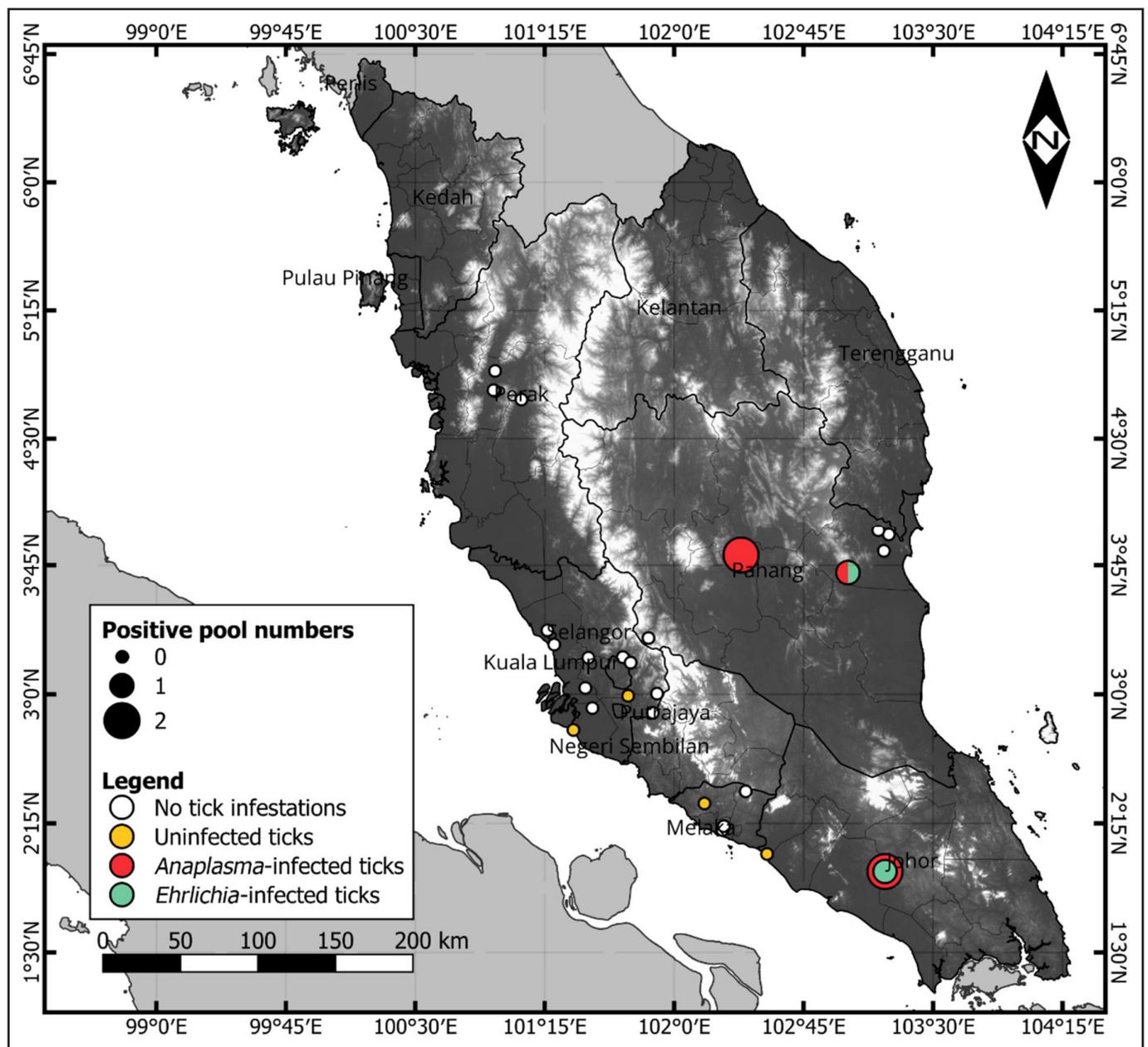


Figure 1. Map of the Peninsular Malaysia, illustrating the visited farms and the geographical distribution of *Anaplasma* and *Ehrlichia*. Map shapefiles of Peninsular Malaysia and other neighbouring countries were downloaded from <https://www.gadm.org>. The digital elevation model (DEM) data for Peninsular Malaysia was obtained from the United States Geological Survey (USGS) website.

sheep) were examined for tick infestations. Ticks were removed using fine tweezers and preserved in tubes containing 90% ethanol, then transported to the parasitology laboratory at the Institute of Medical Molecular Biotechnology (IMMB), UiTM Sungai Buloh Campus, for morphological identification. Specimens were examined under an Olympus SZX7 Zoom stereo microscope (Olympus Europa SE & Co. KG, Germany) and identified using taxonomic keys from Anastos (1950), Kohls (1957), Trapido et al. (1964), Tanskul and Inlao (1989), and Walker et al. (2000).

DNA extraction and molecular analyses of tick-borne pathogens (TBP)

Ten ticks were pooled for DNA extraction, while fully engorged females and nymphs were processed individually. After morphological identification, different species were kept separate throughout the extraction process. The ticks were first washed with distilled water and dried using KIMWIPES delicate wipers (Kimberly-Clark Professional, CA), then transferred to 1.5 mL microcentrifuge tubes and dissected with sterile surgical scissors (S.S. Pakistan, Pakistan). DNA extraction was carried out using the DNEasy® Blood and Tissue Kit (QIAGEN®, California) according to the manufacturer's protocol. The eluted DNA was subjected to conventional PCR with three sets of 16S rRNA primers targeting *Anaplasma* and *Ehrlichia*, and one primer set targeting the BSCP31 gene for *Brucella* (Table 1).

PCR was performed in 25 µL reaction volumes, each containing 12.5 µL of GoTaq® Green Master Mix (Promega, Wisconsin), 4 µL of DNA template, 1 µL each of forward and reverse primers, and 6.5 µL of nuclease-free water (QIAGEN®, California). Amplification

followed the cycling conditions specified in reference studies (Table 1) using a Biometra TAdvanced Twin 48 thermal cycler (Analytik Jena GmbH+Co. KG, Germany). A negative control was included in every PCR run to check for contamination. Amplicons were analyzed by electrophoresis on a 1.7% agarose gel stained with 1.5 µL FloroSafe DNA stain (1st BASE, Singapore) and visualized under UV light. PCR products were sent to Apical Scientific Sdn. Bhd. (Selangor, Malaysia) for sequencing. Sequences were aligned and trimmed using BioEdit software (Hall, 1999) and analyzed for similarity using BLAST on the NCBI website.

RESULTS AND DISCUSSION

All bacteria sequences were submitted to the GenBank database with their respective accession codes: *Ehrlichia* (PQ865284–PQ865285) and *Anaplasma* (PQ865286–PQ865290).

A total of 1,241 ticks were collected from 674 farm ruminants in Peninsular Malaysia, comprising *Rhipicephalus microplus* (1,229/1,241; 99.03%), *Rhipicephalus haemaphysaloides* (6/1,241; 0.48%), *Haemaphysalis bispinosa* (5/1,241; 0.40%), and *Haemaphysalis wellingtoni* (1/1,241; 0.08%). For molecular screening of *Anaplasma*, *Ehrlichia*, and *Brucella*, 130 tick pools were prepared (Table 2). Five pools (3.85%) tested positive for *Anaplasma*, and two pools (1.54%) were positive for *Ehrlichia*, all from *R. microplus*. No bacterial DNA was detected in *R. haemaphysaloides*, *H. bispinosa*, or *H. wellingtoni*, and no *Brucella* was detected in any pool.

Table 1. Primers used for the detection of *Anaplasma*, *Ehrlichia*, and *Brucella*

| Target gene | Primer name | Primer sequence ¹ | Base pair (bp) length | Reference |
|--------------------------------------------------|-------------|-------------------------------------------|-----------------------|------------------------|
| <i>Anaplasma/Ehrlichia</i> 16S rRNA ² | AE1-F | F: AAG CTT AAC ACA TGC AAG TCG AA | ~1400 | Oh et al. (2009) |
| | AE1-R | R: AGT CAC TGA CCC AAC CTT AAA TG | | |
| <i>Anaplasma</i> 16S rRNA ³ | EE3 | F: GTC GAA CGG ATT ATT CTT TAT AGC TTG C | ~950 | Barlough et al. (1996) |
| | EE4 | R: CCC TTC CGT TAA GAA GGA TCT AAT CTC C | | |
| <i>Ehrlichia</i> 16S rRNA ³ | HE1 | F: CAA TTG CTT ATA ACC TTT TGG TTA TAA AT | ~360 | Lee et al. (2005) |
| | HE3 | R: TAT AGG TAC CGT CAT TAT CTT CCC TAT | | |
| <i>Brucella</i> BSCP31 | B4 | F: TGG CTC GGT TGC CAA TAT CAA | ~220 | Baily et al. (1992) |
| | B5 | R: CGC GCT TGC CTT TCA GGT CTG | | |

¹F: Forward primer; R: reverse primer.

²First run of nested PCR.

³Second run of nested PCR.

Table 2. Allocation of tick pools for DNA extraction and PCR, and the number of pools positive for *Anaplasma*, *Ehrlichia*, and *Brucella*

| Region | Farm | Tick species | Number of ticks | Total pools | Total positive for <i>Anaplasma/Ehrlichia/Brucella</i> |
|--------------------------------|------|---------------------------------------|-----------------|-------------|--------------------------------------------------------|
| Central | 4 | <i>Rhipicephalus haemaphysaloides</i> | 5 | 1 | 0/0/0 |
| | | <i>Rhipicephalus microplus</i> | 14 | 2 | 0/0/0 |
| | 10 | <i>Rhipicephalus microplus</i> | 130 | 13 | 0/0/0 |
| Southern | 6 | <i>Haemaphysalis bispinosa</i> | 2 | 1 | 0/0/0 |
| | | <i>Rhipicephalus microplus</i> | 5 | 1 | 0/0/0 |
| | 7 | <i>Rhipicephalus microplus</i> | 190 | 19 | 2/1/0 |
| Eastern | 5 | <i>Haemaphysalis bispinosa</i> | 2 | 1 | 0/0/0 |
| | | <i>Haemaphysalis wellingtoni</i> | 1 | 1 | 0/0/0 |
| | | <i>Rhipicephalus microplus</i> | 730 | 73 | 1/1/0 |
| | 6 | <i>Rhipicephalus haemaphysaloides</i> | 1 | 1 | 0/0/0 |
| <i>Rhipicephalus microplus</i> | | 130 | 13 | 2/0/0 | |
| Northern | 2 | <i>Haemaphysalis bispinosa</i> | 1 | 1 | 0/0/0 |
| | | <i>Rhipicephalus microplus</i> | 30 | 3 | 0/0/0 |
| Total | | | 1241 | 130 | 5/2/0 |

Two of the *Anaplasma* sequences (A123 and A137) showed 100% identity with *Anaplasma marginale* isolate 9803C-2t from Taiwan (OL660541), while two others (A36 and A113) matched 100% with *Anaplasma platys* isolates from China (KU586175) and South Africa (MK814414), respectively. The remaining sequence (A118) showed 99.77% similarity to *Candidatus "Anaplasma boleense"* isolate C13 genotype Cab1 from South Africa (MK814450). *Anaplasma marginale* is one of the causative agents of bovine anaplasmosis, of which infected cattle show signs of anaemia, fever, anorexia, jaundice, abortion, weight loss, and reduced milk production (Salinas-Estrella *et al.*, 2022). While *A. marginale* has been previously reported in bovine sera in Malaysia (Tay *et al.*, 2014; Koh *et al.*, 2018; Ola-Fadunsin *et al.*, 2018), not much is known about its prevalence in cattle ticks, especially *R. microplus* which is a known biological vector of this species (de la Fournière *et al.*, 2023).

Anaplasma platys, typically a parasite of dogs vectored by *Rhipicephalus sanguineus* sensu lato, has also been reported in cattle and ruminants in Algeria, Egypt, Nigeria, Tunisia, and Vietnam (Dahmani *et al.*, 2015; Said *et al.*, 2017; Chien *et al.*, 2019; Tumwebaze *et al.*, 2020; Kamani *et al.*, 2022). Piloto-Sardibas *et al.* (2023) reported mixed infections of *A. marginale* and *A. platys* in Cuban cattle, suggesting that *A. platys* may also contribute to bovine anaplasmosis and that *R. microplus* could serve as a vector.

Candidatus "A. boleense" was first identified in *Hyalomma asiaticum* ticks in China (previously designated as *Anaplasma* sp. BL099-6, BL099-11, and BL102-7) (Kang *et al.*, 2014), and later in *R. microplus* ticks infesting cattle, buffalo, deer, goats, and sheep (Kang *et al.*, 2014; Guo *et al.*, 2016; Xu *et al.*, 2023; Khan *et al.*, 2024). In Malaysia, strains identical to *Ca. "A. boleense"* have been detected in deer (*Rusa timorensis*), buffalo (*Bubalus bubalis*), and cattle (*Bos taurus*) (Koh *et al.*, 2018). Despite its wide detection across hosts and tick species (Seo *et al.*, 2020; Sebastian *et al.*, 2023; Khan *et al.*, 2024), its pathogenicity, transmission routes, and reservoir hosts remain unknown.

Both *Ehrlichia* sequences (E36 and E85) demonstrated 100% identity with *E. ewingii* isolate Aa2FT175 from North Carolina, USA (KJ942192). *E. ewingii* is the causative agent of granulocytic ehrlichiosis in humans and dogs (Harrus *et al.*, 2021), with clinical signs in dogs including lethargy, fever, lameness, reluctance to move, stiff gait, joint effusion, and joint pain, while human cases may present with headache, fever, thrombocytopenia, and occasionally leukopenia (Sykes, 2014). *E. ewingii* has typically been reported in *Amblyomma americanum*, *Dermacentor variabilis*, and *R. sanguineus*, but it has also been detected in *R. microplus* infesting cattle (Matysiak *et al.*, 2016). Its ecology in *R. microplus* and cattle is still poorly understood, which is concerning given the potential exposure risk for farm workers who frequently handle cattle and come into contact with ticks.

Out of six positive pools (4.62%), only one has *Anaplasma* and *Ehrlichia* co-infection (*A. platys* + *E. ewingii*). Breitschwerdt *et al.* (2014) has previously reported a co-infection of *A. platys* and *E. ewingii* in a case study involving a family and their dog in Chicago, United States. In this study, molecular testing revealed the presence of *A. platys*, *E. chaffeensis*, and *E. ewingii* DNA in the blood of two asymptomatic family members and their pet dog. Despite the absence of typical symptoms associated with anaplasmosis or ehrlichiosis, the infections persisted intravascularly, as confirmed by sequential PCR tests over several months. Following doxycycline treatment, both the dog and one family member tested negative for these pathogens. To our knowledge, this is the first report of *A. platys* and *E. ewingii* co-infection in ticks infesting cattle. Consequently, it is crucial to conduct more comprehensive pathogen screening on both these animals and farm personnel, while factoring in co-infections during diagnostic evaluations, even in the absence of clinical signs.

This study has several important limitations that should be acknowledged. First, because no blood samples were collected from the cattle, it remains unknown whether the pathogens detected in the ticks were present in their midguts (indicating true infection of the ticks) or were simply acquired transiently during feeding on infected hosts. This gap limits our ability to determine the true vector competence of the tick species studied. Second, because sampling was conducted opportunistically rather than through a systematic year-round approach, the study could not assess seasonal patterns in tick infestation rates or pathogen prevalence. Such information is crucial for understanding infection risk periods and developing targeted control strategies. Third, the use of pooled tick samples, while cost-efficient, reduced the ability to determine individual infection rates and may have masked low-level pathogen presence, further constraining the precision of prevalence estimates.

In this study, *Brucella* bacteria were not detected in any of the four tick species examined. Although *Brucella* detection in ticks has raised concern due to their potential role in transmitting brucellosis, findings vary across regions and host species. A six-year study in Spain reported *Brucella* DNA in 5.17% of *Dermacentor marginatus* and *Dermacentor reticulatus* collected from wild boars, but not from ticks on other ungulates, suggesting possible host specificity (Rebollada-Merino *et al.*, 2024). Additionally, a review of 83 studies reported *Brucella* DNA in 16 tick species with an overall prevalence of 33.87%, indicating widespread occurrence in tick populations (Ma *et al.*, 2024). These studies emphasize the need to consider ticks in brucellosis epidemiology and support integrated surveillance efforts in Malaysia.

Conclusively, this study represents the first screening of *Anaplasma*, *Ehrlichia*, and *Brucella* in ticks infesting farm ruminants in Peninsular Malaysia. Three species of *Anaplasma* (*A. marginale*, *A. platys* and *Ca. "A. boleense"*) and one species of *Ehrlichia* (*E. ewingii*) were identified in *R. microplus* ticks, while no *Brucella* were detected in all four tick species. More studies are needed to study the pathogen interaction in cattle ticks, particularly understudied pathogens such as *Ca. "A. boleense"*, and pathogens that are dog-associated such as *A. platys* and *E. ewingii*.

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Declaration of competing interests

All authors declared no competing interests.

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