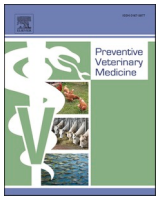
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Rickettsiae of the spotted fever group in dogs of the Americas: A systematic review and meta-analysis

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ABSTRACT

Sentinel animals are defined as sensitive indicators of environmental hazards that provide an early warning system for public health interventions. Spotted fever group rickettsioses are zoonotic tick-borne diseases that are considered endemic in different American countries with significant rates of morbidity and lethality, mainly when involving species such as *Rickettsia rickettsii* and *Rickettsia parkeri*. Dogs have been recognized as good sentinels for these rickettsioses, since they are hosts to different species and stages of ticks, and they sustain a good immunological response after infection. Data from epidemiological studies conducted on dogs in the Americas are dispersed and have not been integrated. In this paper, we present a systematic review and meta-analysis that aimed to present a pooled seroprevalence of *Rickettsia* sp. in dogs and summarize other relevant data. Literature was reviewed in three databases (PubMed, Scopus, and Web of Science) by different authors, using specific eligibility criteria, and subsequently submitted for meta-analysis to obtain pooled seroprevalences for *Rickettsia* spp. and different *Rickettsia* antigens. The systematic search yielded 700 documents, and 49 were selected for review and analysis (years: 2001–2025). Brazil (59.2%) was the country with the highest number of published studies. The Indirect Immunofluorescence Assay (IFA) was used as the main technique with *R. rickettsii* and *R. parkeri* as the main antigens used. The estimated overall seroprevalence for *Rickettsia* sp. was 26.2% (95% CI: 17.8% – 36.8%), with the highest values for *R. rickettsii* (16.9%, 95% CI: 9.8% – 27.4%), followed by *R. parkeri* (13.2%, 95% CI: 6.9% – 23.6%). The most frequent tick species collected on dogs were *Amblyomma ovale* and *Rhipicephalus sanguineus* s.l. This study confirms the important eco-epidemiological role of dogs as sentinels of rickettsioses. Although this has been studied in some countries, several American countries have not yet addressed it. This could be improved by strengthening surveillance programs focused on rickettsial pathogens that include dogs as sentinels, prioritizing these diseases as relevant zoonoses within a One Health framework.

1. Introduction

Vector-borne diseases pose a major threat to human and animal health worldwide, as there has been an increase in the incidence and spread of zoonotic and veterinary tick-borne diseases in recent decades, generating great concern (Machtinger et al., 2024). For this reason, it has been proposed to implement a One Health approach to the study of tick-borne diseases, focusing on prevention and surveillance based on transdisciplinary epidemiological studies (Garcia-Vozmediano et al., 2022).

The increase in tick-borne diseases is triggered by factors linked mainly to human behavior, changes in land use, as well as constant environmental changes that lead to altered behavioral patterns of amplifying, sentinel, and incidental hosts, favoring the persistence and growth of tick populations and the enzootic occurrence of related pathogens (Alvarez-Hernandez et al., 2019; Diuk-Wasser et al., 2021).

Ticks are obligate hematophagous arthropods that parasitize a broad range of vertebrate animals and are considered extremely important

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vectors in public and animal health, due to their great capacity to transmit pathogens such as viruses, bacteria, and parasites (Parola and Raoult, 2001). Among the pathogens transmitted by ticks, bacteria of the genus *Rickettsia* are characterized as obligate intracellular Gram-negative bacilli, which are phylogenetically classified into five major groups: the *Rickettsia bellii* group, the *Rickettsia canadensis* group, the Typhus group, and two distinct subdivisions within the Spotted Fever Group (SFG I and II) (El Karkouri et al., 2022). The SFG group comprises tick-borne rickettsiae and includes highly pathogenic species such as *Rickettsia rickettsii*, the etiological agent of Rocky Mountain and Brazilian spotted fever (Ricketts, 1906; Monteiro, 1932; Labruna et al., 2014). Currently, in the Americas, four tick-borne rickettsiae belonging to the SFG have been reported as pathogenic in humans: *R. rickettsii*, *Rickettsia parkeri*, *Rickettsia lanei*, and *Rickettsia massiliae* (Garcia-Garcia et al., 2010; Parola et al., 2013; Blanton, 2019; Paddock et al., 2025).

Dogs are highly susceptible to *R. rickettsii* infection under experimental (Piranda et al., 2008; Levin et al., 2014; Binder et al., 2021) and natural conditions (Paddock et al., 2002; Nicholson et al., 2006; Labruna et al., 2009), and also have been recognized as good sentinels for human infection in endemic zones (Moraes-Filho et al., 2009; Pacheco et al., 2011; Foley et al., 2025), and as amplifying hosts in specific ecological scenarios (Binder et al., 2021). As sentinels, dogs develop detectable and quantifiable immune titers upon contact with the pathogen, suggesting the presence of the microorganism in an ecosystem (Halliday et al., 2007; Bowser and Anderson, 2018).

Despite several serological studies on SFG rickettsiae conducted in dogs throughout the Americas, the information in the scientific literature remains dispersed and has not been condensed. For this reason, the aim of this work is to compile all this information through a systematic review and to report pooled seroprevalences for different rickettsiae antigens through a meta-analysis. In addition, other data on vectors, diagnosis, and study distribution are presented.

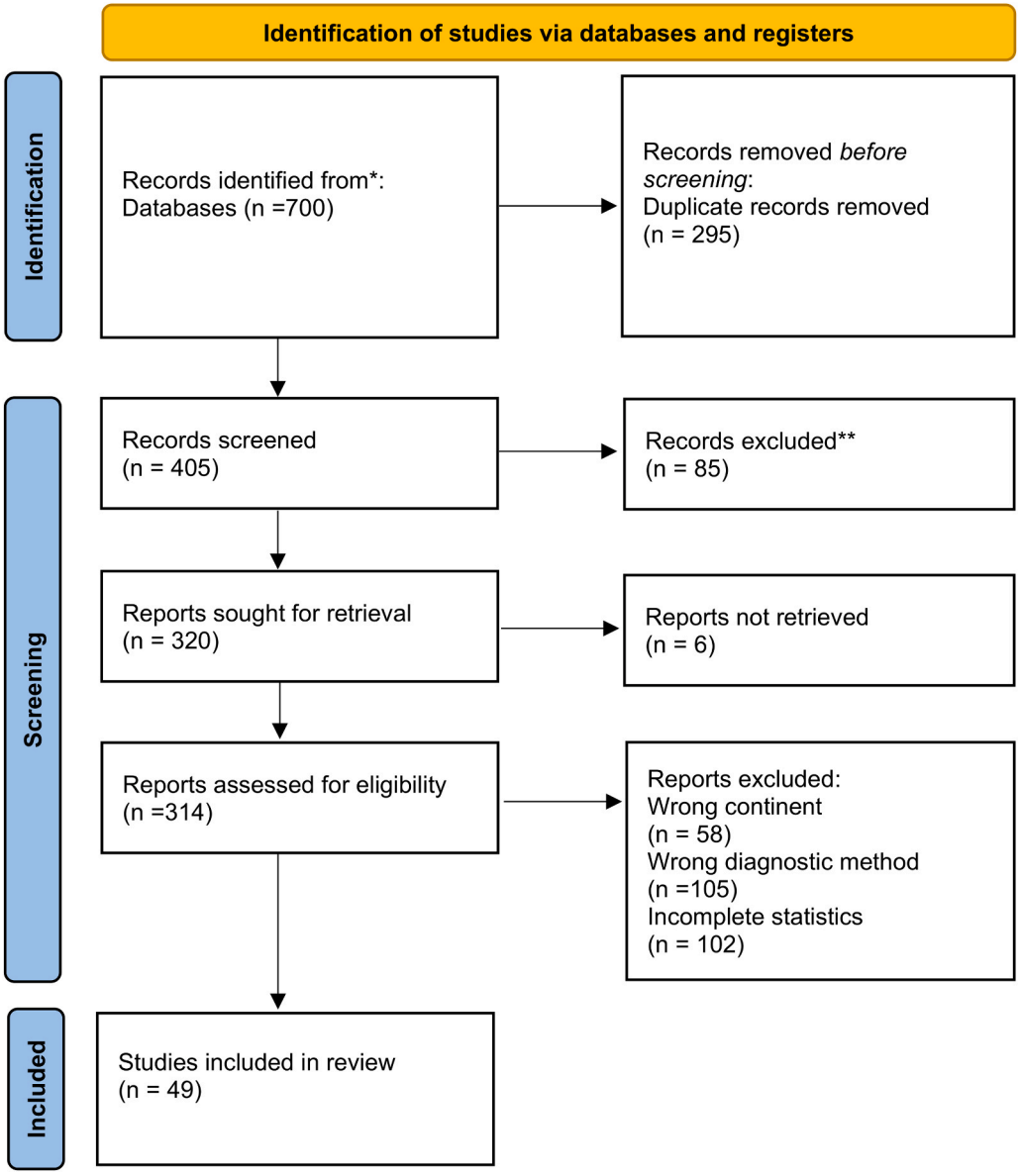


Fig. 1. Preferred Reporting Items for Systematic Reviews and Meta-analysis (PRISMA) flowchart. * Used databases were PubMed, Scopus, and Web of Science. ** Documents were mainly excluded for incorrect geographic scope, incorrect target host species, or detection of rickettsiae exclusively in ticks without serological testing in dogs.

2. Methods

2.1. Databases and search strategy

This systematic review followed the Preferred Reporting Items for Systematic Reviews and Meta-analysis (PRISMA) statement (Fig. 1). The search was performed using MeSH terms and word combinations such as: "Dog", "canid", "canidae", "*Canis lupus familiaris*", "*Rickettsia* sp.", "spotted fever group", "Rocky Mountain spotted fever", "Rickettsiosis", "Rickettsioses", "Brazilian spotted fever", and "Fiebre de Tobia", separately, employing the Boolean operators "AND" and "OR", and adding the geographical terms "Latin America", "South America", "North America", "Central America", and specific countries' names. The search was performed on PubMed, Scopus, and Web of Science. The complete search strategy is attached as supplemental material (Table S1).

2.2. Eligibility criteria

Language or year restrictions were not applied in the search. The titles and abstracts identified by the search were read independently by the authors to determine whether they met the inclusion or exclusion criteria (Table 1).

2.3. Study selection

The systematic review was performed in the three databases to retrieve all results; subsequently, all duplicates were removed. Reviewing authors (by duplicate) discarded studies if the title or abstract indicated other bacterial species or geographical areas outside the Americas. Then, at least two authors evaluated the documents in full text to determine eligibility. The PRISMA flow chart summarizes the process (Fig. 1).

For those studies that met all the inclusion criteria, the following data were extracted: authors, country, year of publication, serological and molecular tests applied, serological antigen used, total number of dogs involved, number of seropositive dogs, maximum immunological titer, possible antigen involved in a homologous reaction (PAIHR), and the identification of ticks parasitizing dogs (when available). In addition, the final selected studies were stratified by *Rickettsia* antigen and climate zone to conduct specific meta-analyses. In the former, spotted fever group antigens were used as the main criteria, and *R. bellii* was included because it is commonly screened in serological studies and commonly circulates in ticks that parasitize dogs. For climatic stratification, the main criterion was the geographical latitude where the study was conducted [i.e., tropical (approx. 0–23.5º); subtropical (approx. 23.5–40º); and temperate (approx. 40–60º)]. If a study had sampling points in climate zone boundaries (or had a zone overlap), the location of most of the geographical points was used to define the corresponding zone.

2.4. Data analysis

The total seroprevalence of studies reporting a single seroprevalence was calculated using the R software with the meta package. The pooling of *Rickettsia* species was performed using a generalized linear mixed model (GLMM) within a random intercept logistic regression framework. The random-effects model was applied using the Hartung-Knapp method to calculate confidence intervals (method.random.ci = "HK"), which provides more robust and conservative interval estimates, particularly in meta-analyses with a small number of studies or high heterogeneity. To estimate the 95% confidence intervals (CIs) for the seroprevalences in individual studies, we used the Clopper-Pearson method. Between-study heterogeneity was assessed using Cochran's Q test and the I^2 statistic, with I^2 values $\geq 60\%$ categorized as high heterogeneity. A p-value < 0.05 in Cochran's Q test was considered indicative of significant heterogeneity. In addition, the climate zone subgroup analysis used a random-intercept logistic regression model with maximum-likelihood estimation for T^2, logit transformation for proportions, t-distribution-based confidence intervals, and continuity correction (0.5) for studies with zero events. For bias assessment, an adapted Newcastle Ottawa Scale was implemented (NOS) (Wells, 2000) (Supplementary Table S2).

Table 1
Inclusion and exclusion criteria used in study selection.

Inclusion Criteria	Exclusion Criteria
Research articles linking canines (and other canids)	Review articles, editorials, letters, and conference abstracts
Studies conducted in the American continent	Studies where the full text was not available
Diagnosis by serological tests	The total number of animals or the prevalence were not specified

3. Results

The systematic search yielded 700 documents in the three databases. After eliminating 295 duplicates, the authors reviewed a total of 405 documents. After selection based on titles and abstracts, 314 documents were evaluated in full text to determine eligibility. Then, 265 studies were eliminated according to the search criteria, resulting in 49 documents that are the basis for this systematic review (Fig. 1).

A total of 49 studies published between 2001 and 2025 were included. Brazil (59.2%) was the country with the highest number of published studies involving dogs; followed by Colombia (10.2%); Mexico and the USA (6.1% each); Chile and Costa Rica (4.1% each); and Bolivia, Canada, Nicaragua, Peru, and Uruguay (2.0% each) (Table 2). Studies with specific results (i.e., PAIHR) on *R. rickettsii* have a broad distribution, from northeastern USA to southern Brazil; for *R. parkeri* were conducted in Brazil and Uruguay; for *R. amblyommatis* in Brazil and Costa Rica; and specific reports for *R. felis*, *R. bellii,* and *R. rhipicephali* were only registered in Brazil. Numerous countries in the continent, mainly from Central and South America, do not report studies (Fig. 2).

Indirect immunofluorescence assay (IFA) was used as the main technique in all studies; among them, 39 (79.6%) reported the maximum titer, and 31 (63.3%) registered the PAIHR.

A total of 12,087 sera were sampled, of which 20.29% (2453 animals) tested seropositive (Table 2). For *R. rickettsii*, sera from 4234 dogs were examined, yielding a seroprevalence of 15.26% (n = 646), and this species was identified as the putative antigen involved in homologous reaction (PAIHR) in 16 studies. For *R. parkeri,* 2289 sera were tested, with a seroprevalence of 24.4% (559), and it was reported as the PAIHR in twelve studies. The species *R. amblyommatis* and *R. bellii* were confirmed as the PAIHR in seven and three studies, respectively, whereas *R. felis* and *R. rhipicephali* were each implicated as the possible antigen in one study.

The estimated total seroprevalence obtained from the random-effects model was 26.2% (95% CI: 17.8% – 36.8%). The observed heterogeneity was reflected by an I^2 value of 97.8% (95% CI: 97.4% – 98.0%). Additionally, the τ^2 value was 2.9 and the H statistic 6.7 (95% CI: 6.3% – 7.1%) (Fig. 3).

In addition, we conducted two subgroup analyses, one stratified by the specific *Rickettsia* antigen evaluated and the other by climate zone. In the antigen-stratified analysis, the highest pooled seroprevalence estimate was observed for *R. rickettsii* (16.9%, 95% CI: 9.8% – 27.4%), followed by *R. parkeri* (13.2%, 95% CI: 6.9% – 23.6%). Lower seroprevalences estimates were obtained for *R. bellii* (6.5%, 95% CI: 3.5% – 11.9%), *R. amblyommatis* (5.0%, 95% CI: 2.6% – 9.2%), *R. felis* (4.5%, 95% CI: 1.0% – 17.4%), and *R. rhipicephali* (3.7%, 95% CI: 1.1% – 11.4%). Between-study heterogeneity was substantial, with I^2 values ranging from 91.8% to 97.9%. The τ^2 estimates differed by species, with the largest values observed for *R. rickettsii* (3.7), *R. felis* (3.5), and *R.*

Table 2
Studies incorporated into the final analysis, stratified by country, including pertinent data on serological findings for *Rickettsia* spp.

Author(s), Year	Country	Total number of canine samples	Total number of *Rickettsia*-positive canines	%	Maximum titer	PAIHR*
Tomassone et al. (2010)	Bolivia	44	30	68.18	N/R	N/R
	Total: 1 (2.04%)					
Albuquerque et al. (2024)	Brazil	60	33	55.00	16384	*R. parkeri*
Barbieri et al. (2014)	Brazil	35	35	100.00	32768	*R. parkeri**
Batista et al. (2010)	Brazil	20	4	20.00	1024	N/R
Campos et al. (2017)	Brazil	155	25	16.13	N/R	N/R
Vieira de Carvalho et al. (2021)	Brazil	289	51	17.65	2048	*R. rickettsii*
Costa et al. (2017)	Brazil	1560	196	12.56	16384	*R. amblyommatis**
da Costa et al. (2021)	Brazil	171	28	16.37	1024	*R. bellii*
Amorim et al. (2013)	Brazil	384	12	3.13	2048	*R. bellii*
de Oliveira et al. (2019)	Brazil	356	58	16.29	1024	*R. parkeri*
de Souza et al. (2023)	Brazil	4	2	50.00	4096	*R. parkeri*
de Souza et al. (2023)**	Brazil	27	2	7.41	2048	*R. parkeri*
Fonsèca et al. (2022)	Brazil	153	20	13.07	2048	*R. amblyommatis*
Fournier et al. (2020)	Brazil	64	51	79.69	2048	N/R
Gonçalves et al. (2022)	Brazil	242	19	7.85	512	*R. bellii* *R. rickettsii* *R. amblyommatis*
Horta et al. (2004)	Brazil	16	5	31.25	1024	*R. rickettsii*
Horta et al. (2007)	Brazil	55	33	60.00	4096	*R. rickettsii* *R. parkeri*
Kmetiuk et al. (2019)	Brazil	170	24	14.12	1024	*R. bellii* *R. amblyommatis*
Krawczak et al. (2023)	Brazil	36	5	13.89	8192	*R. parkeri*
Labruna et al. (2007)	Brazil	317	25	7.89	2048	*R. parkeri*
Mesquita et al. (2023)	Brazil	199	123	61.81	2048	*R. parkeri*
Nieri-Bastos et al. (2016)	Brazil	10	6	60.00	≥ 512	*R. parkeri*
Pacheco et al. (2011)	Brazil	78	53	67.95	131072	N/R
Pinter et al. (2008)	Brazil	25	16	64.00	8192	*R. rickettsii*
Poubel et al. (2018)	Brazil	253	199	78.66	131072	*R. rickettsii*
Rotondano et al. (2017)	Brazil	763	43	5.64	2048	*R. rickettsii* *R. felis* *R. amblyommatis*
Scinachi et al. (2017)	Brazil	270	23	8.52	N/R	*R. rickettsii*
Soares et al. (2014)	Brazil	99	6	6.06	512	N/R
Souza et al. (2020)	Brazil	393	89	22.65	4069	*R. rickettsii*
Tamekuni et al. (2011)	Brazil	173	34	19.65	2048	*R. parkeri* *R. rickettsii*
Toledo et al. (2011)	Brazil	73	2	2.74	2048	*R. rickettsii*
	Total: 29 (59.18%)					
Gary et al. (2006)	Canada	68	3	4.41	2048	N/R
	Total: 1 (2.04%)					
Di Cataldo et al. (2022)	Chile	358	11	3.07	N/R	N/R
López et al. (2007)	Chile	77	27	35.06	2048	N/R
	Total: 2 (4.08%)					
Faccini-Martínez et al. (2017)	Colombia	118	17	14.41	8192	*R. rickettsii*
Gual-Gonzalez et al. (2024)	Colombia	52	13	25.00	>128	N/R
Hidalgo et al. (2009)	Colombia	22	4	18.18	4096	*R. rickettsii*
Londono et al. (2019)	Colombia	7	2	28.57	16384	*R. rickettsii*
Londono et al. (2019)	Colombia	141	135	95.74	N/R	N/R
	Total: 5 (10.20%)					
Moreira-Soto et at. (2016)	Costa Rica	329	18	5.47	2048	*R. amblyommatis* *R. rhipicephali*
Pacheco-Solano et al. (2019)	Costa Rica	399	40	10.03	256	*R. rickettsii* *R. amblyommatis*
	Total: 2 (4.08%)					
Foley et al. (2019)	Mexico	213	184	86.38	1024	N/R
Foley et al. (2024)	Mexico	227	174	76.65	N/R	N/R
Pieracci et al. (2019)	Mexico	1136	69	6.07	1024	*R. rickettsii*
	Total: 3 (6.12%)					
Fiorello et al. (2017)	Nicaragua	77	67	87.01	N/R	N/R
	Total: 1 (2.04%)					
Ferradas et al. (2025)	Peru	123	72	58.54	N/R	*N/R*
	Total: 1 (2.04%)					
Lado et al. (2015)	Uruguay	1000	203	20.30	32768	*R. parkeri*
	Total: 1 (2.04%)					
Estrada et al. (2019)	USA	752	92	12.23	≥ 512	N/R
Hinrichsen et al. (2001)	USA	277	59	21.30	N/R	N/R
Yaglom et al. (2018)	USA	217	11	5.07	1024	N/R
	Total: 3 (6.12%)					
TOTAL	**49 (100%)**	**12087**	**2453**	**20.29**		

**Cerdocyon thous* serum samples
N/R: Not registered
N/A: Not applicable
* Possible Antigen Involved in a Homologous Reaction

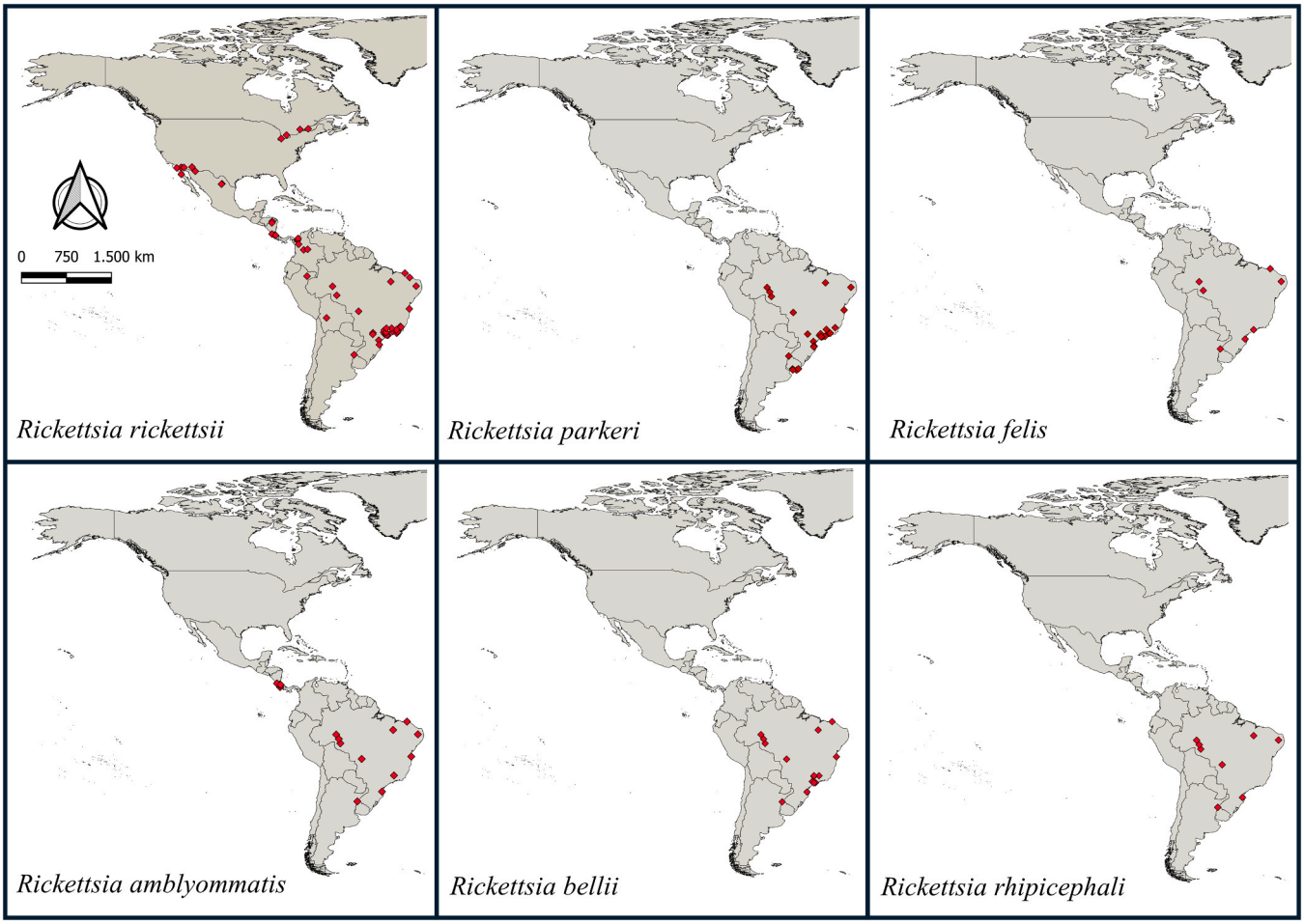


Fig. 2. Maps illustrating the spatial distribution of studies according to the rickettsial antigen potentially involved in a possible antigen-induced homologous reaction (PAIHR).

parkeri (2.7). The test for subgroup differences was statistically significant ($Q = 16.7$, $df = 5$, $p = 0.0052$) (Fig. 4).

When the analysis was stratified by climate zone, the overall pooled seroprevalence estimated using a random-effects model was 26.2% (95% CI: 17.8–36.8%), accompanied by substantial between-study heterogeneity ($I^2 = 97.8\%$, $\tau^2 = 2.891$, $H = 6.69$, $p < 0.001$). Subgroup analyses by climatic zone yielded pooled seroprevalence estimates of 20.7% (95% CI: 10.4–37.1%; $I^2 = 98.1\%$) for subtropical regions (17 studies), 7.0% (95% CI: 0.6–49.2%; $I^2 = 95.6\%$) for temperate regions (3 studies), and 33.2% (95% CI: 20.3–49.1%; $I^2 = 97.7\%$) for tropical regions (30 studies). The differences in seroprevalence among these climatic subgroups were statistically significant ($Q = 7.97$, $df = 2$, $p = 0.019$). Point estimates from individual studies ranged from 2.7% to 100%, indicating pronounced variability attributable to differences in study populations, geographic settings, and diagnostic methodologies (Fig. 5).

Regarding the vectors reported in the articles consulted, the most frequent were *Amblyomma ovale* and *Rhipicephalus sanguineus* s.l., with 57.7% (15 of 26 studies). Other studies reported parasitism by *Amblyomma cajennense* s.l. (6; 23.1%), *Amblyomma sculptum* (5; 19.2%), *Amblyomma oblongoguttatum* (3; 11.5%), and *Amblyomma aureolatum* (3; 11.5%). The species *Amblyomma naponense*, *Rhipicephalus microplus*, and *Ixodes boliviensis* were recorded in two studies each (2; 7.7%). Other registered species were *Amblyomma brasiliense*, *Amblyomma mixtum*, *Amblyomma parvum*, *Amblyomma rotundatum*, *Amblyomma triste*, and *Haemaphysalis juxtakochi*. Tick species, countries, and studies are listed in Table 3.

4. Discussion

The present systematic review and meta-analysis confirm the pivotal eco-epidemiological role of domestic dogs as sentinel hosts for rickettsioses in multiple countries across the American continent. Although other animal species, such as horses and capybaras, have also been implicated as sentinels (Ueno et al., 2016; Luz et al., 2019), dogs in many urban and peri-urban settings exhibit roaming behaviors that encompass both sylvatic and peridomestic habitats. This ecological pattern increases their likelihood of acquiring infected ticks and subsequently introducing them into household environments (Foley et al., 2024, 2025). Moreover, compared to other commonly used sentinel species (e.g., equines), dogs are frequently infested by a wider diversity of tick species (Costa et al., 2025). Importantly, current patterns of close cohabitation between humans and dogs facilitate the transport of ticks into domestic spaces, thereby enhancing the risk of human exposure.

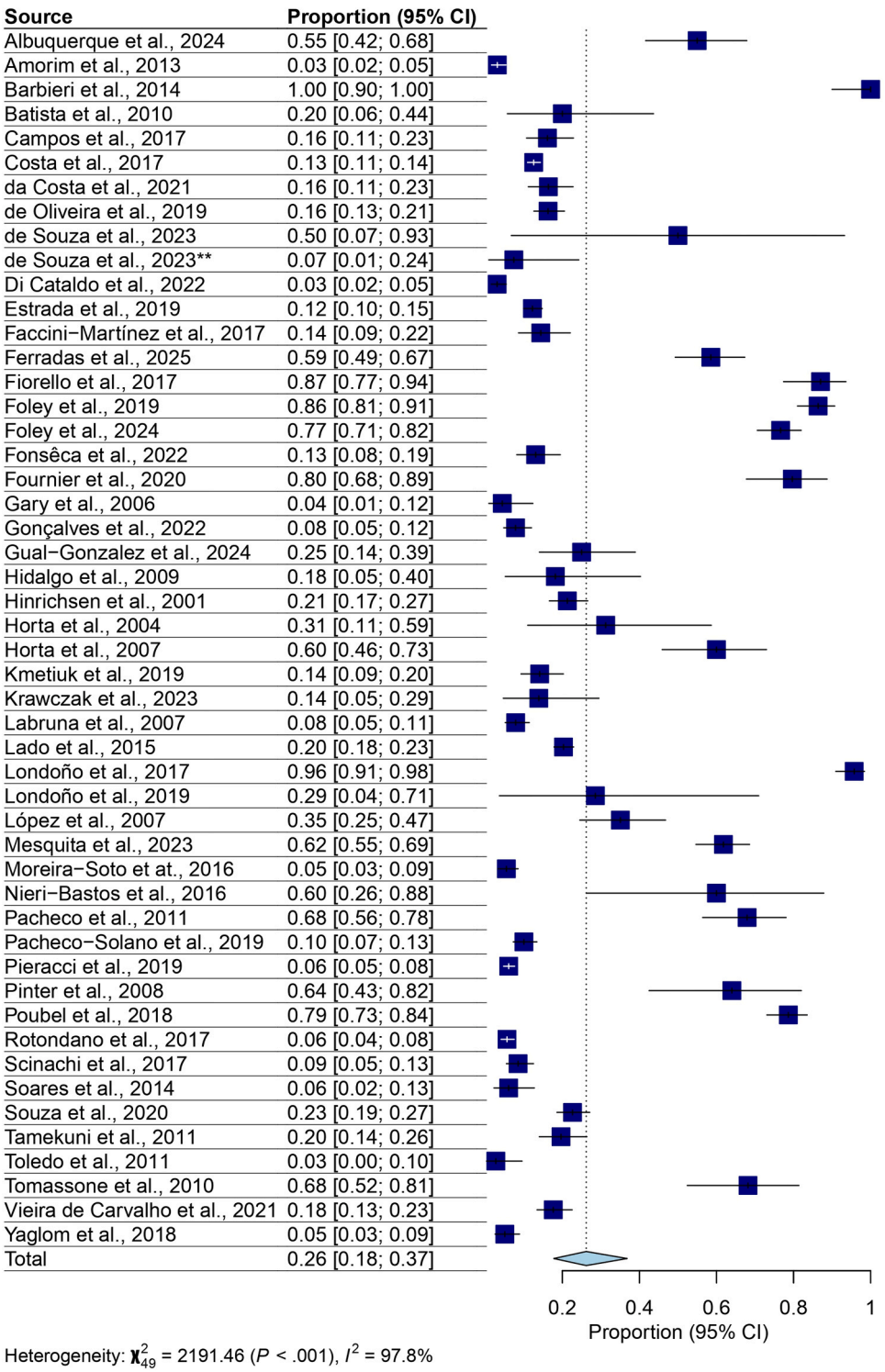


Fig. 3. Overall seroprevalences obtained from the random-effect model. ***Cerdocyon thous* serum samples.

This phenomenon has been extensively characterized for the *R. rickettsii–Amblyomma aureolatum* and *R. rickettsii–Rhipicephalus sanguineus* s. l. systems (Pinter et al., 2008; Saraiva et al., 2014; Foley et al., 2025). In addition, dogs exhibit high susceptibility to infection with *R. rickettsii* (Keenan et al., 1977; Breitschwerdt et al., 1990; Piranda et al., 2008, 2011; Levin et al., 2014; Binder et al., 2021) Consequently, the occurrence of clinical disease in dogs can serve as an early warning indicator of potential human cases, a relationship supported by reports of concurrent rickettsioses in dogs and their owners (Paddock et al., 2002; Hidalgo et al., 2007).

The final number of studies included may be insufficient to accurately represent a comprehensive epidemiological scenario for dog-associated rickettsiae across the American continent. This limitation likely reflects the rigorous application of the exclusion criteria (Table 1), as specified in the Materials and Methods section and detailed in the PRISMA flow diagram (Fig. 1). A substantial number of documents were excluded for reasons such as incorrect geographic scope, detection of rickettsiae exclusively in ticks without serological testing in dogs,

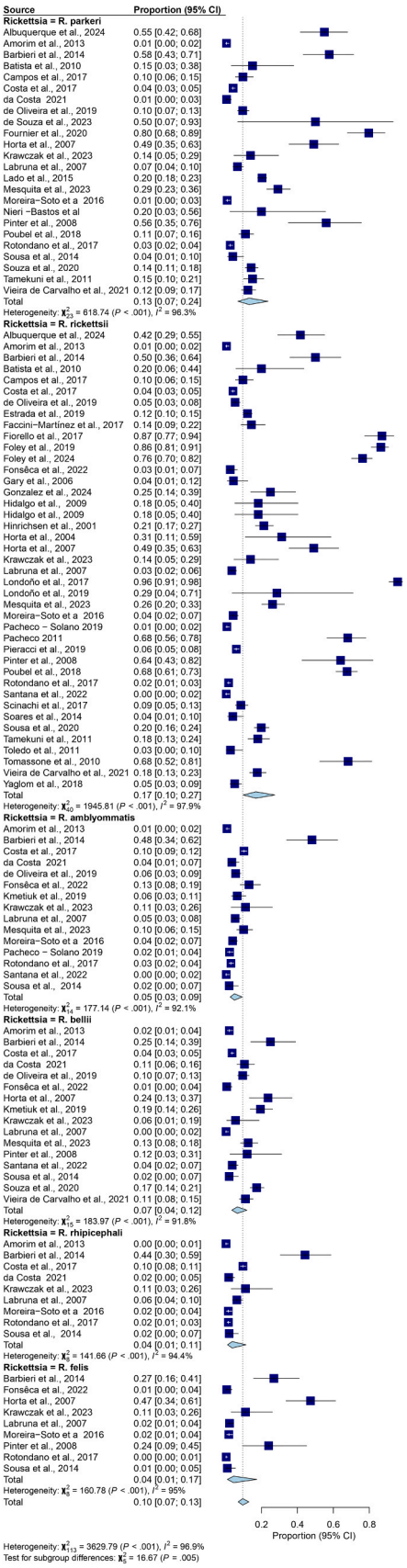


Fig. 4. Seroprevalences obtained from the random-effect model stratified by specific *Rickettsia* antigens (not based on the PAIHR).

ambiguous numbers of sampled animals, or incomplete serological data.

It is noteworthy that Brazil exhibits a prolific body of scientific output in this field. This may be associated with the epidemiological and clinical significance of Brazilian spotted fever (BSF) and other spotted fever group (SFG) rickettsioses in the country, in combination with mandatory case notification and robust epidemiological surveillance systems implemented in specific states (de Oliveira et al., 2016; Faccini-Martinez et al., 2021). This context is further reinforced by the presence of multiple research groups that have enhanced national diagnostic and analytical capacities while also providing support to neighboring countries in the region. Similarly, Mexico has conducted extensive investigations on the role of dogs in particular epidemiological contexts in its northern regions, driven by the elevated incidence of Rocky Mountain spotted fever cases involving dogs and the predominance of *R. sanguineus* s.l. as the principal vector (Tinoco-Gracia et al., 2018; Foley et al., 2019, 2024, 2025). Analogous epidemiological scenarios have been documented in the southwest United States (Demma et al., 2005; Demma et al., 2006). In contrast, several countries in the region have yet to assess the potential epidemiological role of dogs as sentinels for rickettsioses. This gap likely reflects underdiagnosis and/or neglect of these diseases by public health authorities (Walker, 2002; Parola et al., 2005).

Most of the studies identified in the search are cross-sectional and none were longitudinal, which prevents the calculation of risk in sentinel animals (i.e., dogs) and the identification of the factors involved (risk or protective) associated with the circulation of these bacteria in diverse geographical settings throughout the Americas. This continues to represent a knowledge gap in the region that warrants attention. Several works have been longitudinally designed to obtain these data on vertebrate rickettsial hosts (Luz et al., 2019; Goodrich et al., 2020).

Reviewed studies commonly used IFAT as the main serological technique. The Ibero-American Network for Research and Control of Rickettsial Diseases (RIICER) stated in 2014 that the indirect immunofluorescence assay (IFA) is the most commonly used technique by researchers (Oteo et al., 2014), consistent with the reports included in this manuscript. This test is used to detect IgM and IgG immunoglobulins in the acute phase and during convalescence of the disease (La Scola and Raoult, 1997). Despite being considered a gold-standard technique, the antibody cross-reaction between *Rickettsia* species is a limitation that requires using different antigens in the same serum sample to identify the possible antigen involved in a homologous reaction (i.e., PAIHR) and confirm the circulation of pathogenic species (mainly *R. rickettsii* and *R. parkeri*) (Labruna et al., 2007).

The meta-analysis yielded an overall pooled seroprevalence of 26.2% (95% CI: 17.8%–36.8%) using a random-effects model, which reflects the expected range of the true seroprevalence in comparable populations under similar conditions. This confidence interval highlights inherent variability across the included studies. Notably, the analysis revealed a very high degree of heterogeneity (I^2 = 97.8%), indicating that the vast majority of the observed variability arises from genuine differences in study characteristics rather than from sampling error alone (Higgins and Thompson, 2002). Such heterogeneity may stem from variations in study design, population characteristics, diagnostic methods, geographical settings, or temporal factors. The magnitude of τ^2 (2.9) and the H statistic (6.7) provide further quantitative evidence supporting the presence of substantial between-study variability (Higgins and Thompson, 2002). These findings underscore the importance of interpreting the pooled estimate with caution, as the considerable heterogeneity suggests that a single summary seroprevalence may not adequately represent all study contexts. Consequently, future research should consider subgroup analyses or meta-regression to explore potential sources of heterogeneity and to refine the precision and applicability of pooled estimates in this field (Thompson and Higgins, 2002; Harbord and Higgins, 2008).

The test for subgroup differences based on the *Rickettsia* antigen was statistically significant, indicating that the seroprevalences differed

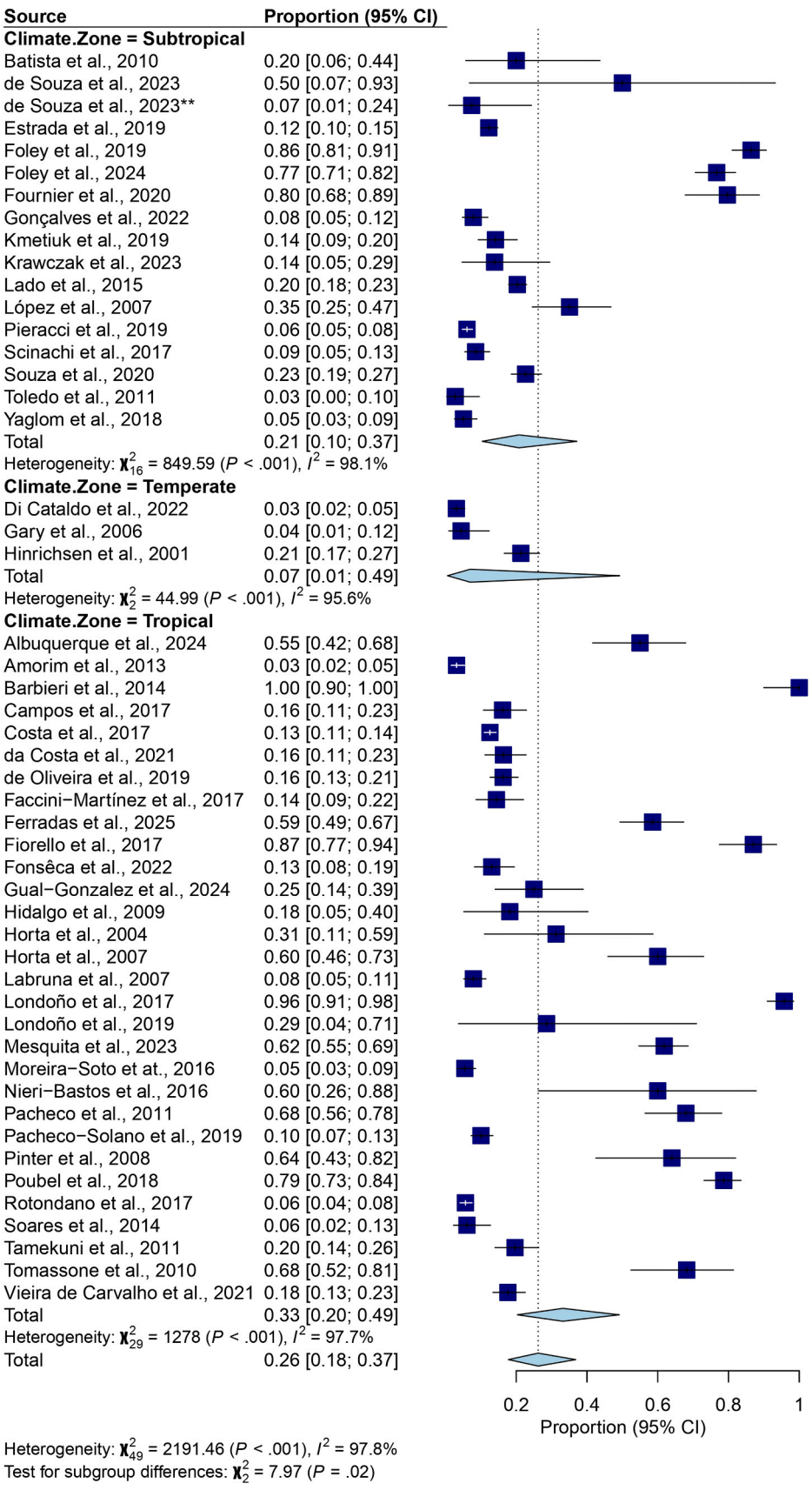


Fig. 5. Seroprevalences obtained from the random-effect model stratified by specific climate zones. ***Cerdocyon thous* serum samples.

Table 3
Tick species identified on dogs in the studies.

Tick species	Country(ies)	Reference(s)
Amblyomma aureolatum	Brazil	(Horta et al., 2007; Barbieri et al., 2014; Vieira de Carvalho et al., 2021)
Amblyomma brasiliense	Brazil	(Soares et al., 2014)
Amblyomma cajennense s.l.	Brazil; Colombia	(Horta et al., 2007; Tamekuni et al., 2011; Toledo et al., 2011; Costa et al., 2017; Faccini-Martinez et al., 2017; Londono et al., 2017)
Amblyomma mixtum	Costa Rica	(Pacheco-Solano et al., 2019)
Amblyomma naponense	Brazil	(Soares et al., 2014; de Oliveira et al., 2019)
Amblyomma oblongoguttatum	Brazil	(Soares et al., 2014; Costa et al., 2017; da Costa et al., 2021)
Amblyomma ovale	Brazil; Colombia; Costa Rica	(Tamekuni et al., 2011; Barbieri et al., 2014; Soares et al., 2014; Costa et al., 2017; Faccini-Martinez et al., 2017; Londono et al., 2017; de Oliveira et al., 2019; Kmetiuk et al., 2019; Pacheco-Solano et al., 2019; Fournier et al., 2020; da Costa et al., 2021; Vieira de Carvalho et al., 2021; Gonçalves et al., 2022; de Souza et al., 2023; Albuquerque et al., 2024)
Amblyomma parvum	Brazil	(Costa et al., 2017)
Amblyomma rotundatum	Brazil	(Costa et al., 2017)
Amblyomma sculptum	Brazil	(Rotondano et al., 2017; de Oliveira et al., 2019; Kmetiuk et al., 2019; Vieira de Carvalho et al., 2021; Gonçalves et al., 2022)
Amblyomma triste	Brazil	(Lado et al., 2015)
Haemaphysalis juxtakochi	Brazil	(Costa et al., 2017)
Ixodes boliviensis	Brazil	(Moreira-Soto et al., 2016; Pacheco-Solano et al., 2019)
Rhipicephalus microplus	Brazil	(Costa et al., 2017; de Oliveira et al., 2019)
Rhipicephalus sanguineus s.l.	Brazil; Colombia; Costa Rica; Mexico; USA; Peru	(Horta et al., 2007; Tamekuni et al., 2011; Toledo et al., 2011; Barbieri et al., 2014; Moreira-Soto et al., 2016; Costa et al., 2017; Faccini-Martinez et al., 2017; Londono et al., 2017; Yaglom et al., 2018; de Oliveira et al., 2019; Foley et al., 2019; Pacheco-Solano et al., 2019; Pieracci et al., 2019; da Costa et al., 2021; Vieira de Carvalho et al., 2021; Fonsêca et al., 2022; Gonçalves et al., 2022; Foley et al., 2024; Ferradas et al., 2025)
Rhipicephalus linnaei	Brazil	(Albuquerque et al., 2024)

significantly between *Rickettsia* species. This suggests that species-specific factors may contribute to the observed variability in infection or detection rates between close groups of antigens such as SFG rickettsiae. For this reason, researchers report in their studies cases where some of the antigens present titers at least four times higher than those of the other rickettsiae in the same group (i.e., PAIHR) (Labruna et al., 2007). Despite these PAIHR reports, our review revealed that several studies did not simultaneously test dog serum samples for different antigens (or species), making it difficult to interpret the results owing to immunological cross-reactivity (Ormsbee et al., 1978; La Scola and Raoult, 1997). It is worth noting that studies reporting *R. bellii* as antigen and PAIHR were included in the review and meta-analysis, as it is commonly screened in serology studies due to cross-reactivity with the spotted fever group species, and also because it is commonly found in neotropical ticks that could parasitize dogs (Vazquez-Guerrero et al., 2023).

The subgroup analysis discriminated by climate zone also revealed a significant difference between the tropical, subtropical, and temperate regions. This approach is more accurate from an ecoepidemiological perspective based on differences in ecosystems, landscapes, vectors, and hosts. The highest pooled prevalence was registered in the studies conducted in tropical regions, followed by subtropical and temperate zones. This could be related to more favorable ecological conditions for ticks, as ectothermic organisms, in tropical and subtropical areas, which contribute to broader geographical distribution and species diversity (Apanaskevich and Oliver, 2014; Alasmari et al., 2025; Valdez-Espinoza et al., 2025). However, this could be biased for the number of studies in each region (mainly in temperate zones) and represents a bare view of a highly complex phenomenon that involves tick-*Rickettsia*-host-environment interactions under climate change scenarios.

Based on the tick species registered in the reviewed studies, dogs were commonly parasitized by *A. ovale* and *R. sanguineus* s.l., which is expected, as both species use dogs as main hosts (all stages for *R. sanguineus* s.l. and mainly adults for *A. ovale*), and are broadly distributed in the region (Guglielmone et al., 2003; Dantas-Torres, 2010). It is worth noting that both species have been incriminated as vectors of *R. parkeri* (strain Atlantic rainforest) and *R. rickettsii* (mainly in Mexico and the southwest United States), respectively (Demma et al., 2006; Szabo et al., 2013). From a One Health perspective, it is relevant to consider and include in surveillance programs these dog-tick-*Rickettsia* interactions, as dogs could act as carriers of infected ticks that potentially infest humans and transmit *Rickettsia*.

5. Conclusion

This systematic review and meta-analysis confirm that various *Rickettsia* species from the Spotted Fever group circulate in dogs throughout the Americas with significant prevalence; however, the lack of antigen availability (probably due to the lack of infrastructure for *Rickettsia* cultivation) has led to numerous studies not presenting robust results and strong conclusions from epidemiological surveys.

Likewise, due to the significant seroprevalence in dogs from countries such as Brazil, Colombia, and Mexico, it could be considered that the lack of evidence of studies in some nearby countries, with similar climatic and ecological conditions, may be related to unexplored regions of the continent rather than the absence of these pathogens and their related diseases. This could be improved by strengthening surveillance programs focused on rickettsial pathogens that include dogs as sentinels and prioritizing these diseases as relevant zoonoses.

Finally, identification of sentinel species for a disease, such as those caused by *Rickettsia*, makes it possible to investigate changes in prevalence or incidence and evaluate control programs. Additionally, it allows confirmation of hypotheses about the ecology or epidemiology of these emerging zoonotic agents within a One Health framework.

CRediT authorship contribution statement

Beatriz Elena Patiño-Quiroz: Writing – original draft, Investigation, Conceptualization, Data curation, Writing – review & editing. **Laura Alejandra Páez-Rojas**: Writing – original draft, Investigation, Data curation, Writing – review & editing. **Jerson Andrés Cuéllar-Sáenz**: Investigation, Data curation, Writing – review & editing. **Nicolás Ernesto Baldrich–Romero**: Writing – original draft, Investigation, Data curation, Writing – review & editing. **Gina Polo**: Writing – original draft, Investigation, Conceptualization, Supervision, Writing – review & editing. **Alejandro Ramírez-Hernández**: Writing – original draft, Investigation, Conceptualization, Supervision, Writing – review & editing.

Ethical approval

Not applicable

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.prevetmed.2026.106881.

Data availability

Data will be made available on request.

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