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RESEARCH ARTICLE

Distribution of tick species parasitizing livestock in Sirumalai, The Eastern Ghats of Tamil Nadu, South India and its implications for public health

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ABSTRACT: Ticks and tick-borne diseases are an important public health problem worldwide. In India, prevalence of many tick-borne pathogens such as Ganjam virus, Kyasanur forest disease virus (KFDV), Crimean Congo hemorrhagic fever (CCHF) virus and *Rickettsia conorii* etc., have been documented. The species composition of ticks infesting domestic animals in the Sirumalai area of the Eastern Ghats in Tamil Nadu, South India has been recorded. A total of 2851 tick specimens were collected, and taxonomical identification revealed that 14 species belong to four genera, viz., *Haemaphysalis*, *Rhipicephalus*, *Amblyomma* and *Hyalomma*. Among the species, *Haemaphysalis intermedia* from goats and *Rhipicephalus microplus* from cattle account for 72.6% and 15.2%, respectively. *Amblyomma integrum* was collected only from cattle (*n*=22). *Rhipicephalus simus*, *Rhipicephalus bursa*, *Hyalomma hussaini* and *Hyalomma kumari* have been recorded for the first time this area. The preliminary results confirms the occurrence of rich diversity of tick fauna in this area and recommend further studies to determine the role of these fauna and their public health relevance to livestock and residents.

Keywords: Ixodida, *Haemaphysalis*, *Amblyomma*, *Rhipicephalus*, *Hyalomma*, domesticated animals, South India
Zoobank: https://zoobank.org/29FC14A3-6557-49D0-A32E-AF56BF3D0546

INTRODUCTION

Ticks (Ixodida) are considered as a serious pest of livestock and involved in transmission of various public health important pathogens to animals and humans. Ticks transmit viral, bacterial, and protozoan pathogens to humans and regarded to be the second-most significant vector after mosquitoes (Zhijun et al., 2015). More than 60% of humans are infected due to the pathogens originated through zoonotic (Rahman et al., 2020). The rise in tick-borne diseases globally is a major concern and causes serious illness in humans as well as animals in terms of morbidity, mortality and economic loss (Ghosh and Nagar, 2014; Wikel, 2018). Tick and tick-borne diseases spread due to rapid urbanization, growth of the human population, cattle trade and continuous evolution of pathogens (Chala and Hamde, 2021). The species composition, systematic, and vector incrimination studies are very scarce when compared to mosquitoes. Globally, the Argasidae (soft ticks) and the Ixodidae (hard ticks) together comprise 900 tick species (Abubakar et al., 2018). In India, approximately 106 tick species have been reported (Geevarghese et al., 1997), and the species *Haemaphysalis spinigera* and *H. turturis* are incriminated as vectors of the Kyasanur forest disease virus (KFDV) (Rajaiah, 2019). Likewise, the other species, such as *Rhipicephalus sanguineus, Rhipicephalus* (*Boophilus*) *microplus* and *Hyalomma* spp. acts as vector for *Rickettsia conorii, Babesia bigemina* and Crimean Congo hemorrhagic fever (CCHF) virus respectively (Ghosh and Nagar, 2014). In addition, Indian tick typhus, transmitted by *Rh. sanguineus* and *Rh.* (*Boophilus*) *decoloratus*, Ganjam virus transmitted by *H. intermedia* and *Rhipicephalus haemaphysaloides* are important tick-borne diseases in India (Sudeep et al., 2009; Ghosh and Nagar, 2014; Negi et al., 2021).

In India, though tick faunistic studies have been carried out in different parts of the country (Gurwattan et al., 1975; Geevarghese et al., 1997; Nataraj et al., 2021) the species composition of the tick fauna in many potential areas remains unexplored due to the underreported or unreported tick-borne diseases (Stewart et al., 2017; Salje et al., 2021). In Tamil Nadu, the geography of the Western Ghats and the adjoining areas are found highly suitable for the breeding and existence of ticks. Considering the recent escalating trend of occurrence of ticks and incidences of tick-borne diseases worldwide, this study to map the species composition of ticks from domestic animals in foot-hill villages near the Western Ghats bordering Dindigul and Madurai districts was carried out. Eventually, such data would shed light on the prevalent tick fauna and the possible risk of tick-borne pathogen transmission to humans and animals in this area.

MATERIALS AND METHODS

Study area

The Sirumalai foothill ranges cover 60,000 acres and located in the Eastern Ghats of Tamil Nadu, South India, at longitude 77.9967043, latitude 10.1942441, and elevation 1093m/3586 feet. The details of the study areas where the survey was carried out have been depicted in (Fig. 1). Many rural villages are situated in the foothill's

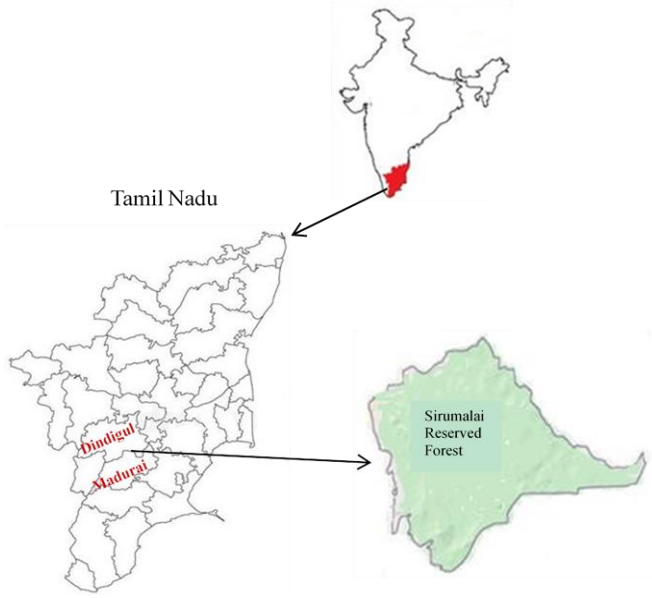

Figure 1. A map of the Sirumalai ticks collected areas.

region of Sirumalai, and house domesticated animals including cattle, sheep, goats, dogs and horses. These domestic animals are often exposed to profuse tick infections while entering the forest areas for foraging. The availability of plenty of vegetation and the existing climatic conditions are highly favorable for the breeding of ticks. This study was duly approved by the Research Institutional Unit (RIU).

Tick Collection and Identification

The ticks were collected from the infested livestock manually using forceps, after obtaining the cattle owner's permission during the daytime. The whole body of the domestic animal, particularly the legs, tail and ears, were thoroughly checked. Before collection, necessary precautionary measures were taken to avoid accidental tick bites. The ticks were collected from cattle, dogs, goats, horses, and sheep. Details of the village, type of host, and date of the collection were labelled on the collection vials. The collected specimens were immediately placed in 70% ethanol in 1.5 ml microtubes and transported to the laboratory for further taxonomic identification. In the laboratory, ticks were grouped by stages and sex before taxonomical identification using a stereo zoom microscope, (Magnus MSZ-TR, India) using standard morphological identification keys as described by (Sharif, 1928; Geevarghese and Dhanda, 1987; Walker et al., 2003; Geevargheese and Mishra, 2011) the genus and species were confirmed. All the taxonomically identified specimens representing species were kept in the institutional tick collection.

RESULTS AND DISCUSSION

A total of 760 domestic animals, viz., goats (*n*=485), sheep (*n*=9), cattle (*n*=237), dogs (*n*=28) and horse (*n*=1) examined, and 2851 tick specimens belonging to various stages were collected. The various stages of ticks collected during the survey included larvae (*n*=86), nymphs (*n*=442), males (*n*=1127) and females (*n*=1196) Table 1. Overall, 14 tick species were recorded from domestic animals, which belonged to 4 genera, viz., *Haemaphysalis*, *Rhipicephalus*, *Amblyomma* and *Hyalomma* (Fig. 3). Among the 14 species, *H. intermedia* and *Rh.* (*B.*) *microplus* account for 72.6%, 15.2%, respectively. The analysis of stagewise tick ratios showed that the females were higher when compared with the males. The hostwise species composition of ticks is depicted in (Fig. 4). The percentage of tick infestation rate among dogs and goats was 57.1% and 54.8%, respectively, followed by cattle (42.6%) and sheep (44.4%) (Fig. 2). The details of the tick species recovered and their vectors potential in the possible transmission of public health important pathogens are presented in Table 2.

The geographical expanding potential of many public health important ticks from their original place of distribution to naive areas and the potential incursion of emerging and re-emergence of tick-borne pathogens is a serious concern globally. According to the estimate, India spends $498.7 million annually to control ticks and tick-borne diseases (TTBD) in domestic animals (Minjauw and McLeod, 2003). Tick-borne diseases are emerging due to climatic changes, rapid urbanization, and human, animal movements etc. (Mourya et al., 2021). The present survey recorded 14 tick species in total in the studied area, the species composition of ticks infesting on domestic animals was indicated. Notable, out of 14 tick species collected 10 of them are well recognized vector of public health importance namely, *Haemaphysalis intermedia*, *H. spinigera*, *H. bispinosa*, *Rhipicephalus haemaphysaloides*, *R. annulatus*, *microplus*, *R. decoloratus*, *R. sanguineus*, *Amblyomma integrum* and *Hyalomma anatolicum*. These tick species have been documented as potential vectors of tick-borne diseases such as Ganjam virus (GANV), Indian tick-typhus, and Anaplasmosis (Negi et al., 2021).

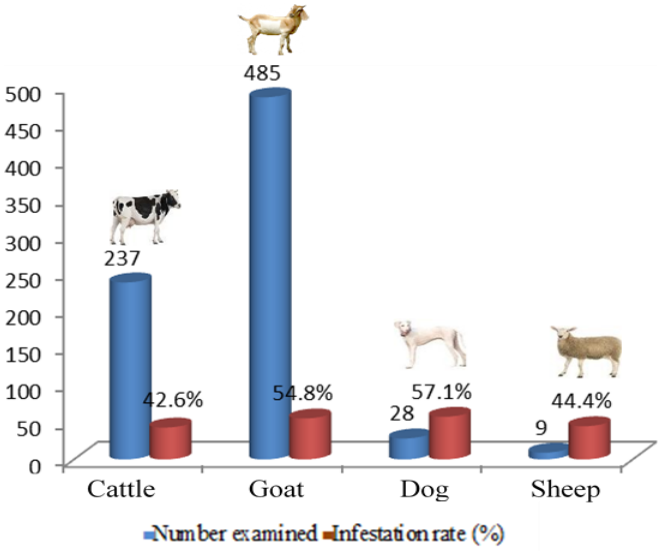

Figure 2. Tick infestation rate in cattle, dogs and sheep.

It is interesting to note that the possible circulation of potential tick-borne pathogens among these vector ticks collected from the study areas. The dominant occurrence (72.6%) of *H. intermedia* in cattle, goats, dogs and sheep indicates that this species has a wider distribution in this area and the availability of specific vertebrate hosts for its

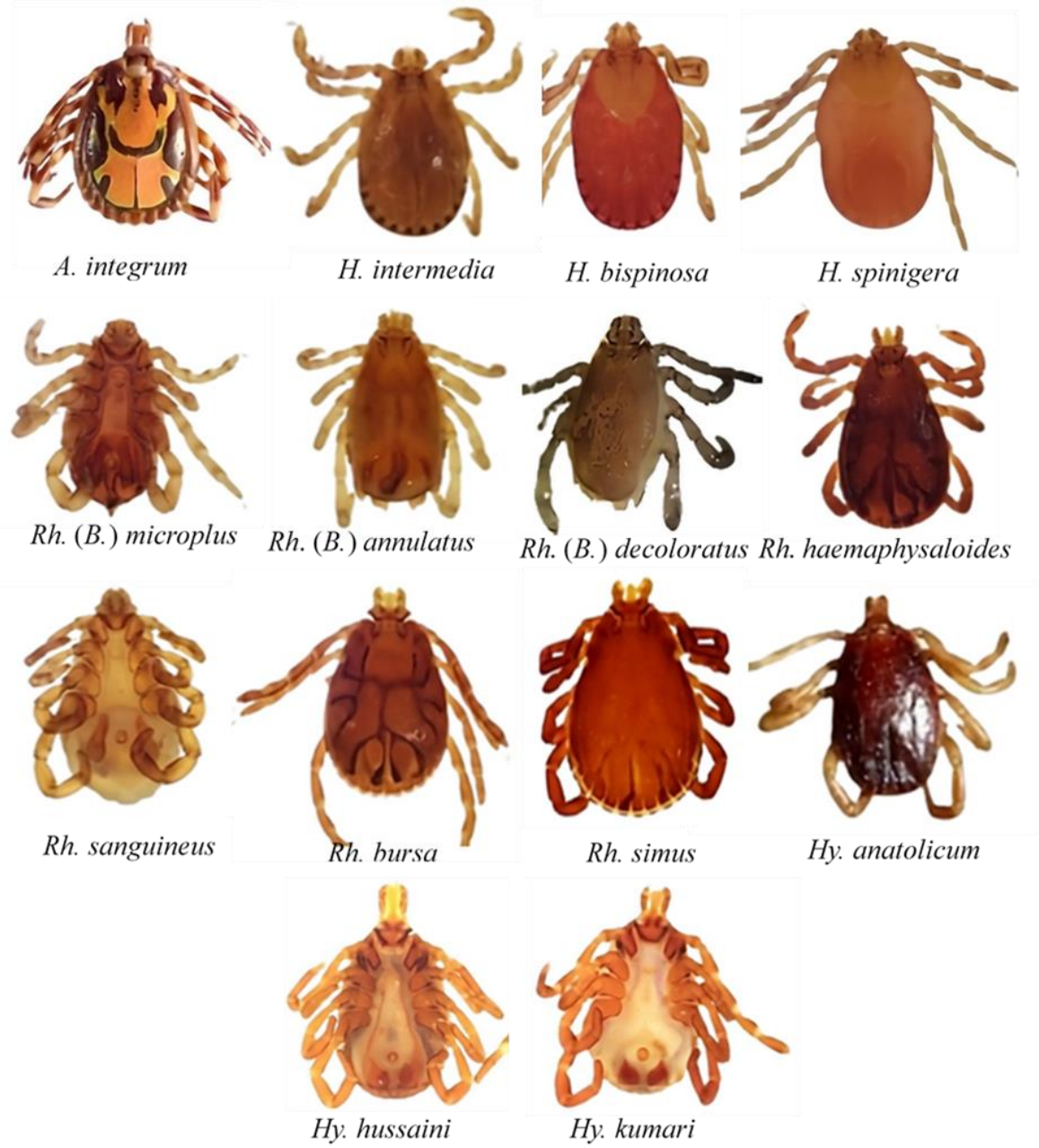

Figure 3. Images of ticks collected from Sirumalai foot hill villages.

feeding and survival. Moreover, the occurrence of *H. spinigera* on cattle and goats and *H. bispinosa* only from goats reveal the availability of a wider variety of host ranges such as birds, cattle and goats (Prakasan and Ramani, 2007). Further, it is noteworthy to understand their association in veterinary and public health in this area, since our recent study have detected laboratory evidences of the circulation of *Rickettsia felis* and *R. raoultii* from *H. intermedia* (Nallan et al., 2023) which have been attributed as the etiological agent of human illnesses namely cat-flea typhus and tick-borne lymphadenopathy (TIBOLA) (Brown and Macaluso, 2016; Mediannikov et al., 2008). However, these vectors *i.e., H. intermedia* has been found transmitting the Nairobi sheep disease virus in Sri Lanka, as well as Bhanja and Ganjam viruses, are new arboviruses in Orissa, India (Perera et al., 1996; Shah and Work, 1969; Dandawate and Shah, 1969). *Rhipicephalus* (*Boophilus*) *microplus* (15.2%) was the most prevalent species recorded in this study and their infestation in cattle causes severe deterioration of animal health and milk production (Jain et al., 2020).

The recording of the *H. spinigera*, a known vector of KFD in India, could indicate the necessity of continuous surveillance for monitoring the possible incursion of KFD viruses in these areas. Although, CCHF cases are not been reported from these areas the recording of *Hy. anatolicum* among cattle, goats and horses recommends strengthening surveillance systems. Every year, 400–500 people in the Western Ghats suffer from diseases transmitted by the *Haemaphysalis* species (Chakraborty et al., 2019). Apart from the potential transmission of viral pathogens by *H. bispinosa*, the data on the possible transmission of other rickettsial pathogens (such as Anaplasmosis), Babesiosis, and tropical Theileriosis are worth understanding as they have already been documented in South-East Asia (SEA) (Senbill et al., 2022).

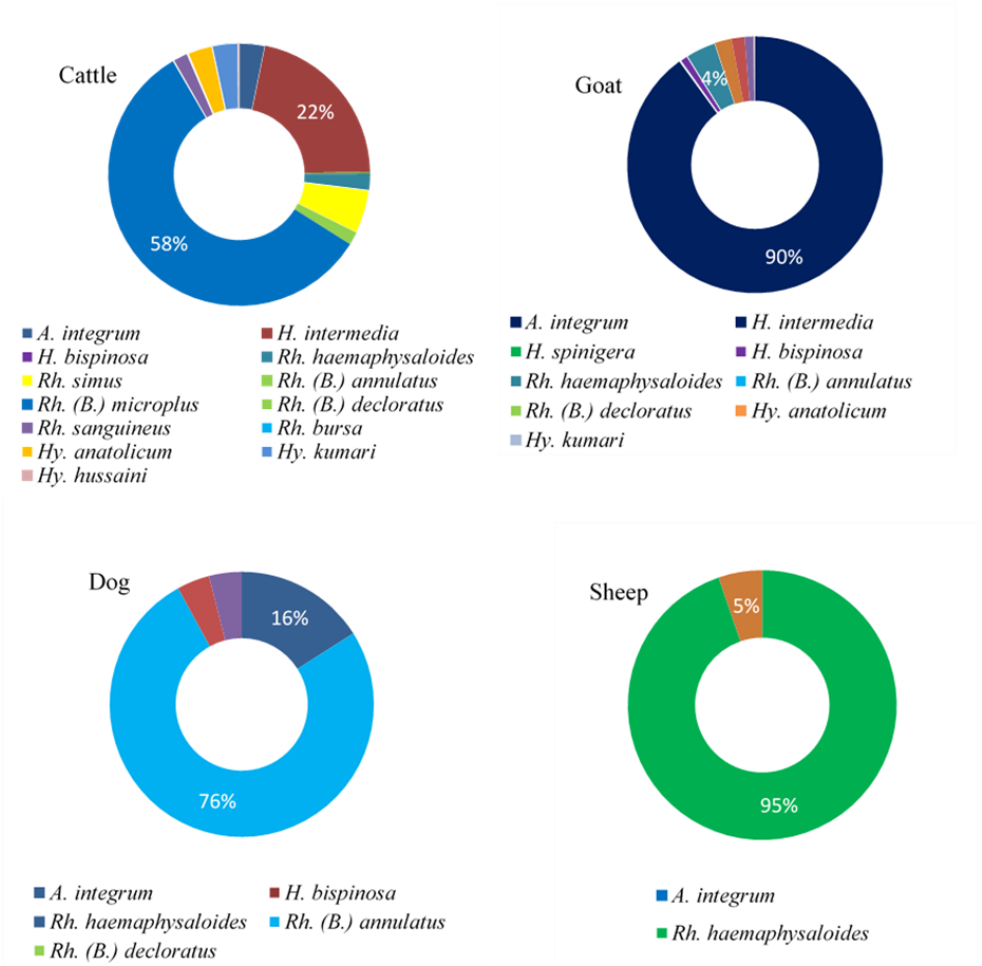

Figure 4. Tick species composition on cattle, goats, dogs and sheep.

Table 1. Details of stagewise tick species collected from animal hosts at Sirumalai

No	Tick species	Ticks stage & gender				Total ticks
		Larva	Nymph	Male	Female	(*n*)
1	*Amblyomma integrum*	0	0	9	13	22
2	*Haemaphysalis intermedia*	85	339	828	818	2070
3	*Haemaphysalis bispinosa*	0	0	15	5	20
4	*Haemaphysalis spinigera*	0	3	1	1	5
5	*Rhipicephalus* (*Boophilus*) *microplus*	0	92	113	228	433
6	*Rhipicephalus* (*Boophilus*) *annulatus*	0	6	4	1	11
7	*Rhipicephalus* (*Boophilus*) *decoloratus*	0	0	1	0	1
8	*Rhipicephalus haemaphysaloides*	0	0	47	50	97
9	*Rhipicephalus sanguineus*	0	0	15	21	36
10	*Rhipicephalus bursa*	0	0	1	0	1
11	*Rhipicephalus simus*	0	0	58	46	104
12	*Hyalomma anatolicum*	1	0	19	5	25
13	*Hyalomma kumari*	0	2	15	8	25
14	*Hyalomma hussaini*	0	0	1	0	1
	Total	**86**	**442**	**1127**	**1196**	**2851**

The prevalence of a significant percentage of *Rh.* (*B.*) *microplus* (58.3%) among the total of 683 ticks, comprising 7 species under the genus *Rhipicephalus* was collected from cattle. This species is considered the most important tick vector since its infection of cattle leads to economic losses in tropical and subtropical regions worldwide (Rodriguez-Vivas et al., 2018). Though the prevalence of *Rh. simus* has been found to be less (3.6%) in this area, the vector has been shown to transmit texas fever (*B. bigemina*) and Anaplosmosis or gall sickness in cattle (*A. marginale*) elsewhere (Tandon, 1990). Interestingly, only *Rh. simus* adult stages were collected from all animals inspected or examined, with a higher infestation rate of 42.3%, 35.5% in goats and cattle, respectively when compared with other animals in this study. Similarly, only adult stages were also recorded

Table 2. Species of ticks collected on domestic animals in the Sirumalai areas, its presence in Indian states and causing diseases.

No	Tick species	Nos collected	Vector-borne diseases	Location	Host	Distributed states in India
1	*A. integrum*	22	Rickettsiosis, Otoacariosis	Dindigul	Cow	6,7,8,10,13,14,16,20,24, 27.
2	*H. intermedia*	2070	Ganjam Virus	Dindigul/ Madurai	Cow, Goat, Dog, Sheep	1,3,4,5,6,7,9,10,11,13, 14,15,18,20,21,24, 28.
3	*H. bispinosa*	20	Kyasanur Forest Disease, Babesiosis	Dindigul	Goat	1,2,3,4,5,7,8,10,11,12, 13,14,15,16,17,19,20, 21,23,24,27.
4	*H. spinigera*	5	Kyasanur Forest Disease	Dindigul	Cow, Goat	1,5,7,13,14,15,16,17, 18,20,24,28.
5	*Rh.* (*B.*) *microplus*	433	Anaplasmosis	Dindigul/ Madurai	Cow, Goat, Dog	1,2,3,4,6,5,7,8,9,10,11, 12,13,15,18,19,20,21, 22,23,24,25,26,27.
6	*Rh.* (*B.*) *annulatus*	11	Anaplasmosis, Babesiosis	Dindigul	Cow	8,11,13,14,24.
7	*Rh.* (*B.*) *decoloratus*	1	Indian tick typhus	Dindigul	Cow	9,11,14.
8	*Rh. haemaphysaloides*	97	Anaplasmosis, Babesiosis	Dindigul/ Madurai	Cow, Goat, Dog	1,2,3,4,5,6,8,9,10,11,12, 13,14,15,16,17,18, 20,21,22,24,27.
9	*Rh. sanguineus*	36	Rocky Mountain & Mediterranean spotted fever	Dindigul/ Madurai	Cow, Goat, Dog	1,2,3,4, 5,8,9,10,11, 12,13,14, 15, 16,19, 20,21,22,24,25,27.
10	*Rh. bursa*	1	Anaplasmosis, Babesiosis	Dindigul	Cow	29.
11	*Rh. simus*	104	East Coast Fever of Cattle, Swine babesiosis,	Dindigul/ Madurai	Cow, Goat, Dog, Sheep Horse	29.
12	*Hy. anatolicum*	25	Crimean Congo Hemorrhagic Fever	Dindigul	Cow, Goat, Horse	1,3,4,5,6,7,8,9,10,11,13, 15,16,20,21,22,24,25,26, 27.
13	*Hy. kumari*	25	Crimean-Congo hemorrhagic fever virus	Dindigul	Cow, Goat	3,4,6,9,10,11,12,14,16, 20,21,22, 25.
14	*Hy. hussaini*	1	Rickettsiosis	Dindigul	Cow	1,4,5,6,8,9,10,11,12,13, 15,16,20,21,22,23,24,25.

1. Andhra Pradesh, 2. Arunachal Pradesh, 3. Assam, 4. Bihar, 5. Chhattisgarh, 6. Delhi, 7. Goa, 8. Gujarat, 9. Haryana, 10. Himachal Pradesh, 11. Jammu and Kashmir, 12. Jharkhand, 13. Karnataka, 14. Kerala, 15. Madhya Pradesh, 16. Maharashtra, 17. Manipur, 18. Meghalaya, 19. Mizoram; 20. Odisha, 21. Punjab, 22. Rajasthan, 23. Sikkim, 24. Tamil Nadu, 25. Uttar Pradesh, 26. Uttarakhand, 27. West Bengal, 28. Andaman and Nicobar Island, 29. Puducherry.

from cattle in Puducherry and presence of this species was confirmed with the DNA partial gene sequencing of ribosomal mitochondrial and 18s rDNA gene (GenBank Acc. No. MW078976 and MW078984) respectively (Nataraj et al., 2021). Another record of *Rh. bursa* (Sharif 1928; Nataraj et al., 2021), the vector of *A. marginale*, *B. bigemina*, *B. motasi*, and *B. bovis* to animals has already been recorded in south India and found distributed in southern Europe, the Near and Middle East. To the best of our knowledge, this study has recorded the prevalence of two public health important species, viz., *Rh. bursa* and *Rh. simus,* as reported earlier (Sharif, 1928; Nataraj et al., 2021) in India. In the earlier study, the vectorial role of *Rh. simus* in the transovarial transmission of *B. trautmanni,* which causes swine babesiosis, has been experimentally demonstrated (Waal et al., 1992). In the present study, we collected *Amblyomma integrum* specimens from cattle. This is the second record in Tamil Nadu. The first occurrence of the tick was recorded in 2017 from a dead bison at Gudalur, the Nilgiris, Tamil Nadu, India (Soundararajan et al., 2017). Since this species freely feeds on wild and domestic animals as well as humans, it can act as a zoonotic vector (Apanaskevich et al., 2016). It transmits *T. annulata*, the apicomplexan parasite, and 250 million cattle are at risk due to the infection of this parasite through the tick vector (Liu et al., 2022). Serological studies on the subclinical to severe clinical outbreaks of bovine tropical theileriosis in cross-bred cattle have been reported in the states of Karnataka, Orissa, Tamil Nadu, Kerala, Uttarkhand, and Punjab (Edith et al., 2018).

A male *Hyalomma hussaini* was collected from horse whereas *Hy. anatolicum* and *Hy. kumari* were collected in equal proportions from cattle and goats. The second two species were known to cause Crimean Congo

Hemorrhagic Fever (CCHF) and *Trypanosoma* (*Megatrypanum*) *theileri*, a weak pathogenic parasite of domestic cattle (Shastri and Deshpande, 1981). These three species were recorded among cattle and sheep in Maharastra state during the ixodid survey in 1976-1978 (Geevarghese and Dhanda, 1995). Information on the prevalence of these species in other states is scanty.

Ticks and tick-borne diseases have become a serious public health problem globally. Ticks are serious livestock pests, they remain the major cause of economic impact. Apart from the country's economic damage, they also transmit various pathogens. Under this scenario of emerging the tick-borne diseases, the current survey described the species composition of tick fauna on domestic animals in Tamil Nadu southern region. The dominant occurrence of *H. intermedia* in the area is unique, and there is a possible public health risk of transmission of pathogens both in humans and animals. The first-ever recording of *Amblyomma* spp. in this area and determining their risk are also worth studying in future. The first-time recording of *Hyalomma* spp., in these areas also paves the way for further studies in order to determine the interaction with the host and humans. The outcome of the pilot study would corroborate the occurrence of important tick fauna in the studied area, which would complement existing knowledge on ticks in screening the tick-borne pathogens and the potential risk of tick-borne diseases.

Authors' contributions

Veerapathiran Ayyavu: Conceptualization, investigation, methodology, data curation, writing original draft. **Krishnamoorthy Nallan:** Investigation, methodology, data curation, draft, review & editing. **Elango Ayyanar:** Taxonomic identification, image processing of ticks, writing original draft. **Balaji Thiruppathi:** Resources, methodology, draft editing. **Ashwani Kumar:** Critical evaluation of the study, supervision, funding acquisition. **Paramasivan Rajaiah:** Conceptualization, project administration, review & editing.

Statement of ethics approval

This study has been approved by the institutional Research Integrity Unity (RIU) of the Vector Control Research Centre, RIU-05/2022.

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Conflict of interest

The authors declare no conflict of interest.

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