

Review

Distribution of *Rhipicephalus sanguineus* and *Haemaphysalis elliptica* dog ticks and pathogens they are carrying: A systematic reviewClara-Lee Van Wyk^a, Senzo Mtshali^b, Tsepo Ramatla^{a,*}, Kgaugelo E. Lekota^a, Xuenan Xuan^c, Oriel Thekiso^a^a Unit for Environmental Sciences and Management, North-West University, Potchefstroom 2531, South Africa^b National Institute of Communicable Diseases, Sandringham 2131, South Africa^c National Research Center for Protozoan Diseases, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido 080-8555, Japan

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ABSTRACT

The role of ixodid ticks especially *Rhipicephalus sanguineus* and *Haemaphysalis elliptica* in the epidemiology of several diseases of veterinary and public health importance have been documented. This study conducted a systematic review focusing on the distribution of *R. sanguineus* and *H. elliptica*, as well as the common tick-borne pathogens they harbour. The Scopus, ScienceDirect, PubMed, and Web of Science databases were used to search for English journal articles published between January 1990 and June 2021. The articles were assessed by following the Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA) guidelines. This systematic review was registered on PROSPERO [(ID no: CRD42022327372)]. Of the studies included in the systematic review, 247 and 19 articles had identified *R. sanguineus* and *H. elliptica* respectively, whereas 15 articles had identified both tick species. There is a reported worldwide distribution of *R. sanguineus* from 64 countries, whereas *H. elliptica* was only reported in the African continent from 6 countries. In total, 120 articles that were included in this systematic review reported detection of tick-borne pathogens from *R. sanguineus* ($n = 118$ articles) and/or *H. elliptica* ($n = 2$ articles) ticks. According to the studies tick-borne pathogens harboured by *R. sanguineus* included protozoa such as *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., and *Theileria* spp., as well as bacteria such as *Acinetobacter* spp., *Anaplasma* spp., *Bacillus* spp., *Borrelia* spp., *Brucella* spp., *Coxiella* spp., and *Staphylococcus* spp. The *H. elliptica* was reported to be harbouring *Babesia* spp., *Ehrlichia* spp. and *Rickettsia* spp. Most of the studies (50%) used the conventional polymerase chain reaction (PCR) technique for the detection of tick-borne pathogens, followed by real-time PCR (qPCR) ($n = 26$), and nested PCR ($n = 22$). This systematic review has shed light on the distribution of two common dog ticks as well as the tick-borne pathogens of veterinary and zoonotic importance they are harbouring. This data will enable surveillance studies that can report whether the distribution of these ticks and their associated tick-borne pathogens is expanding or shrinking or is stable.

1. Introduction

Ticks transmit tick-borne pathogens that affect the health of humans, livestock, wildlife and companion animals (Magnarelli, 2009; Esteve-Gassent et al., 2016; Rana et al., 2023). On a global scale, the threat posed by ticks, as well as the pathogenic organisms they harbour, is increasing (Klingelhöfer et al., 2022; Zhou et al., 2023). In addition, ticks are also responsible for toxic conditions, including allergic reactions, tick paralysis, and irritation (Jongejan and Uilenberg, 2004; Esteve-Gassent et al., 2016). Ticks also contribute to economic losses,

due to hide damage, livestock mortalities, or mounting medical and veterinary costs for humans [due to zoonoses] and companion animals resulting from diseases caused by tick-borne pathogens (Jongejan and Uilenberg, 2004; Magnarelli, 2009; Bekere et al., 2022).

Tick-borne diseases of companion animals have gained increasing interest in research within the last couple of years since the discovery of zoonotic diseases, such as Lyme disease and rickettsiosis (Jongejan and Uilenberg, 2004; Hromníková et al., 2022; Feng et al., 2023). When it comes to their relationships with humans, companion animals perform important functions (Meyer et al., 2022). They can be kept as pets, help

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with livestock care, serve as security dogs, or serve as guide dogs for the visually impaired. Companion animals that are considered stray or community-owned are also in close association with humans (Baneth, 2014; Wall, 2016; Losey, 2022). Often, companion animals are permitted indoor access where they are living in close quarters with humans and outdoor access where they may encounter ticks in the environment or wildlife infected with ticks (Celina and Černý, 2022). This poses a risk to human health as companion animals may bring infected ticks into the indoor environment that may attach to human hosts, and stray dogs may be responsible for vector-transmitted infections inside human communities (Wall, 2016; Jones et al., 2018; Schön, 2022).

The global distribution of ticks is of concern as tick populations are increasing due to changing environmental conditions and their ability to adapt to intense environmental conditions, including unfavourable temperatures and humidity (Estrada-Peña, 2008; Esteve-Gassent et al., 2016; Alkishi et al., 2022; Cunze et al., 2022). In addition, populations of several tick species are introduced to new areas by means of migrating or traveling hosts, where the ticks may establish new niches and inhabit non-endemic areas (Mans, 2023). Often, if the aforementioned happens with ticks infected with blood pathogens, these tick-borne pathogens are introduced to new areas, resulting in novel or co-infections of that area (Esteve-Gassent et al., 2016; Buczek and Buczek, 2020; Cuthbert et al., 2023).

Ticks infesting dogs are of importance because of their close association to humans. In the African continent the two tick species infesting dogs are *R. sanguineus* and *H. elliptica* (Freen and Grayson, 2019; Nogueira et al., 2021; Mucheka et al., 2023; van Wyk et al., 2022; Zygnier et al., 2023). As a result, it is important to us to document the continental and worldwide distribution of these dog ticks in particular. This study is a systematic review that consolidates data published on distribution of two dog ticks, *R. sanguineus* and *H. elliptica* and further gives a comprehensive information reporting on tick-borne pathogens they are carrying.

2. Materials and methods

This systematic review was conducted and written using the guidelines specified by the preferred reporting items for systematic reviews and meta-analysis [PRISMA] (Page et al., 2021a; Page et al., 2021b), as illustrated in Fig. 1. This systematic review was registered on PROSPERO under the following ID: CRD42022327372.

2.1. Review questions

This review aimed to identify, obtain, and evaluate relevant English journal articles published after the 1st of January 1990 until the 1st June 2021 from several scientific databases documenting the distribution or prevalence of *R. sanguineus* and *H. elliptica*, as well as tick-borne pathogens they harbour. The review questions of this systematic review were: “What is the distribution of *R. sanguineus* and *H. elliptica*?” and “Which tick-borne pathogens do *R. sanguineus* and *H. elliptica* harbour?”

2.2. Search strategy and selection criteria

Several databases were searched for literature ranging from the 1st of January 1990 to the 1st of June 2021. The databases used include Scopus, Science Direct, PubMed, and Web of Science. This study used only peer review publications as required by PRISMA 2020 guidelines (Page et al., 2021a; Page et al., 2021b). As part of the search strategy, this study searched for articles published as from 1991 until the end of search which was on the 1st of June 2021. Keywords used when searching the databases included “Ticks”, “dog”, “canine”, “*Canis familiaris*”, “*Rhipicephalus sanguineus*”, “brown dog tick”, “kennel tick”, “pantropical dog tick”, “*Haemaphysalis elliptica*”, “*Haemaphysalis leachi*”, “yellow dog tick”. Previously ticks belonging to the species of *H. elliptica*

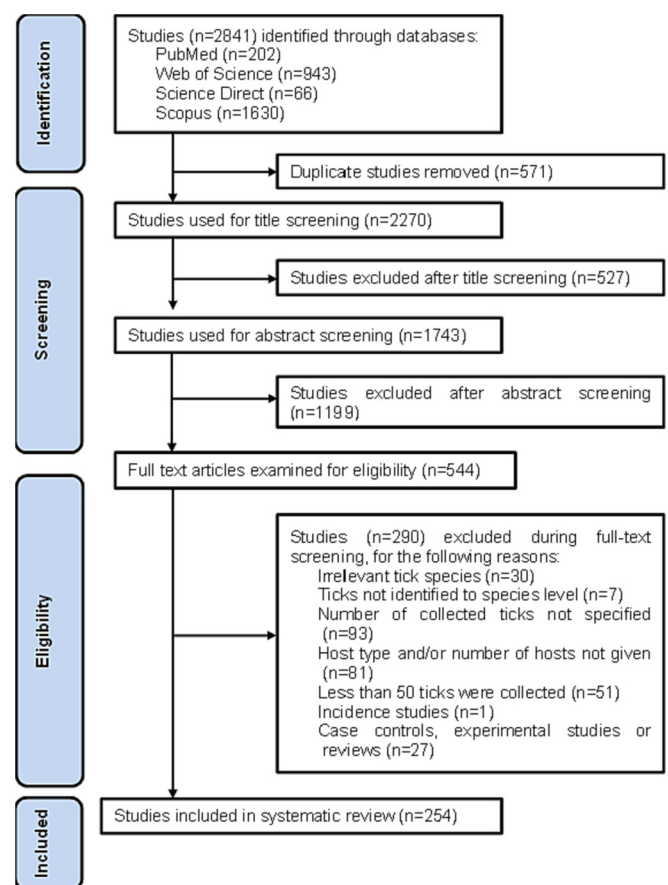


Fig. 1. Flow diagram illustrating eligible studies that were identified during the selection process by following the PRISMA guidelines.

were identified as *H. leachi* until the redescription made by Apana-shevich et al. (2007) where it was re-established as *H. elliptica*. For this reason, *H. leachi* was included as a keyword. Searches on the databases either used the keywords alone or combined them by using the “AND” and/or “OR” operators. After searching each database, the article titles were downloaded and exported to the reference management Mendeley software (Sungur and Seyhan, 2013).

2.3. Exclusion and inclusion criteria

After the journal articles were exported to Mendeley, the duplicated journal articles were removed. Subsequently, the titles and then abstracts of the journal articles were screened for studies that were relevant to the review questions. The full-text screening was then carried out to identify eligible studies that adhered to the specific criteria. The above-mentioned studies were only deemed eligible if: (1) respectively, the source type and document type was a journal article, (2) the journal articles were open access, (3) journal articles were published in English, (4) the articles were published between the 1st January 1990 to 1 June 2021, (5) relevant tick species (*R. sanguineus* and/or *H. elliptica*) were identified in the study, (6) ticks were identified to species level, (7) study locations were specified or spatial data were included, (8) the number of ticks collected during the study was specified, (9) the sampled hosts were specified and enumerated, (10) a minimum of 50 ticks were collected, (11) the study was not an incidence study, (12) and not a case-control, experimental study, or a review. Therefore, journal articles that did not adhere to the aforementioned criteria were excluded.

2.4. Quality assessment (risk of bias)

The quality assessments of the included research studies was conducted using the Joanna Briggs Institute's (JBI) critical appraisal tool for prevalence studies (Munn et al., 2015) (Supplementary Fig. S3) which considers 9 aspects of the studies, and assigns a score of 1 for adhering to each aspect. Subsequently, a score of 5 or above was considered a low risk of bias, whereas a score below 5 was considered a high risk of bias (Azene et al., 2020).

2.5. Data collection and analysis

Data extracted from eligible studies included the author's surnames, year of publication, period the study was conducted, diagnostic method of tick identification, host type and number of hosts sampled, the total number of ticks collected, the prevalence of *R. sanguineus* and/or *H. elliptica*, as well as the presence, species, prevalence, and detection method of tick-borne pathogens from *R. sanguineus* and/or *H. elliptica* ticks. The extracted data was recorded on a spreadsheet. Every step of the systematic review, including eligibility, inclusion, quality assessment, and extraction of data, was carried out by an individual reviewer. In cases where data was not made available in the article but was available as supplementary material, the supplementary material was downloaded and considered during the screening process. No further attempts were made to contact the authors of journal articles for additional or unpublished data.

3. Results

3.1. Article selection

After searching the databases, there were a total of 2841 journal articles (Fig. 1). Thereafter, 571 duplicate articles were removed, leaving 2270 articles that were subsequently used for title screening, which resulted in the removal of 527 articles leaving a total of 1743 articles that were used for abstract screening. Subsequently, a total of 1199 articles were removed, of which 554 remained and were subsequently examined for eligibility by full-text screening. Furthermore, 290 articles were removed as they focused on irrelevant tick species ($n = 30$), the ticks were not identified to species level ($n = 7$), the number of ticks collected during the study was not specified ($n = 93$), the type of host sampled and/or the number of sampled hosts was not specified ($n = 81$), less than 50 ticks were collected during sample collections ($n = 51$), the article was based on an incidence study ($n = 1$), and lastly, the articles were based on case controls, experimental studies or reviews ($n = 27$). After screening, the articles for eligibility 254 studies were included in this systematic review.

3.2. Article characteristics

For the first review question concerning the distribution of *R. sanguineus* and *H. elliptica*, the study characteristics included the authors of each article and year of publication, the country where the study was conducted, the identification method of ticks, sampled hosts and number of hosts sampled, the total number of ticks collected during sampling, as well as the prevalence of *R. sanguineus* and/or *H. elliptica* (Supplementary Table S1). For the second review question concerning the tick-borne pathogens that *R. sanguineus* and/or *H. elliptica* harbour on a global scale, the study characteristics included the authors of each article and year of publication, the geographical location of the study where the infected ticks were collected, the tick-borne pathogens detected in *R. sanguineus* and/or *H. elliptica* ticks, as well as the tick-borne pathogens detection method (Supplementary Table S1).

3.3. Distribution of *R. sanguineus* and/or *H. elliptica*

Of the studies included in this systematic review, respectively, 247 and 19 articles collected and identified *R. sanguineus* and *H. elliptica*, while both tick species were collected and identified in 15 studies (Supplementary Table S2). Based on data from the above-mentioned 195 studies, *R. sanguineus* ticks have been reported globally (Fig. 2), while *H. elliptica* ticks were only found in African countries (Fig. 3). Both tick species were reported from studies conducted in South Africa ($n = 5$), Nigeria ($n = 4$), Mozambique ($n = 3$), Benin ($n = 1$), Ethiopia ($n = 1$), and Uganda ($n = 1$).

Publications included in this systematic review used morphological identification ($n = 222$) and a combination of morphological identification and genetic analysis of PCR amplicons ($n = 29$) to identify the tick species. Of the aforementioned articles, a total of 218 used morphological identification methods for *R. sanguineus* ticks, and 29 used a combination of morphological identification and conventional PCR, whereas 19 articles used morphological identification for *H. elliptica* ticks. Only morphological identification techniques were utilized in the 15 articles that mentioned the existence of both tick species (Fig. 4).

Several studies reported that *R. sanguineus* was collected from domestic dogs ($n = 213$), vegetation ($n = 23$), domestic cats ($n = 17$), goats ($n = 14$), sheep ($n = 14$), cattle ($n = 9$), humans ($n = 5$), deer ($n = 4$), rodents ($n = 3$), hedgehogs ($n = 3$), foxes ($n = 2$), camels ($n = 2$), horses ($n = 2$), wolves ($n = 2$), Black-tailed marmoset ($n = 1$), coyotes ($n = 1$), Croatia ($n = 1$), raccoons ($n = 1$), guinea pigs ($n = 1$), Iberian lynx ($n = 1$), mouflon ($n = 1$), unspecified host ($n = 1$), donkeys ($n = 1$), European pine marten ($n = 1$), Chinese hare ($n = 1$), boars ($n = 1$), ring-necked pheasants ($n = 1$), jackals ($n = 1$), mongoose ($n = 1$), as well as several species of canine hosts ($n = 1$). The articles in the systematic review that reported the presence of *H. elliptica* were collected from domestic dogs ($n = 14$), vegetation ($n = 3$), cheetahs ($n = 2$), rodents ($n = 2$), jackals ($n = 1$), domestic cats ($n = 1$), caracals ($n = 1$), lions ($n = 1$), and leopards ($n = 1$). Of the articles that reported the presence of both *R. sanguineus* and *H. elliptica*, both tick species were collected from domestic dogs ($n = 14$), rodents ($n = 1$), and domestic cats ($n = 1$).

A total of 120 articles that reported the presence of tick-borne pathogen infections within *R. sanguineus* or *H. elliptica* ticks were included in this systematic review (Supplementary Table 2). Respectively, 119 and 2 of the above-mentioned articles reported the presence of tick-borne pathogens within *R. sanguineus* ticks and *H. elliptica* ticks. In addition, only 1 article reported the presence of tick-borne pathogens within both *R. sanguineus* and *H. elliptica* ticks (Fig. 5). Detected tick-borne pathogens within *R. sanguineus* were from Brazil ($n = 20$), Italy ($n = 13$), Turkey ($n = 10$), China ($n = 7$), Taiwan ($n = 7$), Mexico ($n = 6$), United States ($n = 6$), Malaysia ($n = 5$), Spain ($n = 4$), France ($n = 3$), Philippines ($n = 3$), Algeria ($n = 2$), Australia ($n = 2$), Colombia ($n = 2$), Costa Rica ($n = 2$), Cuba ($n = 2$), Nigeria ($n = 2$), Panama ($n = 2$), Portugal ($n = 2$), Romania ($n = 2$), Russia ($n = 2$), South Africa ($n = 2$), Thailand ($n = 2$), Tunisia ($n = 2$), Vietnam ($n = 2$), Argentina ($n = 1$), Cameroon ($n = 1$), Egypt ($n = 1$), Greece ($n = 1$), Indonesia ($n = 1$), Iran ($n = 1$), Israel ($n = 1$), Laos ($n = 1$), Nicaragua ($n = 1$), Palestine ($n = 1$), Serbia ($n = 1$), Singapore ($n = 1$), and Ukraine ($n = 1$). Whilst, tick-borne pathogens detected within *H. elliptica* were from South Africa ($n = 1$) and Uganda ($n = 1$). The study that reported the presence of tick-borne pathogens within both tick species was from South Africa ($n = 1$).

The studies identified the tick-borne pathogen infecting *R. sanguineus* ticks as belonging to *Rickettsia* ($n = 75$) [*Rickettsia* spp. ($n = 28$), *Candidatus Rickettsia asemboensis* ($n = 1$), *C. R. barbariae* ($n = 2$), *C. R. goldwasesrii* ($n = 1$), *R. rickettsia* ($n = 4$), *R. amblyommii* ($n = 1$), *R. asembonensis* ($n = 2$), *R. conorii* ($n = 8$), *R. conorii israelensis* ($n = 1$), *R. massiliae* ($n = 15$), *R. parkeri* ($n = 1$), *R. rhipicephali* ($n = 1$), *R. felis* ($n = 2$), *R. rickettsi* ($n = 1$), *R. monacensis* ($n = 3$), *R. raoultii* ($n = 2$), *R. sibirica* subsp. *Mongolitimonae* ($n = 1$), and *R. slovacica* ($n = 1$)], *Babesia* ($n = 36$) [*Babesia* spp. ($n = 3$), *B. canis* ($n = 2$), *B. capreoli* ($n = 1$), *B. capreoli/divergens* ($n = 1$), *B. gibsoni* ($n = 3$), *B. microti* ($n = 2$), *B. rossi*

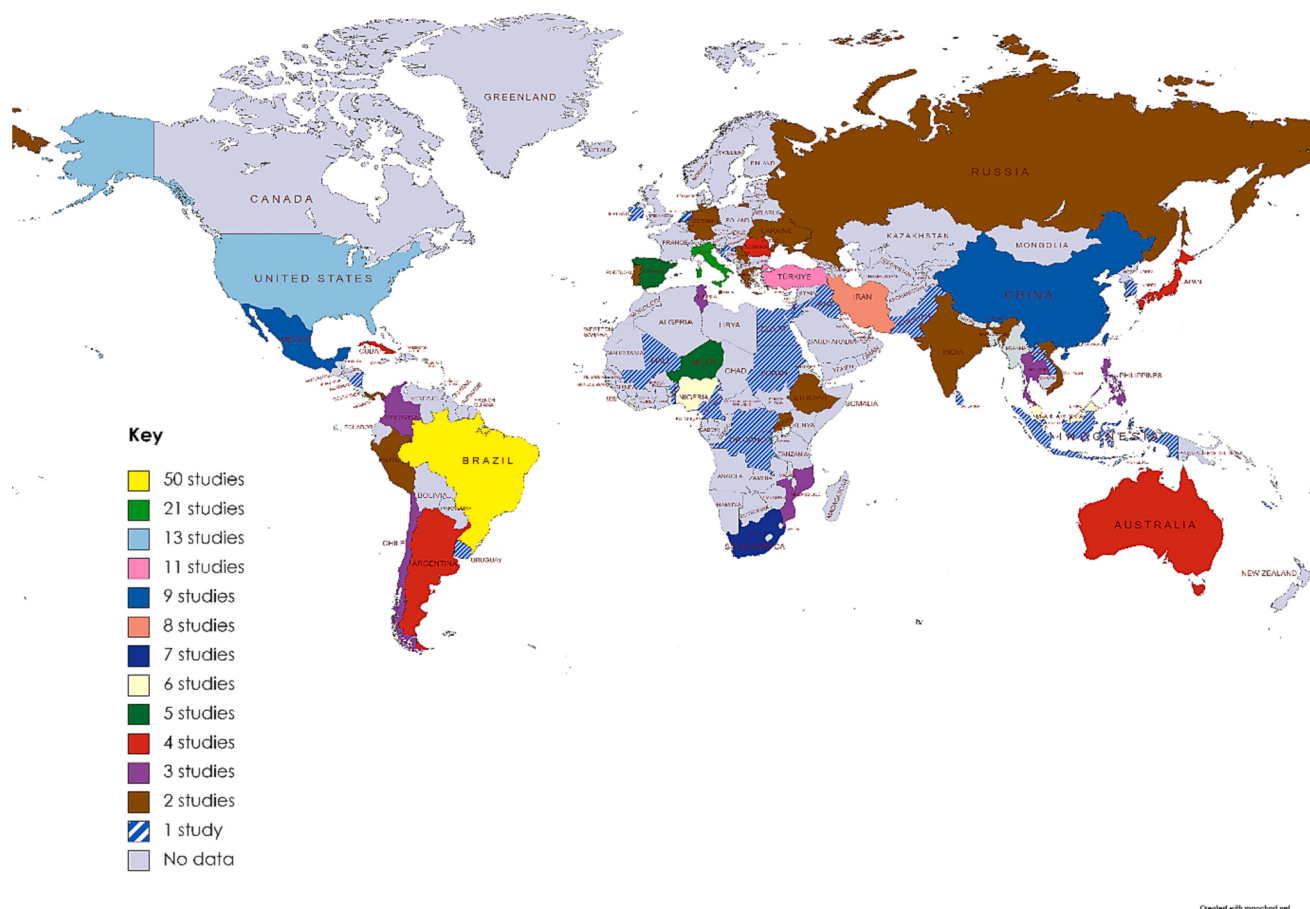


Fig. 2. World map showing number of articles from different countries which reported the *R. sanguineus* tick occurrence (<https://www.mapchart.net/world.html> [accessed on 12 March 2023]).

($n = 1$), *B. venatorum* ($n = 1$), *B. vogeli* ($n = 19$), *B. vulpes* ($n = 1$), and *B. ovis* ($n = 2$), *Ehrlichia* ($n = 36$) [*Ehrlichia* spp. ($n = 6$), *Ehrlichia* spp. HF ($n = 1$), *E. canis* ($n = 27$), *E. chaffeensis* ($n = 1$), and *E. ewingii* ($n = 1$)], *Anaplasma* ($n = 33$) [*Anaplasma* spp. ($n = 6$), *A. ovis* ($n = 2$), *A. phagocytophilum* ($n = 6$), and *A. platys* ($n = 19$)], *Hepatozoon* ($n = 21$) [*Hepatozoon* spp. ($n = 2$) and *H. canis* ($n = 19$)], *Leishmania infantum* ($n = 6$), *Theileria* ($n = 6$) [*Theileria* spp. ($n = 1$), *T. buffeli/sergenti/orientalis* ($n = 1$), *T. cervi* ($n = 1$), *T. equi* ($n = 1$), and *T. ovis* ($n = 2$)], *Bartonella* ($n = 5$) [*Bartonella* spp. ($n = 3$), *B. rochalimae* ($n = 1$), and *B. clarridgeiae* ($n = 1$)], *Coxiella* ($n = 5$) [*Coxiella* spp. ($n = 2$) and *C. burnetii* ($n = 3$)], *Borrelia* ($n = 4$) [*Borrelia* spp. ($n = 1$) and *B. burgdorferi* ($n = 3$)], *Staphylococcus* ($n = 3$) [*S. cohnii* ($n = 1$), *S. epidermidis* ($n = 1$), and *S. saccharitidis* ($n = 1$)], *Bacillus* ($n = 2$) [*B. clausii* ($n = 1$) and *B. megaterium* ($n = 1$)], *Brucella* spp. ($n = 1$), *Acinetobacter iwoffii* ($n = 1$), *Ehrlichia/Anaplasma* ($n = 1$). There were 8 articles reporting co-infections of haemoparasites of *R. sanguineus* including co-infections between *B. gibsoni* and *E. canis* ($n = 2$), *Anaplasma* spp., and *Babesia* spp. ($n = 1$), *B. gibsoni* and *A. platys* ($n = 1$), *E. canis* and *A. platys* ($n = 1$), *E. canis*, *A. platys* and *B. burgdorferi* ($n = 1$), *E. chaffeensis* and *E. canis* ($n = 1$), as well as *R. rickettsia* and *R. rhipicephali* ($n = 1$). The studies identified the haemoparasites infecting *H. elliptica* ticks as belonging to *Rickettsia* ($n = 2$) [*Rickettsia* spp. ($n = 1$) and *R. africae* ($n = 1$)], *B. rossii* ($n = 1$), *Ehrlichia* spp. ($n = 1$), and *Ehrlichia/Anaplasma* ($n = 1$) (Fig. 6).

The articles that reported detection of tick-borne pathogens within *R. sanguineus* used molecular techniques as shown in Fig. 7, and bacterial culturing using the streak plate method performed on blood agar, trypticase soy agar, Baird-Parker agar, and mannitol salt agar ($n = 1$). Studies that detected tick-borne pathogens within *H. elliptica* used molecular techniques including reverse line blot hybridization (RLB) ($n =$

1) and qPCR ($n = 1$). The article that discovered the presence of tick-borne pathogens in both *R. sanguineus* and *H. elliptica* ticks used RLB ($n = 1$).

3.4. Quality assessment (risk of bias) of studies

All of the studies in this systematic review had a quality score ranging from 5 to 8 and were considered a low risk of bias (Supplementary Table S3).

4. Discussion

Based on data from published articles used in this systematic review, *R. sanguineus* has worldwide distribution, whilst *H. elliptica* is restricted to the African continent. There were 64 countries that reported the presence of *R. sanguineus*, whereas *H. elliptica* was only reported in 6 countries. On the other hand, *H. elliptica* is documented to be present only on the African continent, with the majority of studies included in this systematic review reporting the presence of *H. elliptica* mainly in South Africa. It is widely considered that *R. sanguineus* has a global prevalence, mainly in tropical or subtropical regions (Wall, 2016). The global prevalence of *R. sanguineus* is largely associated with their hosts and adaptation abilities (Gray et al., 2013; Wall, 2016). This tick is mainly associated with Canidae hosts (mainly dogs) but is also documented to infest a wide selection of hosts, including several mammals, reptiles, and birds. The adaptive ability of *R. sanguineus* is so good that they are most often located inside urban areas, usually inside cracks and crevices or vegetation used by the hosts. In addition, the close proximity between *R. sanguineus* and traveling hosts (such as humans and domestic

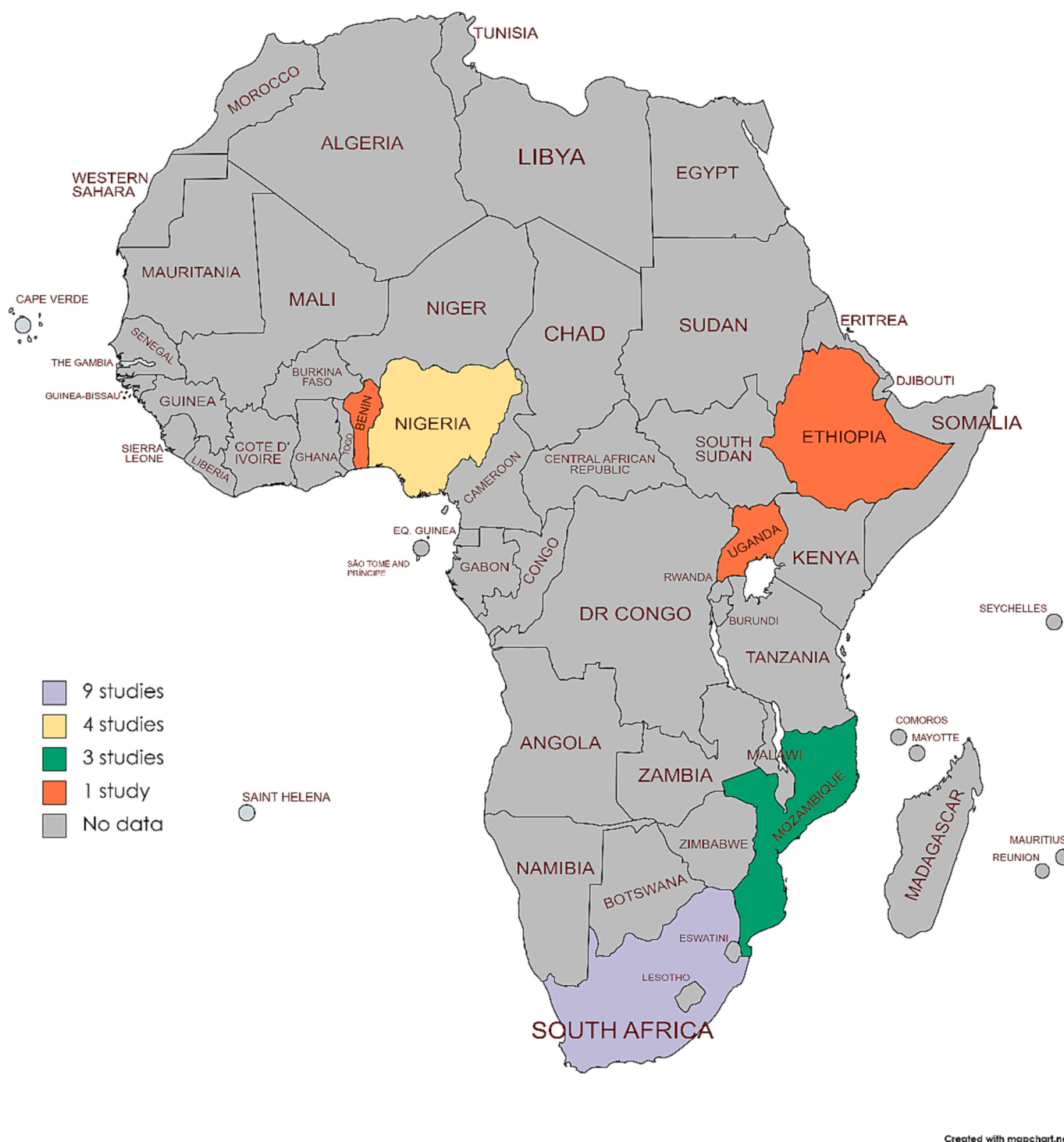


Fig. 3. African continent map showing the number of articles from different countries that reported the occurrence of *H. elliptica* tick (<https://mapchart.net/africa.html> [Accessed on 12 March 2023]).

dogs) or migratory hosts (such as birds), is one of the contributors to the global distribution of this tick (Dantas-Torres, 2008; Gray et al., 2013). Buczek and Buczek (2020) suggested that ticks may be transported to other areas within the same continent or to other continents by several means. This includes owners traveling with infected companion animals (Dutto and Selmi, 2009; Jameson et al., 2010; Claerebout et al., 2013; Hansford et al., 2014, 2016), the importation of exotic infected wild animals, or eggs and ticks unattached from the host incidentally imported with transport containers containing animal fur (Keirans and

Durden, 2001; Sparagano et al., 2015).

Data obtained from published articles shows that majority of tick-borne pathogens by far were detected within *R. sanguineus*, which has been reported in 38 countries, whereas tick-borne pathogen infections within *H. elliptica* were only reported in 2 countries. In addition, tick-borne pathogen infections within both tick species were detected in 1 country. The *R. sanguineus* is thought to be diverse throughout the world, so it stands to reason that the infections it harbours are also widespread (Jongejan and Uilenberg, 2004; Wall, 2016), explaining the wide variety

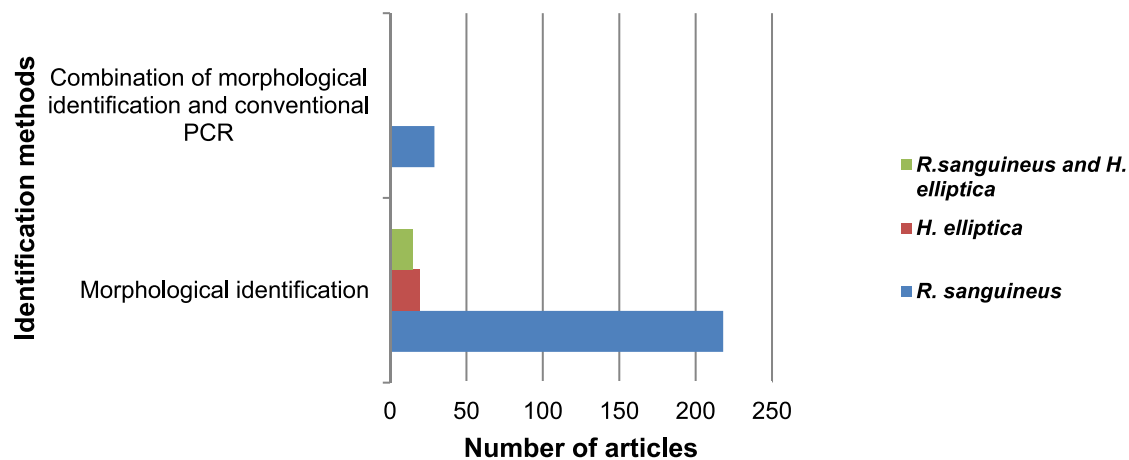


Fig. 4. Frequency of identification methods of *R. sanguineus* and/or *H. elliptica* ticks.

of *R. sanguineus*-borne pathogens identified by studies used in this systematic review. Tick-borne pathogens detected within *H. elliptica* were only reported in South Africa and Uganda (Probst et al., 2015; Kolo et al., 2016), whilst there is information gap of which pathogens this tick species may be harbouring in other countries where its presence has been reported including Mozambique, Ethiopia, Nigeria and Benin. Tick-borne pathogens may be introduced to new niches when traveling with infected ticks or infected tick hosts. Migration of tick-infested animals, including migratory birds flying between continents, is the primary route of transmission for ticks that may be carrying pathogens. Birds can easily navigate obstacles, making them more likely than other migratory animals to spread ticks. In the larval and nymphal developmental stages, when ticks are transmitted most frequently by migratory birds, they have the potential to detach from their avian hosts, transition to the next developmental stage, and adhere to a new native host, resulting in a tick infestation (Sparagano et al., 2015). While Socolovschi et al. (2012) demonstrated the distribution of *R. sanguineus* and *Haemaphysalis* spp. infected with *Rickettsia* spp. to southern Europe, Wallménius et al. (2022) demonstrated the distribution of *Haemaphysalis* spp. infected with *Rickettsia* spp. to western Europe via migrating birds.

Numerous tick species, including *R. sanguineus* and *H. elliptica*, may adapt to new environments with favourable environmental conditions such as adequate vegetation coverage, temperature, moisture, photoperiod, and compatible hosts (Dantas-Torres, 2015). Changes in temperature brought on by climate change may be one of the primary forces driving tick adaptation, particularly when taking questing ticks into consideration. As a result of climate change, tick populations may grow in already-infested areas, some tick species may exhibit longer seasonal activity cycles, and tick developmental stages may be shortened. High temperature in existing tropical regions may cause unsuitable habitats and be disastrous for certain tick species, compelling these ticks to leave and search for newly suitable areas (Dantas-Torres, 2015). These ticks may consist of *R. sanguineus*, that are highly physiologically adaptable to dry areas with low humidity (Parola et al., 2008; Dantas-Torres, 2015). Spring and autumn seasons that are increasingly becoming longer along with the winter season becoming warmer may contribute to the increasing distribution of several tick species to higher altitudes and towards northern latitudes (Dantas-Torres, 2015). Climate may also result in shorter tick developmental stages or hastened life cycles, increases in tick populations in already-infested areas, as well as longer seasonal activity of several tick species (Randolph, 2010; Bouchard et al., 2019).

Numerous tick species rely on wild rodents as hosts during the immature stages, including *H. elliptica* ticks, whereas other tick species require wildlife as hosts during the adult stages to lay eggs (Penzhorn et al., 2020). The distribution of wildlife and rodents, which serve as

hosts for ticks and reservoir hosts for diseases carried by ticks, is also impacted by rising temperatures, in addition to the distribution of ticks (Parola et al., 2008; Dantas-Torres, 2015; Bouchard et al., 2019). Climate change also increases the contact of humans with ticks as people spend longer time outdoors and in areas as potential habitats of ticks, which prolongs exposure of humans to ticks (Randolph, 2010; Bouchard et al., 2019).

Articles included in this systematic review reported the presence of *R. sanguineus* and *H. elliptica* collected on from few different hosts. Majority of the articles ($n = 203$ studies) reported *R. sanguineus* infesting dogs, followed by collections from vegetation ($n = 22$ studies), some collections from livestock ($n = 18$ studies) and humans ($n = 6$ studies), as well as the least collections from different wildlife species ($n = 17$ studies) [Supplementary Table S2]. Most articles reported the collection of *H. elliptica* from domestic animals, followed by collections from vegetation, and the least collections were from different wildlife species. Both tick species were collected from companion animals and rodents. Both *R. sanguineus* and *H. elliptica* are three-host ticks, that require a new host with each blood meal to molt to the new developmental stage (Dantas-Torres, 2008; Gray et al., 2013). Dogs are *R. sanguineus*' primary preferred hosts because they lack the necessary immune system mechanisms needed to effectively defend themselves against ticks (Baneth, 2014). In certain instances, these ticks display opportunistic host selection where the larval and nymphal developmental stages feed on small mammals, like rodents, and the adult developmental stages feed on large animals and humans (Dantas-Torres, 2008). The larval and nymphal developmental stages of *H. elliptica* prefer to infest rodents, whereas the adult developmental stage prefers companion animals, as well as some wild canine species as hosts (Penzhorn et al., 2020). These ticks are more prevalent on farms or large domestic plots, mainly because of the presence of rodents and companion animals that serve as hosts for all developmental stages of *H. elliptica* (Fourie et al., 2010; Penzhorn et al., 2020). Some of the articles included in this systematic review reported the collection of *R. sanguineus* and/or *H. elliptica* from vegetation, this is because three-host tick species spend the majority of their life cycle (approximately 94 to 97%) off of hosts (Dantas-Torres, 2008).

Numerous *Theileria* spp. were detected in *R. sanguineus* ticks including *T. ovis* (responsible for ovine theileriosis in sheep and goats) (Zaeemi et al., 2011), *T. equi* (responsible for equine piroplasmosis in horses and donkeys) (Kappmeyer et al., 2012), *T. cervi* (responsible for theileriosis in deer) (Pavón-Rocha et al., 2020), as well as the *T. buffeli/sergenti/orientalis* group (responsible for bovine theilerioses in buffaloes and cattle) (Chisu et al., 2021).

The *Staphylococcus* genus detected within *R. sanguineus* was also reported by some articles used in this systematic review. *Staphylococcus* is

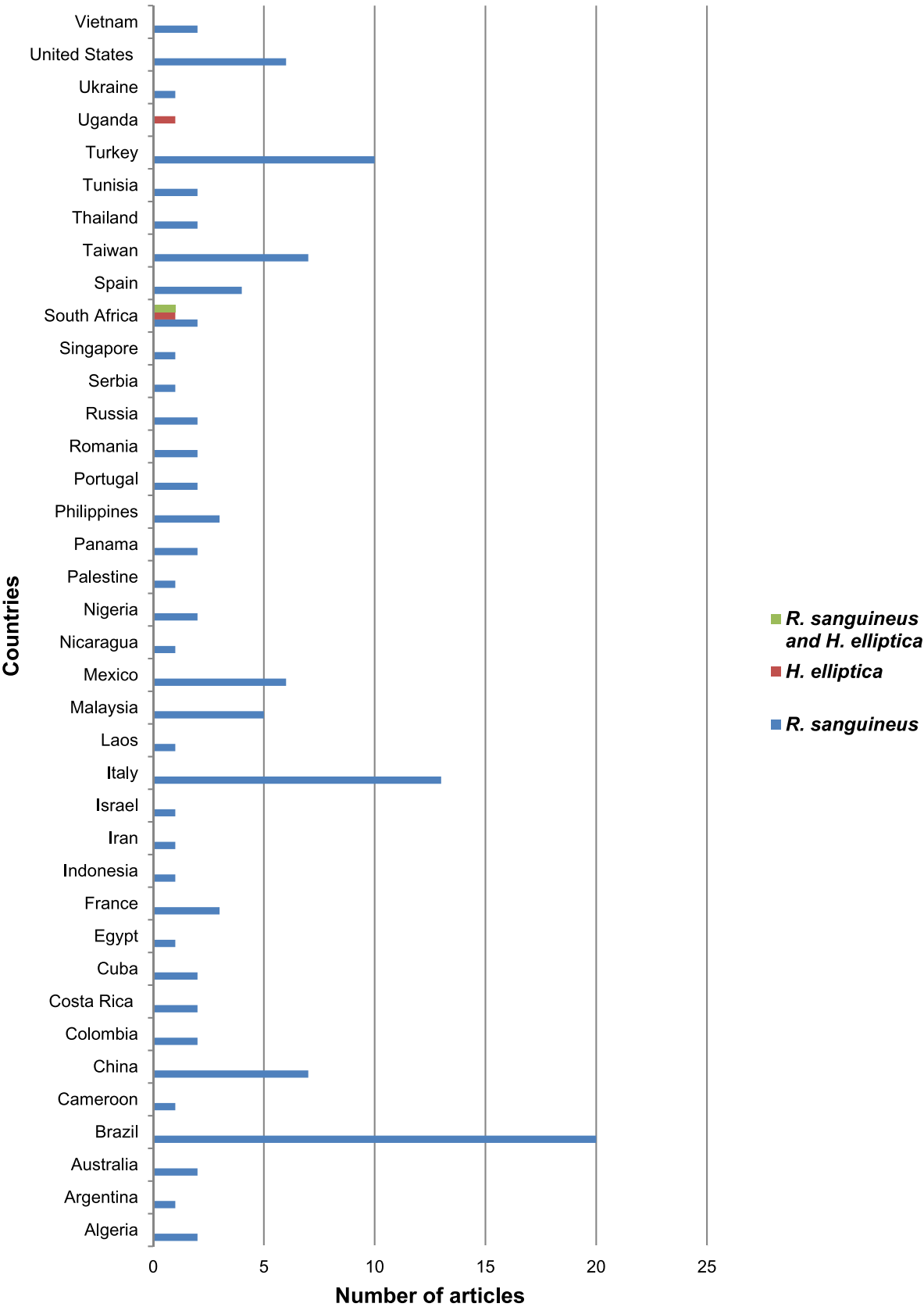


Fig. 5. Frequency of countries of tick-borne pathogens harboured by *H. elliptica* or *R. sanguineus*.

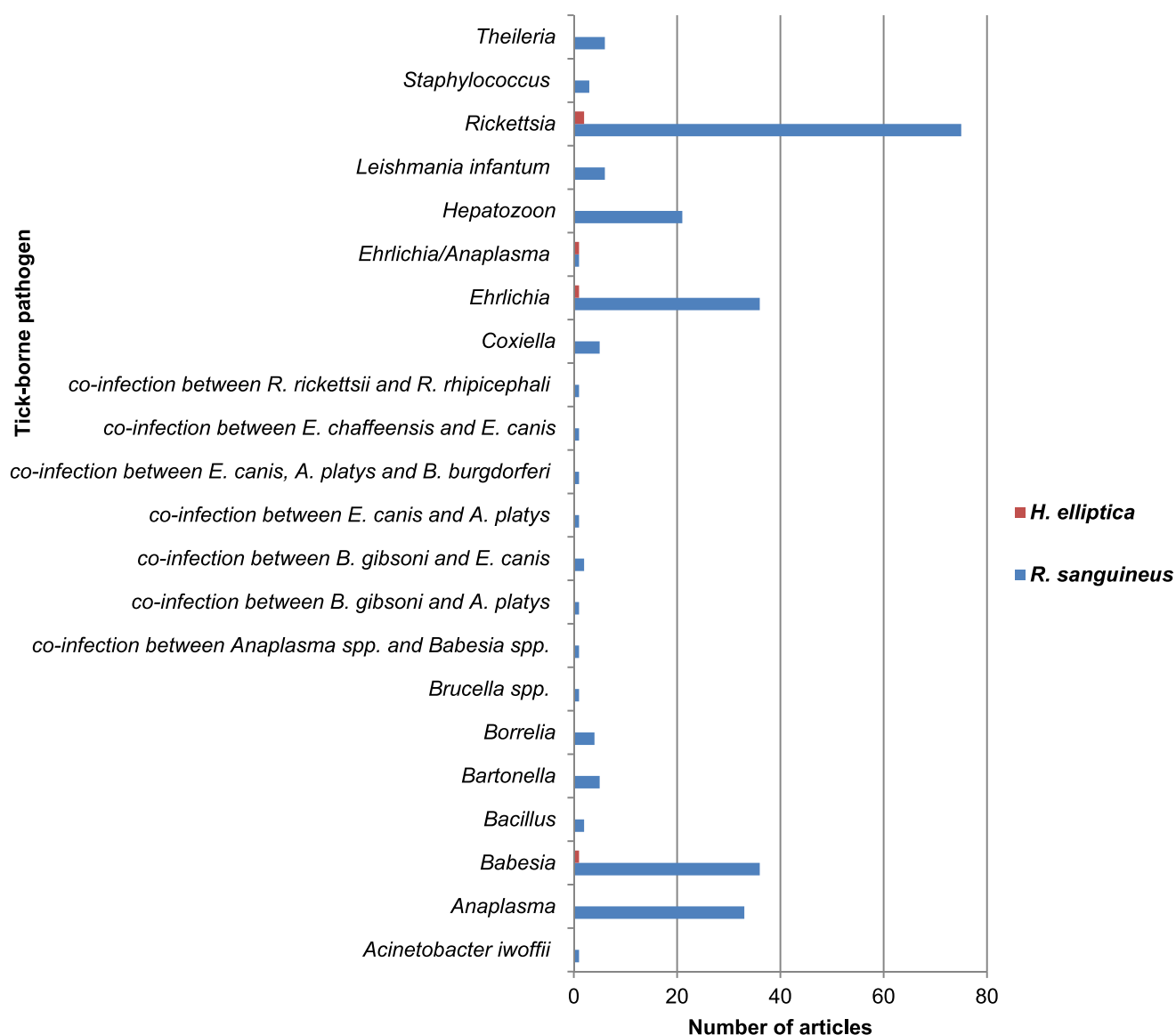


Fig. 6. Frequency of tick-borne pathogens harboured by *H. elliptica* or *R. sanguineus*.

often found in common areas such as vegetation, soil, water, and food, as well as on the mucus membranes and skin of humans and mammals. Since it is generally in areas associated with ticks, it may be transmitted from ticks to hosts during a blood meal (Olayide and Bamidele, 2008). The following species were found in the systematic review's articles: *S. cohnii* (opportunistic pathogen causing meningitis, endocarditis, and bloodstream infections in humans) (Mendoza-Olazarán et al., 2017), *S. epidermidis* (emerging pathogen responsible for nosocomial infections in humans) (Ahmad et al., 2022), and *S. saccharitidis* (occasionally responsible for prosthetic valve infectious endocarditis, device-related joint and bone infections, as well as catheter-related bloodstream infections in humans) (Brooks et al., 2019).

In this systematic review, *Acinetobacter iwoffii* was also detected in *R. sanguineus* ticks and is considered a bacterium that normally forms part of the human skin microbiota. It was also previously reported in water, food products, and hospitals due to its ability to survive extremely low temperatures, low pH levels, dry conditions, irradiation, desiccation, and disinfectants (Malta et al., 2020). Although it is part of the skin microbiota, human infections were previously reported, specifically gastroenteritis and catheter-associated infections of hospitalized immunocompromised patients (Regalado et al., 2009).

A few species of the *Rickettsia* genus were detected within *R. sanguineus* and *H. elliptica* ticks. The *Rickettsia* genus is globally distributed and has a wide range of hosts, including arthropods (Behravesh and Massung, 2016). It is widely considered that most *Rickettsia* spp. are endosymbionts that are not pathogenic to their hosts. Mammals and humans are considered to be accidental hosts of *Rickettsia*, due to pathogen transmission of infected ticks, mites, or fleas during a blood meal (Ahantarig and Trinachartvanit, 2013). Of the articles included in the systematic review, within *H. elliptica* ticks, *R. africae* that is responsible for African tick-bite fever in humans was detected. On the other hand, among the *Rickettsia* species found in *R. sanguineus*, there is *R. sibirica* subsp. *Mongolitimona*, which causes human cases of North Asian tick typhus, *R. rickettsii* (responsible for Rocky Mountain spotted fever in humans), *R. rhipicephali* (may cause moderately severe illness in meadow voles), *R. raoultii* and *R. slovaca* (responsible for scalp eschar and neck lymphadenopathy after a tick bite, or SENLAT, syndrome in humans), *R. parkeri* (causes mild, eschar associated rickettsiosis or *R. parkeri* rickettsiosis), *R. monacensis* and *R. massiliae* (causes spotted fever in humans), *R. helvetica* (causes an unnamed rickettsiosis in humans), *R. felis* (responsible for flea-borne spotted fever or cat-flea typhus in humans), *R. conorii israelensis* (responsible for Israeli tick

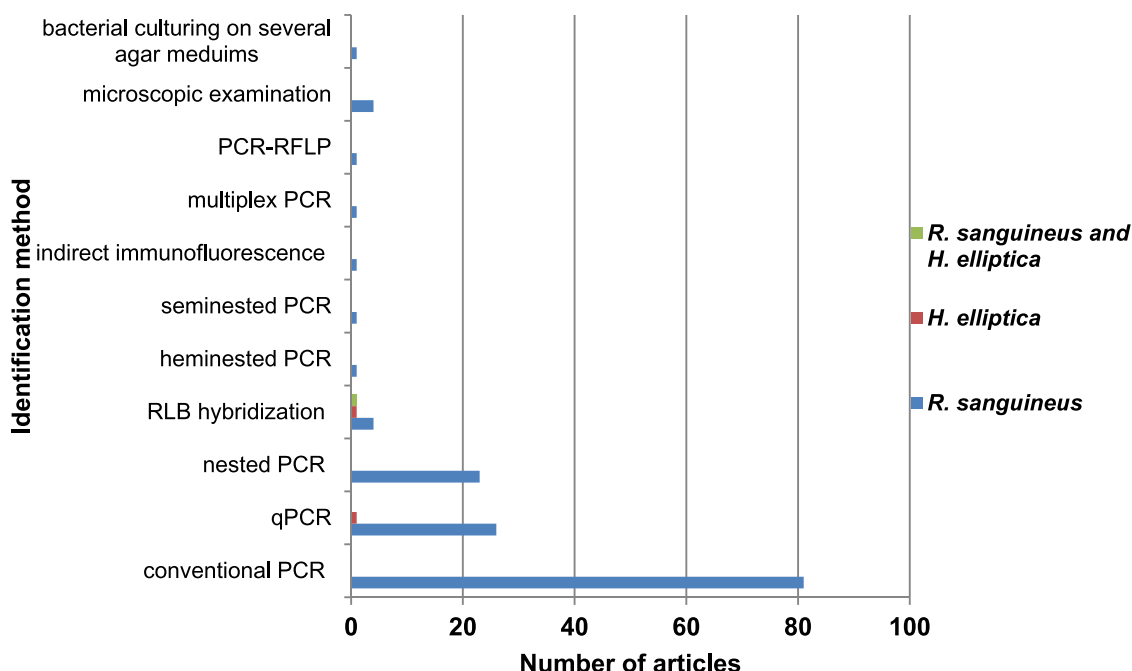


Fig. 7. Frequency of detection of tick-borne pathogens harboured by *R. sanguineus* and/or *H. elliptica* ticks.

typhus or Israeli tick bite fever), *R. conorii* (Mediterranean spotted fever or Boutonneuse fever) (Parola et al., 2013).

Two articles included in this systematic review also reported the presence of *Leishmania infantum* (responsible for canine visceral leishmaniasis, and less commonly cutaneous leishmaniasis in humans) within *R. sanguineus* ticks. Domestic dogs and various wild canids act as natural reservoirs of this pathogen and it is transmitted by the *Lutzomyia longipalpis* sandfly. This pathogen may also be transstadially transmitted to humans, especially in the presence of potentially infected dogs. Although *L. longipalpis* sandflies are considered the only recognized vector, transmission by means of other arthropods, including ticks was previously considered a possibility (Campos and Costa, 2014). Previously, *L. infantum* was reported in *R. sanguineus* ticks but the association between *L. infantum* and *R. sanguineus* is not yet fully understood (Solano-Gallego et al., 2012).

Some of the articles in the systematic review reported the presence of *Hepatozoon* spp. within the *R. sanguineus* ticks. *Hepatozoon* is a well-documented and recognized pathogen of veterinary importance, especially among companion animals. Mainly, *H. canis* and *H. americanum* are considered as veterinary important. *Hepatozoon americanum* is also documented as an emerging pathogen. Respectively, *H. canis* and *H. americanum* are transmitted mainly by *R. sanguineus* and *Amblyomma maculatum* ticks (Baneth et al., 2003). Although quite a few articles in this systematic review identified the species as *H. canis* which is associated with canine hepatozoonosis in dogs and possibly other members of canines and cats (Behravesh and Massung, 2016).

Multiple *Ehrlichia* spp. were detected in *R. sanguineus* and *H. elliptica* ticks by some studies included in this systematic review. Some species of *Ehrlichia* transmitted by ticks are well-documented and are of veterinary importance, especially *E. canis*, and some are considered zoonotic pathogens, such as *E. ewingii* and *E. chaffeensis* (Lin et al., 2021). Some articles included in this systematic review have reported detection of *Ehrlichia* spp. in *H. elliptica* ticks, whilst *Ehrlichia* sp. HF (responsible for laboratory mice acute fatal infection, sharing similarities with acute fatal human monocytic ehrlichiosis from *E. chaffeensis*) has been detected from *R. sanguineus* (Lin et al., 2021), as well as *E. ewingii* (responsible for *Ehrlichiosis ewingii* infection or *Ehrlichia ewingii* ehrlichiosis in humans), *E. chaffeensis* (responsible for human monocytic ehrlichiosis) (Lin et al., 2021), *E. canis* (responsible for canine monocytic

ehrlichiosis, or CME, in dogs, and animals classified under the family Canidae) (Harrus et al., 2016).

A few articles of this systematic review have detected *Coxiella* spp. and *Coxiella burnetii* (responsible for Q fever in humans and subclinical infections in dogs and cats) from *R. sanguineus* (Angelakis and Raoult, 2010; Rezaei et al., 2016). The *C. burnetii* can spread with aerosol particles contaminated with spores but is also transmitted by arthropods, especially ticks, which is vital for wildlife reservoir cycles (Pfeffer et al., 2016).

One article included in the current study has reported presence of *Brucella* spp. in *R. sanguineus* ticks. Some of the species of *Brucella* genus are pathogenic to humans and also infect other animals. Transmission to animal or human hosts occur mainly by consumption of contaminated food or water. *Brucella* may also be present in all of the developmental stages of ticks, from eggs to adults. Therefore tick transmission of *Brucella* to other hosts is possible when ticks take a blood meal (Jia et al., 2022).

The current study has also used articles which have reported presence of *Borrelia* spp. within *R. sanguineus* ticks. Some members of the *Borrelia* genus are well-documented pathogens of zoonotic and veterinary importance, whereas others are considered non-pathogenic. A few of the articles included in this systematic review identified *B. burgdorferi* which is associated with Lyme disease in humans and animals. Certain birds and wild mammals serve as reservoirs of some subspecies of *B. burgdorferi*, that maintain the pathogen in wildlife reservoir cycles (Radolf et al., 2021). Multiple *Bartonella* spp. were detected within *R. sanguineus* ticks by some articles in this systematic review and were identified as *B. rochalimae* and *B. clarridgeiae*. These species are associated with companion animals as *B. rochalimae* is a newly recognized emerging pathogen of dogs (Ernst et al., 2020) and the maintenance host of *B. clarridgeiae* are domestic cats and possibly other felines (Birtles, 2016).

The *Bacillus* genus consists of certain species that inhabit a wide variety of natural environments. Generally, most *Bacillus* spp. are considered to be non-pathogenic, with the exception of *B. cereus* and *B. anthracis*. The *B. cereus* causes food poisoning, while *B. anthracis* is responsible for anthrax (Ehling-Schulz et al., 2019). In this systematic review, one study detected *B. megaterium* and *B. clausii* in *R. sanguineus* ticks. Although *B. megaterium* is not considered as pathogenic, it was

reported to be responsible for a soft tissue infection in a human (Bocchi et al., 2020). Additionally, the prolonged use of *B. clausii* in an immunocompetent child resulted in bacteremia (Khatri et al., 2021).

Babesia spp. mainly infects domestic dogs and cats, as well as wild canines and felids. Additionally, *Babesia duncani*, *Babesia microti*, and *Babesia divergens* were reported to infect humans and *B. microti* is recognized as an emerging zoonotic tick-borne pathogen of humans (Irwin, 2016). In multiple articles used in this systematic review, *Babesia rossi* was detected in both *R. sanguineus* and *H. elliptica* ticks. Furthermore, *Babesia vulpes*, *Babesia vogeli*, *Babesia venatorum*, *Babesia ovis*, *B. microti*, *Babesia gibsoni*, *Babesia capreoli/divergens*, *Babesia capreoli*, and *Babesia canis* were detected in *R. sanguineus* ticks by numerous studies. Even though most of the above-mentioned *Babesia* spp. cause mild forms of infection, *B. rossi* is known to cause a severe form of babesiosis in South African dogs (Leisewitz et al., 2019).

Anaplasma spp. are mainly of veterinary importance, although, some species infect humans as well. Some articles included in this systematic review detected the following *Anaplasma* spp. from *R. sanguineus* ticks: *A. platys* (responsible for infectious canine cyclic thrombocytopenia mainly in dogs), *A. phagocytophilum* (responsible for granulocytotropic anaplasmosis in humans and animals), and *A. ovis* (responsible for ovine anaplasmosis mainly in sheep and goats) (Harrus et al., 2016).

A few of the articles in this systematic review reported co-infections within *R. sanguineus* ticks between *B. gibsoni* and *E. canis*, *Anaplasma* spp. and *Babesia* spp., *B. gibsoni* and *A. platys*, *E. canis* and *A. platys*, *E. chaffeensis* and *E. canis*, *R. rickettsii* and *R. rhipicephali*, as well as *E. canis*, *A. platys* and *B. burgdorferi*. Certain arthropods may maintain certain pathogens through multiple generations by acting both as a reservoir and a vector. Co-infections of companion animals and humans may result in severe diseases. In addition, these co-infections are difficult to diagnose by means of clinical signs as it may result in an incorrect diagnosis (Beasley et al., 2021).

The articles included in this systematic review identified *R. sanguineus* and/or *H. elliptica* using mainly morphological methods, as well as a combination of morphological identification and conventional PCR. The presence of tick-borne pathogens within *R. sanguineus* and/or *H. elliptica* was determined by microscopic examination, bacterial culturing on different agar media, and molecular methods including different PCR assay types. Overall, a combination of PCR and sequencing approach is increasingly been used as an identification method of ticks and tick-borne pathogens due to its sensitivity, specificity and reliable accuracy (Mtshali et al., 2015; Bailet et al., 2019; van Wyk et al., 2022). This systematic review was conducted to expand on our knowledge of the prevalence of dog ticks with special attention to *R. sanguineus* and *H. elliptica*, as well as the tick-borne pathogens that they are harbouring. There are several limitations of the systematic review such as: (i) multiple articles often use the pooling of samples, especially when screening for the presence of pathogens, which may result in heterogeneity; (ii) low number of samples from some studies; (iii) the scarcity of data in some countries, especially concerning the studies focusing on *H. elliptica* is worrisome. Lastly, publication bias is also of concern.

5. Conclusion

Rhipicephalus sanguineus has a worldwide prevalence and distribution and harbours a large array of pathogens including protozoan parasites and bacteria. Whilst it is well known that *R. sanguineus* transmits tick-borne pathogens such as *B. rossi*, *B. vogeli*, *E. canis* and *A. phagocytophilum*, its vectorial capacity (biological or mechanical) for bacteria such as *Bacillus* spp., *Staphylococcus* spp., *Acinetobacter* spp., *Borellia* spp. and *Coxiella* spp. remains to be proven beyond reasonable doubt. The *H. elliptica* is only reported in some African countries and harbours fewer tick-borne pathogens as compared to *R. sanguineus*. The current study has observed that morphological identification of dog ticks is now increasingly supplemented with DNA-based methods. There is a need for an increase in the number of studies on prevalence of dog ticks

in the African and Asian continents, as this will give a clearer picture of the current worldwide distribution of tick species and their associated tick-borne pathogens.

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This work is a systematic review that not needed ethical approval, it was registered on PROSPERO under the following ID: CRD42022327372.

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Declaration of Competing Interest

None.

Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.vprsr.2023.100969>.

References

- Ahantari, A., Trinachartvanit, W., 2013. Hard ticks and their bacterial endosymbionts (or would be pathogens). *Folia Microbiol.* 58 (5), 419–428. <https://doi.org/10.1007/s12223-013-0222-1>.
- Ahmad, S., Rahman, H., Qasim, M., Nawab, J., Alzahrani, K.J., Alsharif, K.F., Alzahrani, F.M., 2022. *Staphylococcus epidermidis* pathogenesis: interplay of *icaADBC* operon and MSCRAMMs in biofilm formation of isolates from pediatric bacteremia in Peshawar, Pakistan. *Medicina* 58 (11), 1510. <https://doi.org/10.3390/medicina58111510>.
- Alkhishe, A., Cobos, M.E., Osorio-Olvera, L., Peterson, A.T., 2022. Ecological niche and potential geographic distributions of *Dermacentor marginatus* and *Dermacentor reticulatus* (Acari: Ixodidae) under current and future climate conditions. *Web Ecol.* 22 (2), 33–45. <https://doi.org/10.5194/we-22-33-2022>.
- Angelakis, E., Raoult, D., 2010. Q fever. *Vet. Microbiol.* 140, 297–309. <https://doi.org/10.1016/j.vetmic.2009.07.016>.
- Apanashevich, D.A., Horak, I.G., Camicas, J.-L., 2007. Redescription of *Haemaphysalis (Rhipistoma) elliptica* (Koch, 1844), an old taxon of the *Haemaphysalis (Rhipistoma) leachi* group from East and southern Africa, and of *Haemaphysalis (Rhipistoma) leachi* (Audouin, 1826) (Ixodida, Ixodidae). *Onderstepoort J. Vet. Res.* 74, 181–208. <https://hdl.handle.net/10520/EJC86301>.
- Azene, A.G., Aragaw, A.M., Wassie, G.T., 2020. Prevalence and associated factors of scabies in Ethiopia: systematic review and meta-analysis. *BMC Infect. Dis.* 20, 380. <https://doi.org/10.1186/s12879-020-05106-3>.
- Bailet, B., Bouchez, A., Franc, A., Frigerio, J.M., Keck, F., 2019. Molecular versus morphological data for benthic diatoms biomonitoring in Northern Europe freshwater and consequences for ecological status. *Metabarcoding Metagenom.* 3, 21–35. <https://doi.org/10.3897/mbmg.3.34002>.
- Baneth, G., 2014. Tick-borne infections of animals and humans: a common ground. *Int. J. Parasitol.* 44 (9), 591–596. <https://doi.org/10.1016/j.ijpara.2014.03.011>.
- Baneth, G., Mathew, J.S., Shkap, V., Macintyre, D.K., Barta, J.R., Ewing, S.A., 2003. Canine hepatozoonosis: two disease syndromes caused by separate *Hepatozoon* spp. *Trends Parasitol.* 19, 27–31. [https://doi.org/10.1016/s1471-4922\(02\)00016-8](https://doi.org/10.1016/s1471-4922(02)00016-8).
- Beasley, E.A., Pessoa-Pereira, D., Scorza, B.M., Petersen, C.A., 2021. Epidemiologic, clinical and immunological consequences of co-infections during canine leishmaniasis. *Animals* 11 (11), 3206. <https://doi.org/10.3390/ani11113206>.
- Behravesh, C.B., Massung, R., 2016. Rickettsial infections. In: Day, M.J. (Ed.), *Infectious Diseases of the Dog and Cat*, 2nd ed. CRC Press, pp. 189–196.
- Bekere, H.Y., Tamanna, N., Hossen, M., Abebe, D., Harun, M., Yusuf, Y., 2022. Identification and affliction of ixodid tick species in domestic animals. *Int. J. Agric. Vet. Sci.* 4 (2), 38–45. <https://doi.org/10.34104/ijavs.022.039045>.
- Birtles, R., 2016. Bartonellosis. In: Day, M.J. (Ed.), *Infectious Diseases of the Dog and Cat*, 2nd ed. CRC Press, pp. 153–166.
- Bocchi, M.B., Perna, A., Cianni, L., Vitiello, R., Greco, T., Maccauro, G., Perisano, C., 2020. A rare case of *Bacillus megaterium* soft tissues infection. *Acta Biomed.* 91 (S. 14), e2020013 <https://doi.org/10.23750/abm.v91i14-S.10849>.
- Bouchard, C., Dibbernardo, A., Koffi, J., Wood, H., Leighton, P.A., Lindsay, L.R., 2019. Increased risk of tick-borne diseases with climate and environmental changes. *Can. Commun. Dis. Rep.* 45 (4), 81–89. <https://doi.org/10.14745/ccdr.v45i04a02>.
- Brooks, D., Thomas, V., Snowden, J., 2019. *Staphylococcus capitis* osteomyelitis: case report. *Glob. Pediatr. Health.* 6, 1–4. <https://doi.org/10.1177/2333794X19833736>.
- Buczek, A., Buczek, W., 2020. Importation of ticks on companion animals and the risk of spread of tick-borne diseases to non-endemic regions in Europe. *Animals* 11, 6.

- Campos, J.H.F., Costa, F.A.L., 2014. Participation of ticks in the infectious cycle of canine visceral leishmaniasis, in Teresina, Piauí, Brazil. *Rev. Inst. Med. Trop. São Paulo* 56 (4), 297–300. <https://doi.org/10.1590/S0036-46652014000400005>.
- Celina, S.S., Cerný, J., 2022. *Coxiella burnetii* in ticks, livestock, pets and wildlife: a mini-review. *Front. Vet. Sci.* 9, 1068129. <https://doi.org/10.3389/fvets.2022.1068129>.
- Chisu, V., Loi, F., Mura, L., Tanda, A., Chessa, G., Masala, G., 2021. Molecular detection of *Theileria sergentii/orientalis/buffeli* and *Ehrlichia canis* from aborted ovine and caprine products in Sardinia, Italy. *Vet. Med. Sci.* 7 (5), 1762–1768. <https://doi.org/10.1002/vms3.510>.
- Claerebout, E., Losson, B., Cochez, C., Casaert, S., Dalemans, A.C., De Cat, A., Madder, M., Saegerman, C., Heyman, P., Lempereur, L., 2013. Ticks and associated pathogens collected from dogs and cats in Belgium. *Parasit. Vectors* 6, 183. <https://doi.org/10.1186/1756-3305-6-183>.
- Cunze, S., Glock, G., Kochmann, J., Klimpel, S., 2022. Ticks on the move—climate change-induced range shifts of three tick species in Europe: current and future habitat suitability for *Ixodes ricinus* in comparison with *Dermacentor reticulatus* and *Dermacentor marginatus*. *Parasitol. Res.* 121 (8), 2241–2252. <https://doi.org/10.1007/s00436-022-07556-x>.
- Cuthbert, R.N., Darriet, F., Chabrierie, O., Lenoir, J., Courchamp, F., Claeys, C., Robert, V., Jourdain, F., Ulmer, R., Diagne, C., Ayala, D., Simard, F., Morand, S., Renault, D., 2023. Invasive hematophagous arthropods and associated diseases in a changing world. *Parasites Vectors* 16, 291. <https://doi.org/10.1186/s13071-023-05887-x>.
- Dantas-Torres, F., 2008. The brown dog tick, *Rhipicephalus sanguineus* (Latreille, 1806) (Acari: Ixodidae): from taxonomy to control. *Vet. Parasitol.* 152 (3–4), 173–185. <https://doi.org/10.1016/j.vetpar.2007.12.030>.
- Dantas-Torres, F., 2015. Climate change, biodiversity, ticks and tick-borne diseases: the butterfly effect. *Int. J. Parasitol. Parasites Wildl.* 4 (3), 452–461. <https://doi.org/10.1016/j.ijppaw.2015.07.001>.
- Dutto, M., Selmi, M., 2009. Report on ticks (Acari: Ixodidae) collected on dogs in Piedmont: the potential transmission of tick-borne pathogens to man. *Parassitologia* 51, 113–117.
- Ehling-Schulz, M., Lereclus, D., Koehler, T.M., 2019. The *Bacillus cereus* group: *Bacillus* species with pathogenic potential. *Microbiol. Spectr.* 7 (3), 3–32. <https://doi.org/10.1128/microbiolspec.GPP3-0032-2018>.
- Ernst, E., Qurollo, B., Olech, C., Breitschwerdt, E.B., 2020. *Bartonella rochalimae*, a newly recognized pathogen in dogs. *J. Vet. Intern. Med.* 34 (4), 1447–1453. <https://doi.org/10.1111/jvim.15793>.
- Esteve-Gassent, M.D., Castro-Arellano, I., Feria-Arroyo, T.P., Patino, R., Li, A.Y., Medina, R.F., de León, A.A.P., Rodríguez-Vivas, R.I., 2016. Translating ecology, physiology, biochemistry, and population genetics research to meet the challenge of tick and tick-borne diseases in North America. *Arch. Insect Biochem. Physiol.* 92, 38–64. <https://doi.org/10.1002/arch.21327>.
- Estrada-Peña, A., 2008. Climate, niche, ticks, and models: what they are and how we should interpret them. *Parasitol. Res.* 103 (1), S87–S95. <https://doi.org/10.1007/s00436-008-1056-7>.
- Feng, J., Lin, T., Mihalca, A.D., Niu, Q., Oosthuizen, M.C., 2023. Editorial: coinfections of Lyme disease and other tick-borne diseases. *Front. Microbiol.* 14, 1140545. <https://doi.org/10.3389/fmicb.2023.1140545>.
- Fourie, J.J., Fourie, L.J., Horak, I.G., Snyman, M.G., 2010. The efficacy of a topically applied combination of cyphenothrin and pyriproxyfen against the southern African yellow dog tick, *Haemaphysalis elliptica*, and the cat flea, *Ctenocephalides felis*, on dogs. *J. S. Afr. Vet. Assoc.* 81, 33–36. <https://doi.org/10.4102/jsava.v81i1.93>.
- Frean, J., Grayson, W., 2019. South African tick bite fever: an overview. *Dermatopathology* 6 (2), 70–76. <https://doi.org/10.1159/000495475>.
- Gray, J., Dantas-Torres, F., Estrada-Peña, A., Levin, M., 2013. Systematics and ecology of the brown dog tick, *Rhipicephalus sanguineus*. *Ticks Tick Borne Dis.* 4 (3), 171–180. <https://doi.org/10.1016/j.ttbdis.2012.12.003>.
- Hansford, K.M., Pietzsch, M.E., Cull, B., Medlock, J.M., 2014. Importation of *Rhipicephalus sanguineus* into the UK via dogs. *Vet. Rec.* 175, 385–386. <https://doi.org/10.1136/vr.g6226>.
- Hansford, K.M., Medlock, J.M., Atkinson, B., Santos-Silva, M.M., 2016. Importation of a *Hyalomma lusitanicum* tick into the UK on a dog. *Vet. Rec.* 179 (16), 415. <https://doi.org/10.1136/vr.i5645>.
- Harrus, S., Waner, T., Björnsdóttir, A., 2016. Ehrlichiosis and anaplasmosis. In: Day, M.J. (Ed.), *Infectious Diseases of the Dog and Cat*, 2nd ed. CRC Press, pp. 167–188.
- Hromníková, D., Furka, D., Furka, S., Santana, J.A.D., Ravingerová, T., Klöcklerová, V., Žitňan, D., 2022. Prevention of tick-borne diseases: challenge to recent medicine. *Biologia* 77 (6), 1533–1554. <https://doi.org/10.1007/s11756-021-00966-9>.
- Irwin, P., 2016. Babesiosis and cytauxzoonosis. In: Day, M.J. (Ed.), *Infectious Diseases of the Dog and Cat*, 2nd ed. CRC Press, pp. 77–96.
- Jameson, L.J., Phipps, L.P., Medlock, J.M., 2010. Surveillance for exotic ticks on companion animals in the UK. *Vet. Rec.* 166 (7), 202–204. <https://doi.org/10.1136/vr.b4786>.
- Jia, W., Chen, S., Chi, S., He, Y., Ren, L., Wang, X., 2022. Recent progress on tick-borne animal diseases of veterinary and public health significance in China. *Viruses* 14 (2), 355. <https://doi.org/10.3390/v14020355>.
- Jones, E.H., Hinckley, A.F., Hook, S.A., Meek, J.I., Backenson, B., Kugeler, K.J., Feldman, K.A., 2018. Pet ownership increases human risk of encountering ticks. *Zoonoses Public Health* 65 (1), 74–79. <https://doi.org/10.1111/zph.12369>.
- Jongejan, F., Uilenberg, G., 2004. The global importance of ticks. *Parasitology* 129 (S1), S3–S14. <https://doi.org/10.1017/S0031182004005967>.
- Kappmeyer, L.S., Thiagarajan, M., Herndon, D.R., Ramsay, J.D., Caler, E., Djikeng, A., Gillespie, J.J., Lau, A.O., Roalson, E.H., Silva, J.C., Silva, M.G., Suarez, C.E., Ueti, M.W., Nene, V.M., Mealey, R.H., Knowles, D.P., Brayton, K.A., 2012. Comparative genomic analysis and phylogenetic position of *Theileria equi*. *BMC Genet.* 13, 603. <https://doi.org/10.1186/1471-2164-13-603>.
- Keirans, J.E., Durden, L.A., 2001. Invasion: exotic ticks (Acari: Argasidae, Ixodidae) imported into the United States. A review and new records. *J. Med. Entomol.* 38 (6), 850–861. <https://doi.org/10.1603/0022-2585-38.6.850>.
- Khatiri, A.M., Rai, S., Shank, C., McInerney, A., Kaplan, B., Hagmann, S.H., Kainth, M.K., 2021. A tale of caution: prolonged *Bacillus clausii* bacteraemia after probiotic use in an immunocompetent child. *Access Microbiol.* 3 (3), 000205. <https://doi.org/10.1099/acmi.0.000205>.
- Klingelhöfer, D., Braun, M., Brüggemann, D., Groneberg, D.A., 2022. Ticks in medical and parasitological research: globally emerging risks require appropriate scientific awareness and action. *Travel Med. Infect. Dis.* 50, 102468. <https://doi.org/10.1016/j.tmaid.2022.102468>.
- Kolo, A.O., Sibeko-Matjila, K.P., Maina, A.N., Richards, A.L., Knobel, D.L., Matjila, P.T., 2016. Molecular detection of zoonotic rickettsiae and *Anaplasma* spp. in domestic dogs and their ectoparasites in Bushbuckridge, South Africa. *J. Vector Borne Dis.* 16 (4), 245–252. <https://doi.org/10.1089/vbz.2015.1849>.
- Leisewitz, A., Goddard, A., De Gier, J., Van Engelshoven, J., Clift, S., Thompson, P., Schoeman, J.P., 2019. Disease severity and blood cytokine concentrations in dogs with natural *Babesia rossi* infection. *Parasite Immunol.* 41 (7), e12630. <https://doi.org/10.1111/pim.12630>.
- Lin, M., Xiong, Q., Chung, M., Daugherty, S.C., Nagaraj, S., Sengamalai, N., Ott, S., Godinez, A., Tallon, L.J., Sadzewicz, L., Fraser, C., Dunning Hotopp, J.C., Rikihisa, Y., 2021. Comparative analysis of genome of *Ehrlichia* sp. HF, a model bacterium to study fatal human Ehrlichiosis. *BMC Genomics* 22, 11. <https://doi.org/10.1186/s12864-020-07309-z>.
- Losey, R.J., 2022. Domestication is not an ancient moment of selection for prosociality: insights from dogs and modern humans. *J. Soc. Archaeol.* 22 (2), 131–148. <https://doi.org/10.1177/14696053211055475>.
- Magnarelli, L.A., 2009. Global importance of ticks and associated infectious disease agents. *Clin. Microbiol. Newsl.* 31 (5), 33–37. <https://doi.org/10.18502/ijph.v5i112.11457>.
- Malta, R.C.R., Ramos, G.L.D.P.A., dos Santos Nascimento, J., 2020. From food to hospital: we need to talk about *Acinetobacter* spp. *Germes* 10 (3), 210–217. <https://doi.org/10.18683/germes.2020.1207>.
- Mans, B.J., 2023. Paradigms in tick evolution. *Trends Parasitol.* 39 (6), P457–P486. <https://doi.org/10.1016/j.pt.2023.03.011>.
- Mendoza-Olazarán, S., García-Mazcorro, J.F., Morfín-Otero, R., Villarreal-Treviño, L., Camacho-Ortiz, A., Rodríguez-Noriega, E., Bocanegra-Ibarias, P., Maldonado-Garza, H.J., Dowd, S.E., Garza-González, E., 2017. Draft genome sequences of two opportunistic pathogenic strains of *Staphylococcus cohnii* isolated from human patients. *tand. Genom. Sci.* 12, 49. <https://doi.org/10.1186/s40793-017-0263-1>.
- Meyer, I., Forkman, B., Fredholm, M., Glanville, C., Guldbrandtsen, B., Ruiz Izaguirre, E., Palmer, C., Sandøe, P., 2022. Pampered pets or poor bastards? The welfare of dogs kept as companion animals. *Appl. Anim. Behav. Sci.* 251, 105640. <https://doi.org/10.1016/j.applanim.2022.105640>.
- Mtshali, K., Khumalo, Z.T.H., Nakao, R., Grab, D.J., Sugimoto, C., Thekiso, O.M.M., 2015. Molecular detection of zoonotic tick-borne pathogens from ticks collected from ruminants in four South African Provinces. *J. Vet. Med.* 77 (12), 1573–1579.
- Mucheka, V.T., Pillay, A., Mukaratirwa, S., 2023. Prevalence of tick-borne pathogens in *Rhipicephalus* species infesting domestic animals in Africa: a systematic review and meta-analysis. *Acta Trop.* 246, 106994. <https://doi.org/10.1016/j.actatropica.2023.106994>.
- Munn, Z., Moola, S., Lisy, K., Riitano, D., Tufanaru, C., 2015. Methodological guidance for systematic reviews of observational epidemiological studies reporting prevalence and incidence data. *Int. J. Evid. Based Healthc.* 13 (3), 147–153. <https://doi.org/10.1097/XEB.0000000000000054>.
- Nogueira, L.R., Regianni, D.G., Pinter, A., Moraes-Filho, J., 2021. *Rhipicephalus sanguineus* complex: Review. *Braz. J. Global Health* 1 (2), 28–31. <https://doi.org/10.56242/globalhealth.1;2;28-31>.
- Olayide, A.J., Bamidele, A.A., 2008. Transmission of bacterial isolates through all the developmental stages of dog ticks (bacteriological evidence). *J. Anim. Vet. Adv.* 7 (8), 959–962.
- Page, M.J., Moher, D., Bossuyt, P.M., Boutron, I., Hoffmann, T.C., Mulrow, C.D., Shamseer, L., Tetzlaff, J.M., Akl, E.A., Brennan, S.E., Chou, R., Glanville, J., Grimshaw, J.M., Hróbjartsson, A., Lalu, M.M., Li, T., Loder, E.W., Mayo-Wilson, E., McDonald, S., McKenzie, J.E., 2021a. PRISMA 2020 explanation and elaboration: updated guidance and exemplars for reporting systematic reviews. *BMJ* 372, n160. <https://doi.org/10.1136/bmj.n71>.
- Page, M.J., McKenzie, J.E., Bossuyt, P.M., Boutron, I., Hoffmann, T.C., Mulrow, C.D., Shamseer, L., Tetzlaff, J.M., Akl, E.A., Brennan, S.E., Chou, R., Glanville, J., Grimshaw, J.M., Hróbjartsson, A., Lalu, M.M., Li, T., Loder, E.W., Mayo-Wilson, E., McDonald, S., Moher, D., 2021b. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *Syst. Rev.* 10, 89. <https://doi.org/10.1186/s13643-021-01626-4>.
- Parola, P., Socolovschi, C., Jeanjean, L., Bitam, I., Fournier, P.E., Sotto, A., Labauge, P., Raoult, D., 2008. Warmer weather linked to tick attack and emergence of severe rickettsioses. *PLoS Negl. Trop. Dis.* 2 (11), e338. <https://doi.org/10.1371/journal.pntd.0000338>.
- Parola, P., Paddock, C.D., Socolovschi, C., Labruna, M.B., Mediannikov, O., Kernif, T., Abad, M.Y., Stenos, J., Bitam, I., Fournier, P.E., Raoult, D., 2013. Update on tick-borne rickettsioses around the world: a geographic approach. *Clin. Microbiol. Rev.* 26 (4), 657–702. <https://doi.org/10.1128/CMR.00032-13>.
- Pavón-Rocha, A.J., Cárdenas-Flores, A., Rábago-Castro, J.L., Barrón-Vargas, C.A., Mosqueda, J., 2020. First molecular evidence of *Theileria cervi* infection in white-

- tailed deer (*Odocoileus virginianus*) in Mexico. *Vet. Parasitol. Regional Studies Rep.* 22, 100482 <https://doi.org/10.1016/j.vprsr.2020.100482>.
- Penzhorn, B.L., Harrison-White, R.F., Stoltz, W.H., 2020. Completing the cycle: *Haemaphysalis elliptica*, the vector of *Babesia rossi*, is the most prevalent tick infesting black-backed jackals (*Canis mesomelas*), an indigenous reservoir host of *B. rossi* in South Africa. *Ticks Tick Borne Dis.* 11 (2), 101325 <https://doi.org/10.1016/j.ttbdis.2019.101325>.
- Pfeffer, M., Dobler, G., Leschnik, M., 2016. Rare arthropod-borne infections of dogs and cats. In: Day, M.J. (Ed.), *Infectious Diseases of the Dog and Cat*, 2nd ed. CRC Press, pp. 198–209.
- Proboste, T., Kalema-Zikusoka, G., Altet, L., Solano-Gallego, L., Fernández de Mera, I.G., Chirife, A.D., Muro, J., Bach, E., Piazza, A., Cevitanes, A., Blanda, V., Mugisha, L., de la Fuente, J., Caracappa, S., Millán, J., 2015. Infection and exposure to vector-borne pathogens in rural dogs and their ticks, Uganda. *Parasit. Vectors.* 8, 306. <https://doi.org/10.1186/s13071-015-0919-x>.
- Radolf, J.D., Strle, K., Lemieux, J.E., Strle, F., 2021. Lyme disease in humans. *Curr. Issues Mol. Biol.* 42, 333–384. <https://doi.org/10.21775/cimb.042.333>.
- Rana, V.S., Kitsou, C., Dumler, J.S., Pal, U., 2023. Immune evasion strategies of major tick-transmitted bacterial pathogens. *Trends Microbiol.* 31, 62–75. <https://doi.org/10.1016/j.tim.2022.08.002>.
- Randolph, S.E., 2010. To what extent has climate change contributed to the recent epidemiology of tick-borne diseases? *Vet. Parasitol.* 167 (2–4), 92–94. <https://doi.org/10.1016/j.vetpar.2009.09.011>.
- Regalado, N.G., Martin, G., Antony, S.J., 2009. *Acinetobacter lwoffii*: bacteremia associated with acute gastroenteritis. *Israel Med. Infect. Dis.* 7 (5), 316–317. <https://doi.org/10.1016/j.tmaid.2009.06.001>.
- Rezaei, M., Khalili, M., Akhtardanesh, B., Shahheidaripour, S., 2016. Q fever in dogs: an emerging infectious disease in Iran. *J. Med. Microbiol.* 5 (1–2), 1–6.
- Schön, M.P., 2022. The tick and I: parasite-host interactions between ticks and humans. *JDDG-J. German Soc. Dermatol.* 20 (6), 818–853. <https://doi.org/10.1111/ddg.14821>.
- Socolovschi, C., Reynaud, P., Kernif, T., Raoult, D., Parola, P., 2012. Rickettsiae of spotted fever group, *Borrelia valaisiana*, and *Coxiella burnetii* in ticks on passerine birds and mammals from the Camargue in the south of France. *Ticks Tick Borne Dis.* 3 (5–6), 354–359. <https://doi.org/10.1016/j.ttbdis.2012.10.019>.
- Solano-Gallego, L., Rossi, L., Scroccaro, A.M., Montarsi, F., Caldin, M., Furlanello, T., Trotta, M., 2012. Detection of *Leishmania infantum* DNA mainly in *Rhipicephalus sanguineus* male ticks removed from dogs living in endemic areas of canine leishmaniasis. *Parasit. Vectors* 5, 98. <https://doi.org/10.1186/1756-3305-5-98>.
- Sparagano, O., George, D., Giangaspero, A., Špitálská, E., 2015. Arthropods and associated arthropod-borne diseases transmitted by migrating birds. The case of ticks and tick-borne pathogens. *Vet. Parasitol.* 213 (1–2), 61–66. <https://doi.org/10.1016/j.vetpar.2015.08.028>.
- Sungur, M.O., Seyhan, T.Ö., 2013. Writing references and using citation management software. *Turk. J. Urol.* 39 (1), 25–32. <https://doi.org/10.5152/tud.2013.050>.
- van Wyk, C., Taioe, M.O., Mtshali, K., Terera, S., Bakkes, D., Ramatla, T., Xuan, X., Thekisoe, O., 2022. Detection of ticks and tick-borne pathogens of urban stray dogs admitted at Potchefstroom Animal Welfare Society in South Africa. *Pathogens* 11, 862. <https://doi.org/10.3390/pathogens11080862>.
- Wall, R., 2016. Arthropod vectors of infectious disease: Biology and control. In: Day, M.J. (Ed.), *Infectious Diseases of the Dog and Cat*, 2nd ed. CRC Press, pp. 1–14.
- Wallménus, K., Barboutis, C., Fransson, T., Jaenson, T.G., Lindgren, P.-E., Nyström, F., Olsen, B., Salaneck, E., Nilsson, K., 2022. Spotted fever *Rickettsia* species in *Hyalomma* and *Ixodes* ticks infesting migratory birds in the European Mediterranean area. *Parasit. Vectors* 7, 318. <https://doi.org/10.1186/1756-3305-7-318>.
- Zaeemi, M., Haddadzadeh, H., Khazraeiinia, P., Kazemi, B., Bandehpour, M., 2011. Identification of different *Theileria* species (*Theileria lestoquardi*, *Theileria ovis*, and *Theileria annulata*) in naturally infected sheep using nested PCR–RFLP. *Parasitol. Res.* 108 (4), 837–843. <https://doi.org/10.1007/s00436-010-2119-0>.
- Zhou, H., Xu, L., Shi, W., 2023. The human-infection potential of emerging tick-borne viruses is a global public health concern. *Nat. Rev. Microbiol.* 21, 215–217. <https://doi.org/10.1038/s41579-022-00845-3>.
- Zygner, W., Gójska-Zygner, O., Bartosik, J., Górski, P., Karabowicz, J., Kotowski, G., Norbury, L.J., 2023. Canine babesiosis caused by large *Babesia* species: global prevalence and risk factors- a review. *Animals* 13 (16). <https://doi.org/10.3390/ani13162612>.