Current Tropical Medicine Reports (2023) 10:94–137
https://doi.org/10.1007/s40475-023-00288-7

Coxiella burnetii Infection in Livestock, Pets, Wildlife, and Ticks in Latin America and the Caribbean: a Comprehensive Review of the Literature

Loïc Epelboin[1,2] · Mateus De Souza Ribeiro Mioni[3] · Aurelie Couesnon[4] · Mona Saout[5] · Edith Guilloton[2] · Salma Omar[2] · Vincent Pommier De Santi[6] · Bernard Davoust[7,8] · Jean Lou Marié[7,9] · Anne Lavergne[10] · Damien Donato[10] · Alexandro Guterres[11] · Sebastien Rabier[2] · Justin Destoop[12] · Felix Djossou[1] · Xavier Baudrimont[13] · Antoine Roch[13] · Gabriel Leonardo Cicuttin[14] · Tatiana Rozental[11,15] · Mathieu Nacher[2] · Javier Millán[16,17,18] · Elba R. Sampaio De Lemos[11] · Jorlan Fernandes[11] · Olivier Duron[19] · Benoit De Thoisy[10,20] · Elodie Rousset[4]

Accepted: 17 April 2023 / Published online: 15 June 2023

Abstract

Purpose of the Review Q fever, a bacterial zoonosis caused by *Coxiella burnetii*, is reported very heterogeneously in humans in Latin America. The objective of this study was to review the data on *Coxiella burnetii* Infection in animals in Latin America and the Caribbean.

Recent Findings A comprehensive literature review was carried out in the 47 countries and territories of Latin America on various search engines and grouped into four groups: livestock, pets, wildlife, and ticks.

Summary Thus, 113 studies were selected between 1950 and 2022. Among the 47 countries, only 25 (53%) had at least one publication related to *C. burnetii* infection in animals. The most productive country was Brazil ($N=51$), followed by French Guiana ($N=21$), and Colombia ($N=16$). Studies in livestock from 20 countries have shown widely varying country-to-country rates of seroprevalence, ranging from 0 to 67%. Some studies from seven countries, especially French Guiana and Brazil, found antibodies and sometimes positive PCR in dogs and cats, generally in the context of investigations around human clustered cases. Knowledge remained fragmented about infection in wildlife from only five countries (Chile, Colombia, Brazil, French Guiana, and Uruguay). *C. burnetii* infection was identified by PCR in Chiroptera (7 species), Rodentia (6 species), Suina (2 species), Xenartha (1 species), Cingulata (1 species), and Perissodactyla (1 species). Studies on *Coxiella* sp. in ticks have been performed in 11 countries, mostly in Brazil, and mainly found *Coxiella*-like endosymbionts. Thus, data on *C. burnetii* infection in animals are sparse and incomplete in Latin America and the Caribbean, and more research is warranted.

Keywords *Coxiella burnetii* · Latin America · Caribbean · Animal health · Zoonosis · Wildlife · Ticks · Cattle

Introduction

Q fever is a zoonosis caused by the strict intracellular bacterium *Coxiella burnetii*, which is maintained in the environment by animals, especially mammals [1–3]. Humans generally become infected through air-borne transmission of the bacterium from the envirnoment contaminated by animal reservoirs, as a spore-like form allows *C. burnetii* to resist different environmental conditions and disinfectants [4]. This zoonosis is found worldwide, but there is considerable uncertainty about the incidence in different regions of the world and the relative importance of the risk factors of human infection. Potential reservoirs of the pathogen are numerous in wild and domestic species [5–8]. Nevertheless, descriptive studies mainly targeted -cattle, sheep, and goats - which represent the main source of human infection in Europe, while cattle appear to be involved as major reservoirs in Canada and Japan [1, 9, 10]. Other domestic mammals, such as cats and dogs, may also play a role in the transmission to humans, for instance in Canada and Australia [11–17]. Although less frequent, birds, marine mammals, or game may be sometimes implicated in the occurrence of sporadic or clustered human cases [17–20].

This article is part of the Topical Collection on *Emerging Tropical Diseases*.

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Considering that *C. burnetii* infection in humans is largely asymptomatic, Q fever appears to have a limited impact on public health. Nevertheless, it could cause significant disability and possibly long-term consequences due to persistent infection. Approximately 5% of those infected with *C. burnetii* develop a chronic form, now called persistent focalized *C. burnetii* infection, that can develop in patients with heart valve defects or vascular disease, immunosuppressed patients, and pregnant women. Persistent focalized Q fever can occur from a few weeks to several years after the initial infection, with patients presenting with endocarditis, pneumonia, chronic hepatitis, and other manifestations frequently less responsive to antibiotic treatment. Different frequencies of pneumonia and hepatitis have been observed depending on the regions of the world; one hypothesis is an association with local circulating strains [20–22]. Moreover, since the first descriptions in the1990s, chronic fatigue syndrome (CFS) has been described as a sequel directly associated with *C. burnetii* infection (post-acute Q fever) [23–25]. As the clinical manifestations are nonspecific and the diagnosis complex, CFS is probably an underestimated disease that can become a major public health problem. Great difficulties are actually encountered in control, especially during and after large human outbreaks, such as in the Netherlands [26, 27], and in hyperendemic areas, such as in French Guiana [28••]. In addition, *C. burnetii* is classified as a potential inhalational bioterrorism agent [29]. These situations highlight the need for a collaborative effort from human physicians and veterinarians under the umbrella of the "one health" concept to minimize exposure among people [30–32].

In animals, infection is also usually asymptomatic [3]. The spectrum of clinical forms appears less diversified than in humans but is biased by a focus on reproductive disorders leading to substantial economic losses, known as coxiellosis. The association with late-term abortions, stillbirth, prematurity, and low birth weight is clearly demonstrated in sheep, goat, and cattle farms [33–38]. Other manifestations are suspected (infertility, metritis, mastitis) but evidence is still lacking [35]. For other animal species, knowledge on the clinical outcome of *C. burnetii* infection is very limited, but currently appears to include reproductive failure in waterbuck (*Kobus ellipsiprymnus*), roan antelope (*Hippotragus niger*), dama gazelle (*Nanger dama*), and water buffalo (*Bubalus bubalis*) and placentitis in the Pacific harbor seal (*Phoca vitulina richardsi)*, steller sea lion (*Eumetopias jubatus*) and red deer (*Cervus elaphus*) [39]. Overall, knowledge is not fully understood about the pathogenesis and the sites (organs, cells) affected depending on the species. Authors agree on the circulation of *C. burnetii* strains, which appear widespread in cattle, sheep, and goats in most countries. On a technical level, the investigations were first restricted to serology. However, the available serological tests should be optimized and validated for each species [3, 40, 41]. Since the 1990s, more and more research has included direct detection by molecular analysis (PCR). The lack of standardized methods, or at least the lack of knowledge of the performance of sensitivity and diagnostic specificity, and the limited sample size of most of the existing studies could suggest variable bias in reported prevalence rates of *C. burnetii* infection. In addition to the identification of *C. burnetii* infection in different species of animals in different regions, although some results are still questionable, it was possible to acquire descriptive knowledge such as (i) the sites and routes of excretion of ruminants such as feces, urine, vaginal secretions, semen, milk, and placenta, along with serological responses; (ii) potential environmental sources (dust, manure, etc.); and (iii) molecular epidemiological data [37, 38, 42–45]. Studies have shown a higher risk of transmission following an episode of abortion, especially in small ruminants, generating massive bacterial shedding in the environment [46]. Nevertheless, the epidemiology of *C. burnetii* infection is still complex, with particularities according to the regions of the world. A wide range of animal species can play a role in the dissemination or maintenance of the bacterium in the environment. The effective airborne propagation ranges of *C. burnetii* may vary depending on meteorological and topographical factors. It is important to better understand the diversity of epidemiological situations and evolutions around the world.

The presence of *C. burnetii* in several animal species linked to its zoonotic importance justifies the growing recent trend in scientific development related to coxiellosis [47]. The reservoirs of *C. burnetii* have been largely investigated in many countries, especially in Europe [48]. Nevertheless, the implication of wildlife in the transmission of *C. burnetii* to humans and livestock remains poorly understood [35, 48–54]. On the other hand, data on *C. burnetii* in Latin America are scarce, sparse, and extremely heterogeneous, although several studies have been published in the last decade in humans, especially in French Guiana and Brazil. On the one hand, French Guiana contains areas of hyperendemicity and holds the record for the highest annual incidence rate in the world [28••, 55]. Furthermore, there is a specific virulence associated with a pulmonary tropism, likely linked to a specific strain of the MST17 [22, 56–59]. On the other hand, countries such as Brazil have reported few cases, case series, and seroprevalence studies [60–66]. Other countries have performed only exploratory investigations, and most countries have reported none or a few human cases over the last 30 years [28••, 67]. The objective of this work is therefore to carry out a comprehensive review of the literature concerning

animal *C. burnetii* infection in Latin America and the Caribbean.

Methodology and Objectives

Settings

We defined Latin America as Central America, the Caribbean, and South America.

Review of the Literature

A comprehensive literature review was carried out following the PRISMA Reporting Guidelines. The terms "Q fever" and "*Coxiella*" were searched together with the names of each of the 47 countries and territories of South America and the Caribbean in English, French, Spanish, and Portuguese in PubMed (National Institutes of Health's National Library of Medicine) and ScienceDirect (Elsevier), and the terms "*Coxiella*" and "Q fever" in four languages in the databases SciELO (Scientific Electronic Library Online) and LILACS (Scientific Health Information from Latin America and the Caribbean countries), which are more specifically dedicated to the Latin American medical and scientific literature (Fig. 1). We excluded papers on other subjects than *C. burnetii* infection, *C. burnetii* infection in humans only, and studies on *C. burnetii* performed outside of Latin America and the Caribbean. A second time, after selecting the papers according to those inclusion criteria, the references of each paper were analyzed independently by two authors, and the most relevant ones were also included. Lastly, unpublished data concerning *C. burnetii* according to the knowledge of the authors were also added, including, thesis, web papers, and unpublished investigations, especially in Brazil and French Guiana. The bibliography was screened for every paper, and articles without complete text but with informative abstracts or summarized in a literature review were maintained in order not to avoid some not-indexed publications, especially old ones. The research period ranged from 1 January 1950 to 31 December 2022.

The publications were then grouped and discussed into four different groups: (1) livestock (cattle, sheep, goats, equine, swine), (2) pets (mainly dogs and cats), (3) wildlife (any taxon), and (4) ticks and other ectoparasites. For each of these four parts, the results are presented in summary tables. In the second part, a special focus was made on five countries where the infection is more often reported: French Guiana, Brazil, Argentina, Chile and Colombia, and where research on animal fever has been the most abundant.

Results/Discussion

After applying the criteria, 113 studies in French, Spanish, Portuguese or English were selected: (i) 84 published articles found in the databases; (ii) 16 articles not found in the databases but found through the bibliography review of the articles in the previous item, and (ii) 13 articles acquired from other sources, including four theses developed in Brazil and French Guiana, including four PhD theses (Fig. 1).

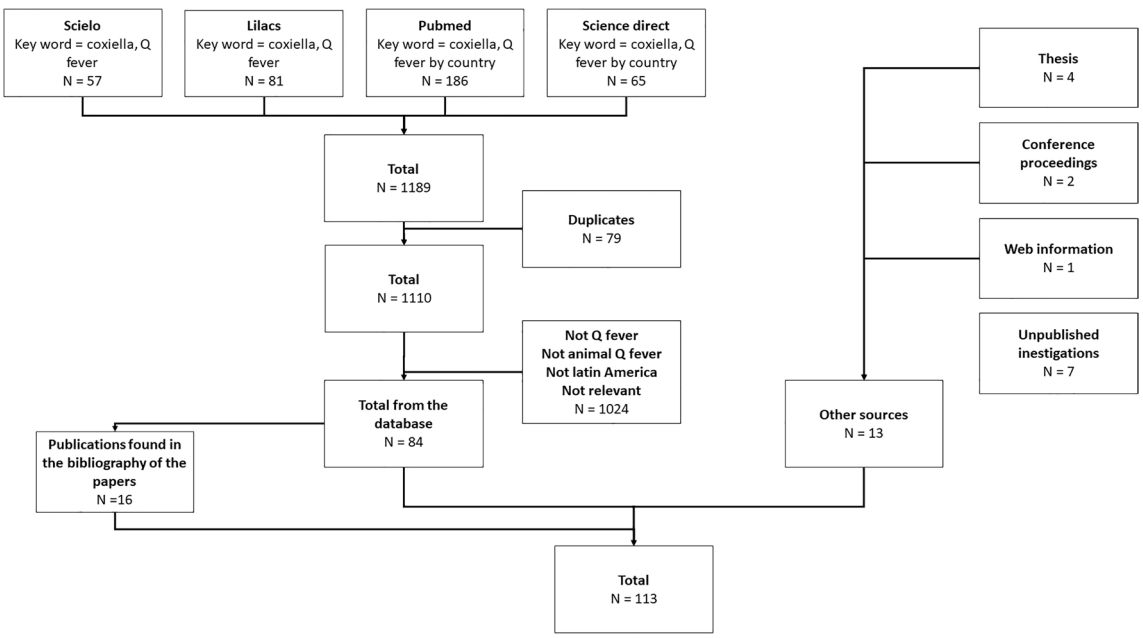

Fig. 1 Flow chart of the study according to the Prisma criterion

Among the 21 countries or territories in continental Latin America, 16 (76%) had at least one publication related to *C. burnetii* detection in animals, and nine (35%) among the 26 Caribbean countries and territories. The most productive country was Brazil ($N=51$), followed by French Guiana ($N=21$), Colombia ($N=16$), Argentina, Chile, and Uruguay ($N=8$), respectively. Five countries had between two and four studies, and fourteen countries or territories had only one study. About 30% of the studies have been published between 2020 and 2022. The more abundant literature was available for livestock, followed by ticks, wildlife, and at last pets.

Animal Coxiella burnetii Infection in Latin America

Livestock

During the study period, there were 64 publications concerning *C. burnetii* from livestock in 20 countries and territories of Latin America and the Caribbean, mainly from Brazil ($N=18$), Colombia ($N=10$), and French Guiana ($N=6$) (Fig. 2). Most of them concerned cattle, sheep, and goats, but also included zebu cattle, buffalo cattle, alpaca, horses, swine, and chicken (Table 1). Most of the studies were seroprevalence surveys in livestock, especially cattle. In cattle, seroprevalence rates varied a lot according to regions and studies, from 0% in the Brazilian state of Mato Grosso do Sul and in several Islands from the lesser Caribbean to 31.8% in Duque de Caxias, state of Rio de Janeiro [72, 83, 101]. Some authors also calculated the herd prevalence in addition to the apparent individual prevalence, with a variation from 46.9 to 82% [102, 105, 122]. Seroprevalence in goats varied a lot, from 0%, in the Caribbean Islands, in French Guiana or Piauí state, Brazil, to 35% in Nuevo Leon, Mexico, 50% in Itaboraí, Brazilian state of Rio de Janeiro, and 60.6% in Venezuela [76, 78, 101, 107, 109, 111, 121]. In most of the studies, the seroprevalence was relatively low, between 0 and 3% [80, 98, 100, 101]. At last, seroprevalence in sheep was highly variable also, from 0% in Argentina and the Caribbean Islands Trinidad and French Guiana, to 17.3% in Uruguay, 26.3% in St. Kitts, and 66% in Itaboraí, Brazilian state of Rio de Janeiro [76, 113–116].

Some had investigated the presence of the *C. burnetii* genome on vaginal swabs [86, 89, 98, 109], fetuses or placenta [86, 88••, 89, 117], serum or blood samples [66, 76, 99], and finally, milk and dairy products [71, 76, 81, 84, 85, 96, 98, 123]. Vaginal carriage of *C. burnetii* has been found in a few studies and implicated as a cause of abortion for different species [63, 88••, 118–120].

C. burnetii infection has been reported elsewhere in other domestic mammals, though less frequently than in livestock [124]. In Latin America, studies among domestic animals, including cattle (including zebu cattle and buffalo cattle),

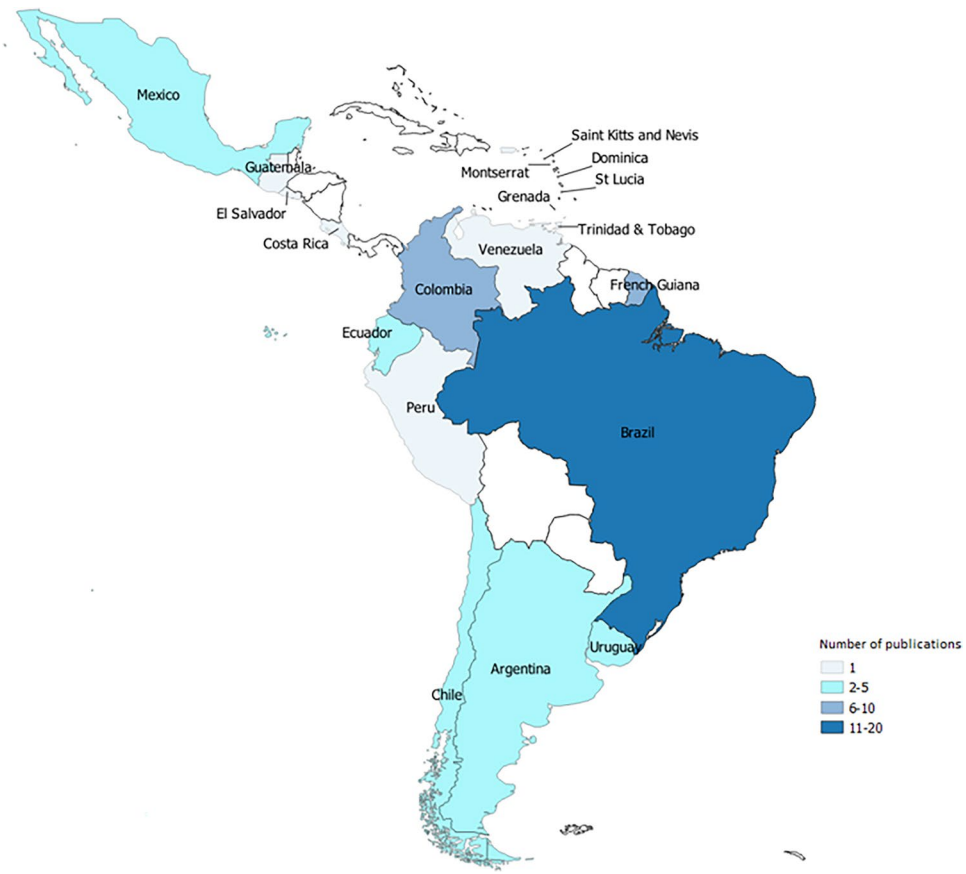

Fig. 2 Map of the publications on *Coxiella burnetii* infection in livestock in Latin America and the Caribbean

Table 1 Data on C*oxiella burnetii* detection in livestock, swine and equine in Latin America

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Babudieri and Kaplan [68, 69]	NA	1952	Spanish	Argentina	–	CFT	Serum	Sheep	0/22	0%		Yes
							Serum	Cattle	2/28	7.1%		
Trezeguet [70]	2007	2010	Spanish	Argentina	Various states	ELISA and CFT	Serum	Goats	33/15,272	0.22%		Yes
Rojas [71]	NA	2013	Spanish	Argentina	NA	RT-PCR (IS1111)	Milk	Cattle	0/1	0%		Yes
Travassos and Kaplan [72, 68]	NA	1954	Portuguese	Brazil	Caixas (vicinity of Rio de Janeiro)	CFT	Serum	Cattle	114/358	31.8%		Yes
Valle [73]	NA	1955	Portuguese	Brazil	São Paulo	CFT	Serum	Cattle	24/171	14%		Yes
Riemann [74]	1972	1975	English	Brazil	7 towns of Minas Gerais State and 12 towns of Goiás State	IHA	Serum	Zebu cattle	45/156	29%	Study in slaughter-house	Yes
Brown [75]	NA	1989	English	Brazil	5 among 9 States in North-east regions	ELISA	Serum	Goats	0/76	0%		Yes
Mares-Guia [76]	2008–2009	2014	English	Brazil	Itaboraí municipality, State of Rio de Janeiro	IFA	Serum	Sheep	2/3	66.6%	Area of the first human case of Q fever in Brazil	Yes
								Horses	0/2	0%		
								Goats	5/10	50%		
						PCR (*htp*AB gene)	Serum	Sheep	0/3	0%		
							Serum	Horses	0/2	0%		
							Milk	Goats	6/10	60%		
Mares-Guia [77]	2011–2012	2015	Portuguese	Brazil	Itaboraí municipality, State of Rio de Janeiro	IFA	Serum	Sheep	2/15	17.1%	Several human cases in the area Unpublished thesis	Yes
						PCR (*htp*AB gene)	Serum	Sheep	0/15	0%		
							Udder	Sheep	1/6	16.7%		

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Guimarães [78]	2013	2017	Portuguese	Brazil	Parque Nacional da Serra das Confusões, Caatinga biome, Piauí	IFA	Serum	Sheep	3/153	2.0%	Not on PubMed	Yes
								Goats	0/202	0%		
De Oliveira [79]	2014–2015	2018	English	Brazil	Agreste mesoregion, Alagoas	ELISA	Serum	Goats	172/312	55.1%	Dairy goats with reproductive disorders	Yes
						PCR (IS1111)	Placenta		2/23	8.7%		
Souza [80]	2016	2018	English	Brazil	Petrolina, Pernambuco State	IFA	Serum	Goats	9/412	2.2%		Yes
								Sheep	9/403	2.1%		
Mioni [81]	2017	2019	English	Brazil	Goiás State	qPCR (IS1111)	Raw milk	Cattle	4/112	3.6%		Yes
Zanatto [82]	2014–2015	2019	English	Brazil	States São Paulo, Minas Gerais Minas, Mato Grosso do Sul, Goiás	IFA	Serum	Cattle	14/102	13.7%	Cows showing a history of reproductive disorders	Yes
Ramos [83]	NA	2020	English	Brazil	Mato Grosso do Sul	IFA	Serum	Zebu cattle				Yes
								Cow	2/200	1.0%		
								Calves	0/200	0%		
Rozental [84, 85]	NA	2020	English Portuguese	Brazil	Serro microregion, Minas Gerais State	PCR (IS1111)	Artisanal cheese	Cattle	5/53	9.4%		Yes
Mioni [86]	NA	2020	English	Brazil	São Paulo	Genotyping (MLVA and MST) #	Vaginal swabs	Sheep	3/3	100%	MST74	Yes
							Vaginal swabs	Goat	1/1	100%		
							Fetus	Cattle	3/3	100%		
Mioni [64]	2014–2015	2020	English	Brazil	São Paulo State	IFA	Serum	Cattle and Zebu cattle	360/1515	23.8%	45/54; 83.3% of the cities had at least 1 seropositive animal	Yes
						qPCR (IS1111)			44/360	12.2%		

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Nascimento [87]	2020	2021	English	Brazil	Municipality of Patos de Minas, Cerrado Mineiro Minas Gerais State	qPCR (IS1111)	Artisanal cheese	NA (likely cattle)	4/87	4.6%		Yes
Mioni [88••]	2013–2019	2022	English	Brazil	São Paulo State University and Universidade Federal do Rio Grande do Sul		Fetuses	Cattle	7/76	9.2%	3 co-infections with *Neospora* spp.	Yes
Mioni [89]	NA	Unpublished	Portuguese	Brazil	São Paulo	qPCR IS1111	Vaginal swabs	Sheep and goats	27/133	20.3%	Sheep: flock with the reproductive disorder (abortions) Goats: asymptomatic flock	No
International Society for Infectious Diseases [90]	2014	2014	English	Chile	NA	ELISA	Serum	Alpaca (*Vicugna pacos*)	13/946	1.4%	Culled after importation in China after being diagnosed with Q fever	No
Cornejo [91]	2017	2019	English	Chile	Metropolitan, Ñuble, Bío-Bío, Araucanía, Los Ríos, and Los Lagos Districts	qPCR IS1111	Raw tank milk from 105 different farms	Cattle	2/105	2.1%		Yes

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Covelli [92]	NA	1961	Spanish	Colombia	Departamentos de Antioquia, Cundinamarca and Meta	CTF	Serum	Cattle	8/1715	0.46%		Yes
San Martin-Berberi [93]	1959	1963	Spanish	Colombia	Valle, Cali	MAT	Milk			"Proof of infection"	Unpublished personal data	No
Vaughn [93]	1963	1967	Spanish	Colombia	Valle, Caldas, Cauca, Tolima, Nariño, Santander, Caquetá, Cundinamarca, and Huila	MAT	Serum	Cattle	110/454	24.2%	Animals from slaughterhouse	Yes
Lorbacher de Ruiz [94]	NA	1977	German	Colombia	Various	CFT	Serum	Horses Cattle	89/357	25.0%	Manuscript not available. Data in a review of the literature	Yes
Perry [95]	NA	1981	Spanish	Colombia	Boyacá Department	CFT	Serum	Sheep Imported Local	197/2501 91/402 106/2099	7.9% 23.0% 5.0%	Blackface sheep recently imported from Great Britain	Yes
Rojas [71]	NA	2013	Spanish	Colombia	NA	RT-PCR (IS1111)	Milk	Cattle	1/4	25%	Ct 37.32	Yes
Contreras [96]	2012	2015	English	Colombia	Montería	IFA qPCR (IS1111)	Milk	Cattle	5/11	45%	Strain CbuK 154Q	Yes
Eraso-Cadena [97]	2014	2017	English	Colombia	North and Magdalena Medio subregions of Antioquia	IFA	Serum	Cattle	104/384	27.1%	48 livestock farms	Yes

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Contreras [98]	2013	2018	English	Colombia	Municipality of Valledupar, department of Cesar	Conventional PCR (IS1111)	Milk	Sheep	4/66	6%	Percentage of identity 100% strain CbuK Q_154	
							Vaginal swabs	Goats	2/328	0.6%	99% strain Guiana Cb175	
Cabrera Orrego [99]	2015	2020	English	Colombia	Magdalena Medio region, Antioquia	qPCR (*IS 1111*) 16SRNA	Serum	Cattle	38/192	19.5%	Risk factors: Location: Municipality (Puerto Nare), female, born on the farm, intended for meat production, spent over 49 months of residence on the farm	Yes
Villagra-Blanc [100]	2013–2017	2018	English	Costa Rica	Central, North Huetar, Atlantic Huetar, Central Pacific, Chorotega, Brunca	ELISA	Serum	Goats Flock	7/391 1/13	1.8% 7.7%	Detected only in 1 flock in the North Huetar Region. 15.2% of the goat positive in this flock	Yes
Johnson [101]	NA	2020	English	Dominica	NA	IFA	Serum	Cattle Sheep Goats	0/83 1/54 0/65	0% 2% 0%		Yes

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Rojas [71]	NA	2013	Spanish	Ecuador	Cruda, Cotopaxi, Carchi, Loja, Chimborazo, Pastaza, Guayas, Galápagos, Imabura	RT-PCR (IS1111)	Milk	Cattle	3/102	2.9%	All in the Chimborazo province Ct: 36.62, 32.73, and 37.10	Yes
Carbonero [102]	2008–2010	2015	English	Ecuador	Azuay, Chimborazo, Cotopaxi, Manabí, Pichincha, Santo Domingo, Tungurahua and Zamora-Chinchipe	ELISA	Serum	Cattle Apparent individual prevalence True prevalence Herd prevalence	 386/2668 181/386	 14.5% 12.6% 46.9% (8% to 100% according to herd)	2668 serum samples from 386 herds Risk factors: females (15.5 vs. 8.5%), cattle > 4 years old (20.2 vs. 10.6%)	Yes
Echeverria [103]	NA	2019	English	Ecuador	Quito area (Andes region) and Santo Domingo de los Tsachilas (tropical region)	ELISA	Serum	Cattle	151/352	42.9%	Dairy cattle	
Changoluisa [104]	NA	2019	English	Ecuador	Santo Domingo Province	ELISA	Serum	Cattle Cows with a first-calf abortion Control cows	91/172 47/95 44/77	52.9% 49.4% 57%		Yes
Rice [105]	NA	1979	English	El Salvador	NA	CFT	Serum	Cattle Positive farms	77/297 27/33	26.0% 82.0%		Yes

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
François [106]	NA	1997	French	French Guiana	The farms tested were randomly selected on the territory	CFT		Cattle	6/355	1.7%	Representing 4% (355/9000 bovines), 14.2% (171/1200 sheep), and 21.6% (108/500 goats) of the whole livestock of French Guiana Grey literature	Yes
								Sheep	0/171	0%		
								Goats	0/108	0%		
Gardon [107]	NA	2001	English	French Guiana		CFT	Serum	Cattle	6/355	1.7%		Yes
								Sheep	0/50	0%		
								Goats	0/21	0%		
								Swine	0/25	0%		
Debin [108]	2007	2007	French	French Guiana	Coastal communities from Montsinéry to Mana	ELISA	Serum	Cattle	0/179	0%	Doubtful serologies considered positive: 2/2 for swine; 2/3 for horses Unpublished thesis	No
								Sheep	0/37	0%		
								Goats	0/16	0%		
								Swine	2/103	0 to 1.9%		
								Horses	3/88	1.1 to 3.4%		
Davoust [109]	2013	2014	English	French Guiana	Montagne du tigre, Cayenne	qPCR (IS1111)	Vaginal swabs	Goats	0/13	0%	Investigation close to a human cluster of Q fever Goats and sheep are small ruminants maintained near the outbreak area	Yes
								Sheep	0/8	0%		
						Serodiagnosis	Milk	Sheep or goat	0/1	0%		
							Serum	Goats and sheep	0/37	0%		

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Roch	2019	2019	French	French Guiana	Montsinery	ELISA	Serum	Cattle	0/31	0%	Herd of a farmer who was infected with Q fever	No
Saout [110]	2015–2017	2022	English	French Guiana	Cayenne, Kourou, Sinnamary	ELISA	Serum	Cattle	152/834	14.2%		Yes
								Goats	15/219	1.8%		
								Sheep	21/175	3.7%		
								Herd	57/86	66.3%		
Johnson [101]	NA	2020	English	Grenada	NA	IFA	Serum	Cattle	0/4	0%		Yes
								Sheep	0/86	0%		
								Goats	1/53	2%		
Richter and Cubes [105]	NA	1966	English	Guatemala	NA	NA	Serum	Cattle	NA	9.0%	Cited in Rice et al. but not found	Yes
Salinas-Meléndez [111]	NA	2002	English	Mexico	Nuevo Leon State	ELISA	Serum	Dairy cattle	126/450	28%		Yes
								Beef cattle	19/190	10%		
								Sheep	36/90	40%		
								Goats	21/60	35%		
Salman [112]	NA	1990	English	Mexico	Ensenada and Tijuana, Baja California State	ELISA	Serum	Cattle	1625/7159	22.7%		Yes
								Positive farms	59/104	56.7%		
Johnson [101]	NA	2020	English	Montserrat	NA	IFA	Serum	Cattle	0/14	0%		Yes
								Sheep	0/53	0%		
								Goats	0/27	0%		
Rojas [71]	NA	2013	Spanish	Perú	NA	RT-PCR (IS1111)	Milk	Cattle	2/3	67%	Ct 36.16	Yes
Johnson [101]	NA	2020	English	Puerto Rico	NA	IFA	Serum	Cattle	0/26	0%		Yes
Johnson [101]	NA	2020	English	Saint Kitts and Nevis	St. Kitts	IFA	Serum	Cattle	0/55	0%		Yes
								Sheep	0/5	0%		
								Goats	1/18	5.6%		
Johnson [101]	NA	2020	English	Saint Kitts and Nevis	Nevis	IFA	Serum	Cattle	0/38	0%		Yes
								Sheep	0/101	0%		
								Goats	0/126	0%		

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Conan [113]	2019	2020	English	Saint Kitts and Nevis	St. Kitts	ELISA and CFT	Serum	Sheep	35/133	26.3%	Local sheep and cattle housed at a veterinary campus	Yes
								Cattle	0/63	0%		
Johnson[114]	NA	2020	English	St. Lucia	NA	IFA	Serum	Cattle	0/72	0%		Yes
								Goats	0/18	0%		
Adesiyun [114]	1992–1995	1996	English	Trinidad and Tobago	San Juan, Tunapuna and Port-of-Spain, Trinidad	CAT by Luoto	Serum	Chickens	3/266	1.1%	At slaughterhouse	Yes
								Cattle	11/256	4.3%		
								Swine	17/151	11.3%		
								Buffalo	5/53	9.4%		
								Sheep	0/16	0%		
								Goats	0/7	0%		
Somma-Moreira [115, 116]	13 studies between 1956 and 1985	1987	English and Spanish	Uruguay	–	CFT, MAT	Serum	Cattle [6]	313/2713	11.5% (0.9 to 30%)	(Number of studies)	Yes
								Horses [2]	33/246	13.4% (5.5 to 21.7%)		
								Swine [2]	83/479	17.3% (0 to 21.2%)		
								Sheep [1]	61/591	10.3%		
Macías-Rioseco [117]	2017	2019	English	Uruguay	Colonia	IHC and PCR	Placenta	Cattle	4/4	100%	Bovine abortions	Yes
							Fetuses		3/3	100%		
Macías-Rioseco [118]	2015–2018	2019	Portuguese	Uruguay	Colonia	IHC and PCR	Fetus [53], fetus + placenta [35], and placenta only [14]	Cattle	6/102	6%	Study not on PubMed	Yes
Rabaza [119]	2017	2021	English	Uruguay	San José	qPCR (IS1111), FISH	Placenta Fetus	Cattle [4]	1/1	100%		Yes
Dorsch [120]	2015–2021	2022	English	Uruguay	NA	Conventional PCR	Fetus [58], fetus + placenta [36], and placenta only [6]	Sheep	0/100	0%		Yes

Table 1 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Publication in a journal
Oropeza [121]	NA	2010	Spanish	Venezuela	Villa Araure, Sabana Grande, Los Aranguez, Lara	ELISA	Serum	Goats	191/315	60.6%	Not on PubMed	Yes

A, not available; *CAT* capillary agglutination test; *CFT*, complement fixation test; *MAT*, microagglutination test; *ELISA*, enzyme-linked immunosorbent assay; *IFA*, immunofluorescence assay; *PCR*, qualitative polymerase chain reaction; *qPCR*, quantitative real-time polymerase chain reaction; *MLVA*, multilocus variable number tandem repeats analysis; *MST*, multispacer sequence type; *IHC*, immunohistochemistry; *IHA*, indirect hemagglutination; *FISH*, fluorescent in situ hybridization

goats, and sheep, were scarce. Thus, we identified one study with 25% seropositivity for *C. burnetii* in horses in Colombia in 1977 and 3.4% in French Guiana in 2007 [108, 125]. Pigs have been found to be positive in two studies: 1.9% in French Guiana in 2007, 11.3% in Trinidad in 1996, and 0 to 21.2% in Uruguay in 1984 and 1985 [115, 116], although their role in the epidemiology of *C. burnetii* remains unclear.

Finally, results vary from region to region, and it is difficult to make broad generalizations about trends on the continent. One may hypothesize a correlation between the seroprevalence of *C. burnetii* infection and animal density. The justification for the higher prevalence of cattle would be in places where there is intensive animal farming [126, 127]. In any case, estimated seroprevalence data are very approximate, which makes it necessary to work on protocols and monitoring devices for *C. burnetii* infections.

Pets

A total of 18 studies from seven countries were performed on detecting *C. burnetii* in pets-dogs and cats -mainly in French Guiana and Brazil (Table 2). These studies included five unpublished works, one thesis in French Guiana and Brazil, respectively, and three unpublished works originating from the investigation of the epidemiology and veterinary department of the French Army following outbreaks in military personnel (Fig. 3). Dogs were found positive in the indirect immunofluorescence assay (IFA) for *C. burnetii in* Argentina, Brazil, and French Guiana, with prevalence from 1.8 to 21.7% according to the region, the study, and the cutoff of the titer of IgG [107, 128, 129, 131, 134]. In Brazil and French Guiana, some dogs have been found to be positive, with higher prevalence rates around human Q fever cases [76, 77, 107, 130]. Although some of these dogs were inquired about during confirmed human Q fever outbreak investigations, they do not seem to be at the origin of these human clusters [76, 107, 130]. Cats have been studied in only three regions :Argentina, Brazil, and French Guiana [77, 107–109, 128–131, 134] with six cats positive, five in Argentina and one in Rio de Janeiro, Brazil [77, 128]. No evidence of *C. burnetii* infection was found in dogs using serology or PCR tests on vaginal swabs in Colombia, Martinique, Nicaragua, and Uruguay [97, 134, 135].

Aside from livestock, pet animals, especially dogs and cats, in close contact with humans are important potential reservoirs of *C. burnetii* during urban Q fever outbreaks [124]. Some cases of human coxiellosis have been reported from infected dogs and cats as a source of infection [14, 138]. At the same time, several pets were found to be positive in the investigation of human clusters without these animals being incriminated in the transmission to humans [76, 107, 130].

Wildlife

A total of 24 studies, to which we must add the unpublished results of two investigations, were published on wildlife from only five countries of Latin America: Chile, Colombia, Brazil, French Guiana, and Uruguay (Fig. 4). Some studies have been performed through serodiagnosis in various mammal species, and most of them were negative, as shown in Table 3. Nevertheless, some species have shown seropositivity, meaning contact with the bacterium, such as free-living cervids (*Blastocerus dichotomous* and *Mazama gouazoubira*) in Mato Grasso do Sul, São Paulo, Goiás, and Paraná, Brazil, rodents and marsupials in French Guiana (*Proechimys* sp., *Philander opossum*, *Didelphis marsupialis* [107, 151]) and Pampas deer (*Ozotocero sbezoarticus*) in the Department of Maldonado of Uruguay. Thus, recent studies conducted in Brazil showed serological evidence of *C. burnetii* infection in *Wiedomys pyrrhorhinos* rodents and *Didelphis albiventris* marsupial from Ceará and Pernambuco states, respectively [131]. These animals were collected from areas where dogs were also found seroreactive to *C. burnetii*, suggesting that wild and peridomestic cycles of *C. burnetii* can be connected by rodents and other wild mammals, a scenario identified in other regions where peridomestic rather than wild cycles have a high impact in coxiellosis cases [131, 157]. The use of molecular biology, mainly PCR targeting the repetitive element IS*1111*, helped identify new positive mammals (Table 4). The results reported in Ct (cycle treshold) were mostly superior to 35, which corresponds to traces in bacterial loads. The animal groups with molecular evidence of *C. burnetii* in Latin America were Chiroptera (7 species), Rodentia (6 species), Suina (2 species), and one species for Pilosa, Cingulata, and Perissodactyla, respectively (Table 4).

Nonflying Mammals In French Guiana, the first studies about *C. burnetii* infection in wildlife date back to the late 1990s, following the discovery of the first human cases. This enthusiasm for the search for an animal reservoir of *C. burnetii* in this small French territory of about 300,000 inhabitants (200,000 inhabitants at the time of the first investigations) and an area of 83,846 km² is due to the real public health burden represented by human Q fever and the occurrence of several clusters in the French military personnel, linked to a very proactive Nation Reference Center in Marseille, in mainland France. Furthermore, these investigations have been enhanced, as all the first studies on animal infection with *C. burnetii* seem to rule out cattle as a source of human infection, so the origin of the epidemics had to be found in wildlife [107, 108, 158]. Although a positive three-toed sloth (*Bradypus tridactylus*) was found positive [109, 154], other animals, such as capybara (*Hydrochoerus hydrochaeris*), were tested and found negative [109, 152], weakening the former hypothesis claiming that the sloth was the single reservoir [151, 159]. Indeed, other species have been found positive between 2005 and 2014 following numerous investigations [153], and several species were found to be positive through the analysis by IS*1111* PCR of the muscular juice of animals collected from hunters. Thus, one nine-banded armadillo (*Dasypus novemcinctus*), three white-lipped peccaries (*Tayassu pecari*), three collared peccaries (*Pecari tajacu*), one south American tapir (*Tapirus terrestris*), and two other capybaras (*Hydrochoerus hydrochaeris*) have already been found to be positive, most of them with Ct superior to 35, but never published. One spiny rat (*Proechimys cuvieri*) was also found positive on liver samples among 29 other rodents [153]. A study is currently underway in French Guiana that has collected over 1000 samples from animals, especially tissues and stools, to better characterize the wildlife reservoir of *C. burnetii* [160].

In Brazil, the first study found on the search for *C. burnetii* in wildlife is a thesis, which is an investigation in domestic animals, wild animals, and arthropods in Itaboraí in the state of Rio de Janeiro around cases of suspected *C. burnetii* infection [77]. Afterward, in a study developed in eight municipalities in the state of Rio de Janeiro, in the Atlantic Forest, between 2007 and 2012, the prevalence of *C. burnetii* DNA in 131 different species of wild rodents was 4.6% [139]. The positive rodents belonged to the species *Akodon cursor* (3/32: 9.4%), *Mus musculus* (1/19: 5.3%), *Oxymycterus dasytrichus* (1/12: 8.3%), and *Oligoryzomys nigripes* (1/16: 6.3%) captured in forest edges and near human dwellings in the municipalities of Piraí and Valença [139]. Other studies have been conducted on other species of nonflying mammals, but all with negative results. Thus studies using PCR have also been performed in several taxa: free-living cervids, free-living wild boars, and different species of Xenarthra in Brazil [141, 145, 146], Darwin's fox (*Lycalopex fulvipes*) in Chile [149], different species of wild canids, rodents, and marsupials in Brazil, French Guiana, and Uruguay [107, 109, 115, 116, 131, 142], and in reptiles and amphibians in French Guiana without the detection of *C. burnetii* DNA [107, 109, 143].

Chiroptera Concerning bats, although the role of these animals in the enzootic cycles of *C. burnetii* has received little attention worldwide, it was possible to find studies developed in Brazil and Chile [147•]. The first study to characterize this proteobacteria in Latin America involved 119 bats from 21 species captured in preserved areas in Rio de Janeiro, Bahia, and Santa Catarina, Brazilian from 2014 to 2015. *Coxiella burnetii* was PCR-detected in specimens of two species from the genus *Artibeus*: the great fruit-eating bat (*Artibeus lituratus*) (3 *C. burnetii*-positive/14 bats) and the fringed fruit-eating bat (*Artibeus fimbriatus*) (1/7) from two different regions: Jacarepaguá (Rio de Janeiro state) (3/44; 7%) and Serra do Tabuleiro State Park (Santa Catarina state) (1/28; 4%) [140]. In the second study, the first report of *C. burnetii* in Chile, PCR positivity of 9.0% (5/55) was observed in Mexican free-tailed bats or Brazilian free-tailed bats (*Tadarida brasiliensis*) sampled in three regions of

the country [147•]. Lastly, a third study was published in 2022 using *IS1111*-qPCR to detect *C. burnetii* in blood samples from 126 bats captured in 2014, 2015, and 2018 in the Macaregua cave, Colombia [161]. Molecular evidence of *C. burnetii* was found in 6.3% of the samples: 3/49 (6.1%) Seba's short-tailed bats (*Carollia perspicillata*), a widespread frugivorous bat; 2/35 (5.7%) ghost-faced bats (*Mormoops megalophylla*); and 3/42 (7.1%) Trinidadian funnel-eared bats (*Natalus tumidirostris*), an insectivorous bat.

There is a strong popular rumor that bats are reservoirs and transmitters of *C. burnetii* to humans in French Guiana. However, no study supported this hypothesis, and it is difficult to know where this rumor originated. In one of the very first studies conducted in the late 1990s, it was shown that seeing bats near one's home was independently associated with the occurrence of Q fever in patients with fever compared to patients supported for dengue fever [107]. Nevertheless, the same team that found the various nonflying mammals positive found six bats belonging to four species positive to *C. burnetii*, spread over the whole territory but with high Ct (> 35): three Seba's short-tailed bat (*Carollia perspicillata*), one Parnell's mustached bat (*Pteronotus parnellii*), a lesser spear-nosed bat (*Phyllostomus elongatus*), and a lesser bulldog bat (*Noctilio albiventris*) [153].

Thus, even though the potential role of these animals as a source of infection for humans and other animals, including cattle, is still unknown, these reports suggest the existence of a complex *C. burnetii* transmission cycle involving a large number of wild mammals [162]. Therefore, further studies must be conducted to better understand their role in *C. burnetii* cycles. The results of this research on species other than domestic ruminants are difficult to interpret because the choices and times of the samples are not homogeneous, and the PCR tests performed in this way on a wide variety of biological matrices (various organs and fluids) allow first-line screening but not a controlled quantification for analytical epidemiology. Methodological developments are required.

Ticks and Ectoparasites

There has been an increasing interest in tick-borne pathogens, including *C. burnetii*, these last few years (Fig. 5). Eleven countries have published at least one study about *C. burnetii* in ticks in Latin America and the Caribbean, with a huge number of studies coming from Brazil, especially in the last 3 years ($N = 19$), followed by French Guiana ($N = 7$) and Colombia ($N = 5$). Although the importance of ticks in the epidemiology of *C. burnetii* infection remains debatable [9], there is no doubt that ticks can be infected by *C. burnetii* and that they can, therefore, act as vectors [6, 163–165]. In natural conditions, several *C. burnetii* strains have been successfully isolated from wild ticks, including from a few South American tick species (Table 5) [6, 173]. The Fiocruz group published a study in which *Amblyomma sculptum* and *Rhipicephalus sanguineus* were PCR-positive for *C. burnetii* [173]. For instance, in the case study by Pacheco et al. (2013) in Argentina, *C. burnetii* infection in two tick species belonging to the *Amblyomma* genus, *A. tigrinum* and *A. parvum*, was confirmed using hemolymph tests, isolation in Vero cells, and multilocus DNA sequencing. The strain At12 was typed as ST 73 in this publication. In Cuba, Noda and colleagues found six *Amblyomma mixtum* from 2 tick pools positive for *C. burnetii* using IS*1111* qPCR [184]. In Brazil and French Guiana, specimens of another *Amblyomma* tick species, *A. geayi*, collected on three-toed sloth infected by *C. burnetii* were also infected [109, 167]. Therefore, a sylvatic cycle based on *C. burnetii* tick-borne transmission seems to be sustainable. However, *C. burnetii* is probably far more frequently transmitted through the airborne route than through ticks [6]. Although most of the studies did not find any sign of infection by *C. burnetii* in South American tick species, recent observations, based on advances in molecular and cell biology, showed that ticks, including those found in South America, commonly harbor *Coxiella*-like endosymbionts (*Coxiella*-LE), closely related but genetically distinct to *C. burnetii*. These *Coxiella*-LE are almost exclusively confined to ticks and, according to current knowledge, pose a much lower infection risk to vertebrates than *C. burnetii* [6]. Extensive molecular surveys have consistently revealed that *Coxiella*-LE predominates in most tick species investigated thus far, with at least two-thirds of tick species being naturally infected [156, 168, 187, 191]. Most importantly, *Coxiella*-LE has been commonly misidentified as *C. burnetii* [6, 192••, 193, 194]. Several *C. burnetii* detection methods are in use, but many are not efficient enough to clearly distinguish between *C. burnetii* and *Coxiella*-LE [192••, 193–195]. Based on the identification of IS*1111* in both *C. burnetii* and the *Coxiella*-LE, Mares-Guia et al. (2018) developed a nested PCR assay, considering that IS*1111* amino-acid sequences in endosymbionts revealed to be genetically divergent, including degraded copies likely to be nonfunctional, providing a specific *C. burnetii* detection [173, 194].

Highlights on the Epidemiological Situation of Specifically Selected Countries

French Guiana

French Guiana is a French overseas territory located in the northeast corner of the South American continent. The territory of 83,534 km^2 is more than 90% covered by the Amazon rainforest, and the population of approximately 300,000 inhabitants (www.insee.fr) is concentrated on the coast, particularly in Cayenne and its surroundings. The human

Table 2 Data on *Coxiella burnetii* in pets in Latin America

Author	Year of the study	Year of publication	Language	Country	State	Biological methodology	Sample type	Species	Number of samples	Result	Comments	Published
Navarro O'Connor [128]	2001–2004	2007	Spanish	Argentina	Buenos Aires	IFA	Serum	Cats	1–5/55	1.8–9%	1 to 5 positive according to the titer used for IgG	Yes
								Dogs	0/16	0%		
Cicuttin [129]	2002–2003	2013	Spanish	Argentina	Buenos Aires	IFA	Serum	Dogs	3–19/123	2.4–15.4%	15.4% (cut-off 1:50)	Yes
											2.4% (cut-off 1:200)	
Lemos [130]	2008	2011	English	Brazil	Rio de Janeiro	IFA	Serum	Dogs	2/13	15.3%	Investigation in the house of a man with Q fever	Yes
Mares-Guia [76]	2008–2009	2014	English	Brazil	City of Itaboraí, Rio de Janeiro State	IFA	Serum	Dogs	2/14	14.2%	Area of the first human case of Q fever in Brazil	Yes
								Cat	0/1	0%		
						PCR (*htp*AB)	Serum	Dogs	2/14	14.2%		
								Cat	0/1	0%		
Mares-Guia [77]	2011–2012	2015	Portuguese	Brazil	Rio de Janeiro	IFA	Serum	Cats	3/13	23.0%	Thesis. Unpublished results	No
								Dogs	1/13	22.2%		
						PCR (*htp*AB)	Anal swab	Cats	1/7	14.3%		
Barboza de Oliveira [131]	2014–2016	2020	English	Brazil	Ceara and Pernambuco (Caatinga biome)	IFA	Serum	Dogs	5/147	3.4%		Yes
Oliveira [132]	2016–2019	2021	English	Brazil	Town of Barra Mansa, Rio de Janeiro State	PCR and nested PCR	Bone marrow	Dogs	0/45	0%	Dogs positive in PCR and IgG positive for *L. infantum*	Yes
Di Cataldo [133]	2006–2019	2022	English	Chile	4 different areas: coastal desert, mountain desert, Steppe-Mediterranean, and Temperate Warm Rainy	IFA	Serum	Dogs	0/358	0%		Yes
Faccini-Martínez [97]	2011	2017	English	Colombia	Villeta, Cundinamarca	IFA	Serum	Dogs	0/118	0%		Yes
Boni [134]	NA	1998	English	French Guiana	NA	IFA	Serum	Dogs	1/19	5.2%	Dogs belonging to the French military	Yes
Gardon [107]	NA	2001	English	French Guiana	Cayenne area	IFA	Serum	Dogs	7/57	12.3%	25/57 and 6/6 belonging to humans with proven Q fever, respectively	Yes
								Cats	0/6	0%		

Table 2 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Biological methodology	Sample type	Species	Number of samples	Result	Comments	Published
Debin [108]	2007	2007	French	French Guiana	Communes du littoral	ELISA	Serum	Dogs	16/63 (including 8 doubtful cases, 4 positive animals, and 2 positive animals belonging to the same owner	9.2 to 21.7%	22 from Kourou kennels and 41 from veterinarians Thesis unpublished	Yes
Davoust	2013	2014	French	French Guiana	Montagne du Tigre, Cayenne	qPCR (IS1111)	Vaginal swabs	Dogs	0/3	0%	Unpublished data	No
								Cat	0/1			
						IFA	Serum	Dog	0/3	0%		
								Cat	0/1			
Davoust	2013	2014	French	French Guiana	Cayenne and Kourou	IFA	Serum	Dogs	2/59	3.4%	Unpublished data	No
Davoust [109]	2013	2014	English	French Guiana	Cayenne	qPCR (IS111)	Vaginal swabs	Dogs	6–18/158	3.8%	6 CT < 35 12 CT > 35	Yes
Marié	NA	2016	French	French Guiana	Cayenne	IFI	Serum	Dogs	1/95	1%	Unpublished data	No
								Cats	0/10	0%		
Wei [135]	2012	2014	English	Nicaragua	Rivas, Southwestern Nicaragua	qPCR	Whole serum	Dogs	0/39	0%		Yes
Somma-Moreira [115, 136, 137]	1956	1987	Spanish	Uruguay	–	CAT and CFT	Serum	Guinea pigs	0/31	0%		Yes

CAT, capillary agglutination test; *CFT*, complement fixation test; *MA*, microagglutination test; *ELISA*, enzyme-linked immunosorbent assay; *IFA*, indirect immunofluorescence assay; *IFI*, indirect immunofluorescence; *PCR*, qualitative polymerase chain reaction; *qPCR*, quantitative real-time polymerase chain reaction; *MLVA*, multilocus variable number tandem repeats analysis; *MST*, multispacer sequence type.; *IHC*, immunohistochemistry; *NA*, data not available

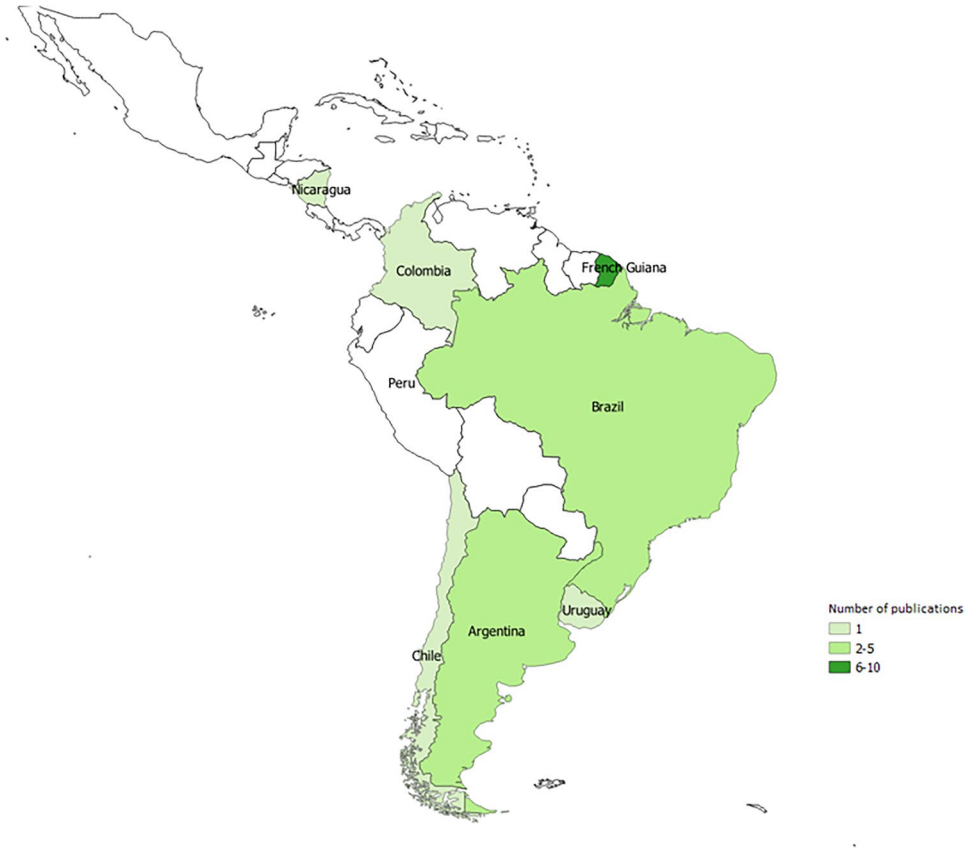

Fig. 3 Map of the publications on *Coxiella burnetii* infection in pets in Latin America and the Caribbean

Q fever situation in French Guiana is unique, with the highest incidence in the world, with a peak in the mid-2000s at more than 150 cases per 100,000 inhabitants per year and a stabilization since 2009 of between 25 and 35 cases per 100,000 inhabitants per year, which is much higher than in the rest of Latin America where the disease is barely reported, making French Guiana a hyper-endemic zone [28••, 55, 67]. For comparison, Q fever incidence in mainland France was 1.9/100,000 inhabitants in 2008–2011, and the incidence reached 69/100,000 inhabitants per year in the Netherlands during the largest outbreak ever in 2009, in the population living within 5 km of an infected dairy goat farm, and 6/100,000 inhabitants per year beyond that distance [21, 196]. The distribution of cases is heterogeneous and is mainly concentrated in the capital, Cayenne, and its surroundings, although a recent seroprevalence study suggests that the infection may be more widely distributed across the country than previously reported [197]. A unique strain was identified a few years ago, found exclusively in French Guiana, MST17, both in humans and animals, when the strain was sequenced [59, 109]. One hypothesis is that the incidence of Q fever in humans is "over-reported" in French Guiana compared to other countries because the more virulent MST17 strain causes a less asymptomatic disease (with atypical symptoms) and that Guianese is therefore "over-diagnosed" compared to other countries. While lung disease usually represents 30 to 50% of cases, it affects more than 90% of patients in this French territory [21, 57]. Finally, one of the most questioning specificities to date of coxiellosis in French Guiana is its animal reservoir, which seems to contrast sharply with the rest of the world. Concerning domestic ruminants, usually considered the main source of transmission of the pathogen to humans, two serological surveys were carried out in the 1990s and 2000, respectively, suggesting a low seroprevalence in ruminants [107, 108, 152]. Ad hoc investigations on farms have been systematically negative, including investigations around cases of Q fever in farmers. The occurrence of several outbreaks of Q fever on the outskirts of Cayenne had raised the possibility of the bacterium being transported by sea winds from certain nearby herds, but this hypothesis has to be corroborated. That is why research has shifted for more than 20 years away from livestock to focus on the search for the bacterium in wildlife surrounding human cases [109, 151, 154]. Nowadays, several individuals from various species of nonflying mammals and bats have been found positive (Table 4), although mostly with Ct > 35, which means that the *C. burnetii* load is detectable but below the limit of quantification. We do not exactly know the link between these species and transmission to humans, apart from the positive sloth incriminated in the epidemic among the military families of Tiger Hill [109, 151]. Moreover, with

Fig. 4 Map of the publications on *Coxiella burnetii* infection in wildlife in Latin America and the Caribbean

the exception of the military clusters reported earlier, the numerous cases of Q fever reported in French Guiana each year are generally isolated cases, without any clustering of cases, which does not facilitate the understanding of the origin of the transmission. One possibility would be the persistence of the bacterium in the environment as a result of different wildlife species emitting it, and that humans could become infected by inhalation of this dust as a result of favorable circumstances like leveling work near the house, gardening, particularly the use of a brush cutter, sweeping, etc. [57, 107, 154].

Recently, two studies have challenged the dogma that there is no link between livestock and Q fever cases in Guiana. On one hand, Saout et al. showed that cattle had a high seroprevalence of Q fever, especially when based not on individual prevalence but on herd prevalence [122]. On the other hand, seroprevalence study for *C. burnetii* of almost 3000 people sampled throughout the country showed that there was a link between high prevalence and proximity to livestock farms [197]. To explain these contradictory results, the old studies focused on a small number of animals and/or herds. In addition, studies conducted in the 1990s used the complement fixation test, currently considered to be weakly sensitive [198]. Moreover, several cases of Q fever were reported among workers at the Cayenne abattoir in 2007 [108]. New studies are therefore needed in French Guiana on livestock to more strictly support these new hypotheses.

In conclusion, the epidemiological cycle of Q fever in French Guiana is still unresolved. Although several species of wild mammals have been identified as carriers of *C. burnetii*, these results remain anecdotal and explain neither the frequency of the disease nor the geographical and ethnic distribution of cases in the territory. Moreover, the dogma that *C. burnetii* was not transmitted by cattle in French Guiana seems questionable. Additional investigations of the animal reservoir, livestock, and wildlife must be carried out to allow a better understanding of the unique phenomenon observed in this small piece of Amazonia.

Brazil

In Brazil, where the first reports of *C. burnetii* infection occurred in the 1950s through serological tests in human and cattle samples [199], Q fever is currently subject to compulsory notification in the context of the differential diagnosis of rickettsioses. However, official data are lacking, which can impact the understanding of the epidemiology of this zoonosis in the country. Furthermore, although some human cases of Q fever have been mandatorily reported, the high incidence of febrile illnesses such as malaria, leptospirosis, dengue, Zika, and chikungunya, can lead to misdiagnosis of Q fever [66].

Table 3 Studies on *Coxiella burnetii* in wildlife in Latin America

Author	Year of the study	Year of publication	Language	Country	Location	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Mares-Guia [77]	2011–2012	2016	Portuguese	Brazil	Municipio de Itaboraí, Rio de Janeiro State	PCR (htpAB)	Spleen	Rodents and marsupials*	0/60	0%	Unpublished thesis	No
Rozental [139]	2007–2012	2017	English	Brazil	8 municipalities of Rio de Janeiro State (Atlantic forest)	PCR (IS1111)	Spleen	Rodents	6/131	4.6%		Yes
								Akodon cursor [3]				
								M. musculus [1]				
								O. dasytrichus [1]				
								O. nigripes [1]				
Ferreira [140]	2013–2015	2018	English	Brazil	Bahia, Rio de Janeiro and Santa Catarina States (Atlantic forest)	PCR (IS1111)	Spleen	Bats	4/119	3.4%		Yes
								A. lituratus [3]				
								A. fimbriatus [1]				
Zanatto [141]	1996–2011	2019	English	Brazil	Mato Grasso do Sul, São Paulo, Goiás and Paraná	PCR (IS1111)	Serum	Free-living cervids*	0/188	0%		Yes
						IFA		*Blastocerus dichotomus*	9/169	5.3%		
								M. gouazoubira	7/129	5.4%		
									2/25	8.0%		
Colle [142]	2014	2019	English	Brazil	Alta Floresta, Sinop and Cláudia, Mato Grosso (Amazonian biome)	PCR *Coxiella* CTP synthase (pyrG)	Liver, spleen, serum	Rodents $	0/78	0%		Yes
								Marsupials $	0/152	0%		
Barboza de Oliveira [131]	2014–2016	2020	English	Brazil	Ceara and Pernambuco (Caatinga biome)	IFA	Serum	Rodents (*Wiedomys pyrrhorhinos*)	1/51	2%		Yes
								Marsupials (*Didelphis albiventris*)	1/18	5.6%		
								Wild canids*	0/1	0%		
						PCR		Rodents	0/51	0%		
								Marsupials	0/18	0%		
								Wild canids	0/1	0%		
Mendoza-Roldan [143]	2015–2018	2020	English	Brazil	States: Acre, Espirito Santo, Mato Grosso, Mato Grosso do Sul, Minas Gerais, Pará, Rio de Janeiro and São Paulo	Conventional PCR (*Coxiella* spp.—capsular polysaccharide biosynthesis protein I-like gene (cap))	48 serum 12 livers	121 reptiles 49 amphibians 60 samples tested for pathogens	0/60	0%		Yes
Ikeda [144]	2017–201	2021	English	Brazil	Campo Grande city, Mato Grosso do Sul state	qPCR (*IS1111*)	133 serum 135 spleen	135 nonheamatophagous bats*	0/135	0%		Yes
Santana [145]	2018–2020	2022	English	Brazil	Municipalities of Barretos, Colina, Guaraci, Jaboticabal, Monte Alto, Monte Azul Paulista,Morro Agudo, Olímpia, and Torrinha, São Paulo State	qPCR (*IS1111*)	Serum	Free-living wild boars (*Sus scrofa*)	0/97	0%		Yes

Table 3 (continued)

Author	Year of the study	Year of publication	Language	Country	Location	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
De Oliveira [146]	2015–2020	2022	English	Brazil	Mato Grosso do Sul, São Paulo, Pará, Rondônia and Rio Grande do Sul	qPCR (*IS1111*)	Serum	Sloths*	0/233	0%	Samples obtained during the necropsy of animals	Yes
							Spleen	Anteaters	0/107	0%	Victims of a vehicular collision on highways	
								Armadillos	0/57	0%		
Muller [147•]	2017–2018	2020	English	Chile	Metropolitan region The Biobío Region La Araucanía Regions	qPCR (*IS1111*)	Spleen for *T. brasiliensis* Serum for the others	Bats	5/55	9%	Quantitation cycle < 37	Yes
								Tadarida brasiliensis	5/9	56%	All positives from the metropolitan region	
Di Cataldo [133]	2006–2019	2022	English	Chile	4 different areas: Coastal Desert, Mountain Desert, Steppe-Mediterranean, and Temperate Warm Rainy	IFA ELISA	Blood	12 South American grey foxes (Lycalopex griseus), 10 Andean foxes (L. culpaeus) and 10 Darwin's foxes	0/32	0%		Yes
Hidalgo-Hermoso [148]	2013–2018	2022	English	Chile	Southern Chile	Serology NA	Serum	Darwin's fox (*Lycalopex fulvipes*)	0/47	0%		Yes
Cabello [149]	2009–2012	2013	English	Chile	Chiloé Island	qPCR	Serum	Darwin's fox (*Lycalopex fulvipes*)	0/30	0%		Yes
Silva-Ramos [150•]	201–-2015, 2018	2022	English	Colombia	Macaregua cave, Las Vueltas village, Municipality of Curiti, Santander Department	qPCR IS1111	Serum	Bats	8/126	6.3%		Yes
								C. perspicillata	3/49	6.1%		
								M. megalophylla	2/35	5.7%		
								N. tumidirostris	3/42	7.1%		

Table 3 (continued)

Author	Year of the study	Year of publication	Language	Country	Location	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Gardon [107]	1998–2000	2001	English	French Guiana	Cayenne and surroundings	IFA	Serum	Rodents	4/117	3.4%	Captured in various areas near the houses of case patients with Q fever Swallows were captured on the roof of the jail at Remire, where many cases of Q fever had been described among guards and prisoners	Yes
								Proechimys sp.	4/26	15.4%		
								Marsupials	5/42	11.9%		
								P. opossum	4/36	11.1%		
								D.marsupialis	1/4	25%		
								Bats	0/86	0%		
								Birds	1/69	0%		
								Batrachians	0/47	1.4%		
						PCR	Lung, liver, or intestine	Rodents	0/42	0%		
								Marsupials	0/117	0%		
								Bats	0/42	0%		
								Birds	0/86	0%		
								Batrachians	0/69	0%		
									0/42	0%		
Davoust [109]	2013–2014	2014	English	French Guiana	Montagne du tigre, Cayenne	qPCR (IS1111)	Feces, spleen	3-toed sloth (female) (*Bradypus tridactylus*)	1/1	100%		Yes
						qPCR (IS1111)	Vaginal swabs	Bats	0/7	0%		
								Birds	0/34	0%		
								Opossum	0/2	0%		
								Iguana	0/4	0%		
								Gecko (species not available)	0/17	0%		
Pommier de Santi [151]	2013	2014	English	French Guiana	Montagne du tigre, Cayenne	IFA	Serum	*Didelphis marsupialis*	2/12	16.6%		Yes
								Philander opossum	1/6	16.6%		
						qPCR (IS1111)	Vaginal swabs [18]	*Didelphis marsupialis*	0/12	0%		
							Serum [14]	*Philander opossum*	0/6	0%		
Pommier de Santi [152]	2014	2014	English	French Guiana	Montagne du tigre (Cayenne) and Macouria Sloths Rescue Center	qPCR (IS1111)	Vaginal and rectal swabs + hairs collected in the perianal area + feces	*Bradypus tridactylus*	0/16	0%	3 collected on the Montagne du Tigre and 13 were sampled in Macouria	Yes

Table 3 (continued)

Author	Year of the study	Year of publication	Language	Country	Location	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Marié [153]	2005–2006	2013	French	French Guiana		qPCR (IS1111)	Muscular juice	*Myoprocta acouchi*	0/1	0%	3 with CT > 35	No
								Tayassu pecari	3/35	8.6%	1 with CT > 35/1 with CT < 35	
								Hydrochoerus hydrochaeris	2/30	6.7%	1 with CT > 35/1 with CT < 35	
								Tapirus terrestris	2/7	28.6%	3 with CT > 35	
								Pecari tajacu	3/13	23.0%	1 with CT > 35	
								Dasypus novemcinctus	1/5	20.0%	1 with CT > 35	
							Liver	Rodents*	1/30	3%	Unpublished data	
								Proechimys cuvieri	1/4	25%		
Davoust [153]	2013	2013	French	French Guiana	Cayenne, Saint Laurent du Maroni, Kourou	qPCR (IS30A)	Vaginal swab samples	Bats*	6/199	3.0%	6 pos but with CT > 35	No
								N. albiventris	1/14			
								P. parnellii	1/37			
								C. perspicillata	3/76	0%		
								P. elongatus	1/13			
Davoust	2013 and 2014		French	French Guiana	Cayenne, Saint Laurent du Maroni, Kourou	ELISA	Serum	Bats	0/41	0%		No
								Species not available				
Christen [154]	2014	2019	English	French Guiana	La Comté river, Roura	qPCR (IS1111)	Stool	Capybara (*Hydrochoerus hydrochaeris*)	1/1	100%	MST 17	Yes

Table 3 (continued)

Author	Year of the study	Year of publication	Language	Country	Location	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Destoop	2018		French	French Guiana	Cayenne	qPCR (IS1111)	Stool	Captive songbirds + +	0/11	0%	Unpublished data	No
Somma-Moreira [115, 116]	1985	1987	English and Spanish	Uruguay	NA	MAT	Serum	Birds	0/66	0%		Yes
Hernandez [155]	2003–2004	2007	English	Uruguay	Dpt of Maldonado	IFA	Serum	Pampas deer (*Ozotoceros bezoarticus*)	5/22	22%	Experimental wildlife breeding station department	Yes

CFT, complement fixation test; *MA*, microagglutination test; *ELISA*, enzyme-linked immunosorbent assay; *IFA*, immunofluorescence assay; *PCR*, qualitative polymerase chain reaction; *qPCR*, quantitative real-time polymerase chain reaction; *MLVA*, multilocus variable number tandem repeats analysis; *MST*, multispacer sequence type.; *IHC*, immunohistochemistry

*Species from Mares-Guia et al. [77]: Rodentia: *Akodon cursor* ($n=10$), *Nectomys squamipes* [1], *Oligoryzomys nigripes* [1], Didelphimorphia: *Didelphis aurita* ($n=9$); *Micoureus (marmosa) paraguayanus* ($n=12$); and *Philander frenatus* ($n=27$). Rodents species from Rozenthal et al. [139]: *Akodon cursor* [32], *Mus musculus* [19], *Oligoryzomys nigripes* [16], *Delomys dorsalis* [14], *Oxymycterus dasytrichus* [12], *Euryoryzomys russatus* [7], *Trinomys iheringi* [6], *Nectomys squamipes* [5], *Akodon lindberghi* [5], *Trinomys dimidiatus* [4], *Akodon montensis* [3], *Oligoryzomys flavescens* [2], *Brucepatersonius iheringi* [1], *Calomys tener* [1], *Necromys lasiurus* [1], *Oecomys catherinae* [1], *Oxymycterus delator* [1], and *Rhipidomys itoan* [1]. Bats species from Ferreira et al. [140]: *Carollia perspicillata* ($n=34$), *Desmodus rotundus* [15], *Artibeus lituratus* [14], *Sturnira lilium* [12], *Artibeus fimbriatus* [7], *Rhinophylla pumilio* [7] *Artibeus planirostris* [5], *Dermanura cinerea* [4], *Phyllostomus discolor* [4], *Artibeus obscurus* [2], *Glossophaga soricina* [2], *Myotis nigricans* [2], *Sturnira tildae* [2], *Vampyressa pusilla* [2], *Anoura caudifer* [1], *Chiroderma doriae* [1], *Lonchophylla peracchii* [1], *Micronycteris minuta* [1], *Micronycteris sp.* [1], *Phyllostonus hastatus* [1], and *Trinycteris nicefori* [1]. Free-living deer species from Zanatto et al. [141]: *Blastocerus dichotomus* [156], *Mazama gouazoubira* [27], *M. bororo* [4], *M. americana* [3], and *Ozotocerus bezoarticus* [11]. Rodents and marsupials species from Colle [142]: rodents: *Euryoryzomys nitidus* [1], *Hylaeamys megacephalus* [5], *Makalata* sp. [1], *Mesomys hispidus* [3], *Mus musculus* [1], *Oecomys bicolor* [18], *Neacomys amoenus* [7], *Necromys lasiurus* [2], *Oecomyscleberi* [3], *Oecomys paricola* [4], *Oecomys roberti* [7], *Oecomys* aff. *Catherinae* [1], *Oligoryzomys* cf. *mattogrossae* [5], *Oxymycterus amazonicus* [1], *Proechimys roberti* [14], and *Proechimys* sp. [5]; marsupials: *Caluromys philander* [6], *Cryptonanus* sp. [10], *Didelphis marsupialis* [34], *Glironia venusta* [1], *Gracilinanu speruanus* [5], *Marmosa constantiae* [64], *Marmosa murina* [2], *Marmosops* [13], *Marmosops* aff. *Pinheiroi* [5], *Metachirus nudicaudatus* [5], *Monodelphis* [4], and *Monodelphis saci* [2]. Mammals species of Barboza de Oliveira et al. [131]: 51 wild rodents: *Thrichomys laurentius* [40], *Rhipidomys cariri* [3], *Calomys expulsus* [2], *Wiedomys pyrrhorhinos* [2], *Galea spixii* [1], *Kerodon rupestris* [1], and *Rattus rattus* [2]; 18 marsupials: *Monodelphis domestica* [9], *Didelphis albiventris* [7], and *Gracilinanus agilis* [2]; and 1 wild canid: *Cerdocyon thous* [1]. Foxes species from Di Cataldo [133]: South American grey foxes (*Lycalopex griseus*) [12] and Andean foxes (*L. culpaeus*) [9] from the Steppe-Mediterranean region (around Santiago city); Darwin's foxes from the Chiloe Island [10] and one from Temperate Warm Rainy area [1]. *Bats species from Muller et al. [147•]: *Myotis chiloensis* [27], *Histiotus montanus* [8], *Lasiurus varius* [7], *Histiotus macrotus* [3], *L. cinereus* [1], and *Tadarida brasiliensis* [9]. Species from Gardon et al. [107]: rodents: *Mus musculus* [58], *Proechimys* sp. (*P. cuvieri* and *P. cayennensis)* [26], *Rattus rattus* [17], and other rodents [16]; marsupials: *Philander opossum* [36], *Didelphis marsupialis* [4], and other marsupials [2]; chiropters: *Molossus molossus* [57], *Phyllostomushastatus* [17], and other marsupials [12]; and birds [83] *Prognechalybea* and *Prognetapera* (swallows from the jail of Rémire-Montjoly, where several human cases were reported (doubtful results)) and batrachians *Buffo marinus* [21], *Leptodactylus pentadactylus* [20], and other batrachians [6]. Rodents species from Marié et al. 2013 [153]: *Micoureus demerarae* [1], *Mus musculus* [3], *Oecomys auyantepui* [3], *Oecomys rutilus* [1], *Proechimys cayennensis* [3], *Proechimys cuvieri* [4], *Proechimys* sp. [4], *Rattus rattus* [6], and *Rhipidomys nitela* [2]. Bats species from Davoust et al. [153]: *Pteropteryx macrotis* [1], *Noctilio albiventris* [14], *Pteronotus gymnonotus* [5], *Pteronotus parnellii* [37], *Pteronotus davyi* [1], *Anoura caudifera* [2], *Anoura geoffroyi* [15], *Glossophaga soricina* [2], *Phyllostomus elongatus* [13], *Carollia perspicillata* [109], *Artibeus planirostris* [8], *Myotis riparius* [1], *Eumops auripendulus* [9], *Molossus barnesi* [4], and *Molossus molossus* [11]. Birds species from Destoop, Edouard, and Epelboin: species: chestnut-bellied seed finch (*Oryzoborus angolensis*) ($n=5$); domestic canary (*Serinus canaria forma domestica*) ($n=1$); ruddy-breasted seedeater (*Sporophila minuta*) ($n=4$); and wing-barred seedeater (*Sporophila americana*) ($n=1$). Species from Mendoza-Roldan [143]: reptiles: snakes: *Chironius multiventris*, *Chironius scurrulus*, *Corallus hortulanus*, *Oxyrphus melanogenys*, *Philodryas viridissima*, *Bothrops insularis*, *Crotalus durissus terrificus*, *Xenodon neuwiedii*, *Dipsas turgidus*, and *Dipsas neuwiedi Bothrops leucurus*; lizards: *Philodryas nattererii*, *Hemidactylus mabouia*, *Salvator merianae*, and *Tropidurus catalanensis.* Species from Ikeda et al. [144]: bats: *Artibeus lituratus*, *Artibeus planirostris*, *Myotis nigricans*, *Platyrrhinus lineatus*, *Eptesicus furinalis*, *Carolia perspicillata*, *Molossus molossus*, *Phyllostomus discolor*, *Molossops temminckii*, *Eumops perotis*, and *Chiroderma villosum.* Mammals species from De Oliveira et al.: *Bradypus tridactylus* [103], *Bradypus* sp. [3], *Choloepus didactylus* [5], *Choloepus* sp. [31], *Tamandua tetradactyla* [40], *Myrmecophaga tridactyla* [67], *Cabassous unicinctus* [4], *Dasypus novemcinctus* [14], *Euphractus sexcinctus* [14], and *Priodontes maximus* [25]

Table 4 Summary of wildlife species with molecular evidence for *Coxiella burnetii* in Latin America

Order/sub-order	Family	Species English name	Species Latin name	Number	Year of publication	Country	Place	Publication	Cycle threshold
Pilosa	Bradypodidae	3-toed sloth	*Bradypus tridactylus*	1	2014	French Guiana	Cayenne	Davoust [109]	23
Cingulata	Dasypodidae	9-banded armadillo	*Dasypus novemcinctus*	1	2013	French Guiana	NA	Marié [153]	> 35
Suina	Tayassuidae	White-lipped peccary	*Tayassu pecari*	3	–	–	–	–	> 35
Suina	Tayassuidae	Collared peccary	*Pecari tajacu*	3	–	–	–	–	> 35
Perissodactyla	Tapiridae	South American tapir	*Tapirus terrestris*	2	–	–	–	–	1 > 35; 1 < 35
Rodentia	Cricetidae	Cursor grass mouse	*Akodon cursor*	3	2017	Brazil	Rio de Janeiro Atlantic forest	Rozental [139]	$
Rodentia	Muridae	House mouse	*Mus musculus*	1	–	–	–	–	$
Rodentia	Cricetidae	Atlantic Forest hocicudo	*Oxymycterus dasytrichus*	1	–	–	–	–	$
Rodentia	Cricetidae	Black-footed pygmy rice rat	*Oligoryzomys nigripes*	1	–	–	–	–	$
Rodentia	Echimyidae	Spiny rat	*Proechimys cuvieri*	1	2013	French Guiana	NA	Marié [153]	> 35
Rodentia	Caviidae	Capybara	*Hydrochoerus hydrochaeris*	1	2019	French Guiana	Comté River, Roura	Christen [154]	31
Rodentia	Caviidae	Capybara	*Hydrochoerus hydrochaeris*	2	2013	French Guiana	NA	Marié [153]	1 > 35; 1 < 35
Chiroptera	Phyllostomidae	Seba's short-tailed bat	*Carollia perspicillata*	3	–	–	Cayenne, Régina, and Saint Jean du Maroni	–	> 35
Chiroptera	Mormoopidae	Parnell's mustached bat	*Pteronotus parnellii*	1	–	–	Cayenne, Régina	–	> 35
Chiroptera	Phyllostomidae	Lesser spear-nosed bat	*Phyllostomus elongatus*	1	–	–	Régina	–	> 35
Chiroptera	Noctilionidae	Lesser bulldog bat	*Noctilio albiventris*	1	–	–	Saint Jean du Maroni	–	> 35
Chiroptera	Phyllostomidae	Fringed fruit-eating bat	*Artibeus fimbriatus*	1	2018	Brazil	Atlantic Forest	Ferreira [140]	$
Chiroptera	Phyllostomidae	Great fruit-eating bat	*Artibeus lituratus*	3	–	–	–	–	$
Chiroptera	Molossidae	Brazilian free-tailed Bats	*Tadarida brasiliensis*	5	2020	Chile	Metropolitan Region	Muller [147•]	33.05, 33.55, 34.06, 35.34, and 36.45

Table 4 (continued)

Order/sub-order	Family	Species English name	Species Latin name	Number	Year of publication	Country	Place	Publication	Cycle threshold
Chiroptera	Phyllostomidae	Seba's short-tailed bat	*Carollia perspicillata*	3	2022	Colombia	Macaregua cave, located in Las Vueltas village, Municipality of Curiti, Santander Department	Silva-Ramos [150•]	NA
Chiroptera	Mormoopidae	Ghost-faced bat	*Mormops megalophylla*	2	–	–	–	–	NA
Chiroptera	Natalidae	Trinidadian funnel-eared bat	*Natalus tumidirostris*	3	–	–	–	–	NA

NA, data not available

$, In this work, we used "conventional" PCR followed by electrophoreses, which is why we will not be able to provide a CT value

Among Latin American countries, Brazil has the largest number of publications, with evidence of *C. burnetii* circulation in livestock, pets, wild animals, and ticks. Bovines are the species with the highest average, followed by sheep, goats, dogs, wild cervids, wild rodents, bats, and ticks. This scenario is probably linked to the economic importance of the sector since Brazil is the second-largest producer of beef cattle and has a large dairy herd. Three papers are related to the detection of *C. burnetii* in animals with reproductive disorders [79, 82, 88••]. The study conducted in the state of Alagoas, in the northeast of Brazil, described a goat herd with high frequency in serology (55.1%) and molecular detection by conventional PCR in two placental samples from seropositive animals (8.7%) [79]. Another survey on cattle aborted fetuses reported 9.2% (7/76) of positivity at qPCR, with 3 positive fetuses from the state of Rio Grande do Sul and 4 positive fetuses from the state of São Paulo, reinforcing the widespread distribution of the pathogen in the country [88••]. In both studies, however, the lack of histopathological assay does not confirm that *C. burnetii* was responsible for the abortions [200]. The vast majority of studies in Brazil are based on serological and molecular detection in convenience samples. Only recently, statistical design studies are being carried out to understand better *C. burnetii* epidemiology [64, 79–81, 140, 141]. In the state of São Paulo, a study with 1515 cattle samples from 54 cities collected in 9 different slaughterhouses reported a seroprevalence of 23.8% using an *in-house* IFA and the detection of *C. burnetii* by qPCR in 12.2% of the seropositive animals, highlighting the risk of infection for abattoir workers [64]. Molecular data suggest the existence of diverse MST and MLVA genotypes of *C. burnetii* in the state of São Paulo (ST74) [86]. In the publication, an ST73 was also detected in samples from Argentina. These genotypes were only reported in South America, reinforcing the need for epidemiological studies aiming at the isolation and characterization of human and animal strains to better understand the real impact on animal and public health [86].

Based on a recent analysis of typing methods and their correlation with the genomic groups [201], cattle and goat strains from Brazil belong to a genomic group (GG)-III, ovine strains from Brazil are correlated with GG-I, the same as ST17 detected in French Guiana, and the Argentinian strain *At12* is placed in GG-IVb-associated, a genomic group with genetic relation with the Australian strains AuQ01, AuQ02, and Namibia (ST-30), which are isolates placed on GG-X, and strains placed in the GG-IV, like the isolate Leningrad-2 (ST-7). Strains from GG-III are usually detected in cattle and are rarely involved in human infection [201, 202]. On the other hand, *C. burnetii* belonging to GG-I can be found across the globe and shows elevated virulence, and strains from GG-IVb and GG-X were mainly isolated from human cases, illustrating the virulence potential of Brazilian ovine strains and the Argentinian isolate At12 described by Pacheco et al. [201, 203].

Although the transmission of *C. burnetii* through the consumption of contaminated milk from dairy animals remains controversial, studies conducted in the last decade in the state of Minas Gerais have shown samples of artisanal Minas cheese contaminated by this proteobacterium [79, 85, 87]. The risk has been assessed; in some cases, the consumption

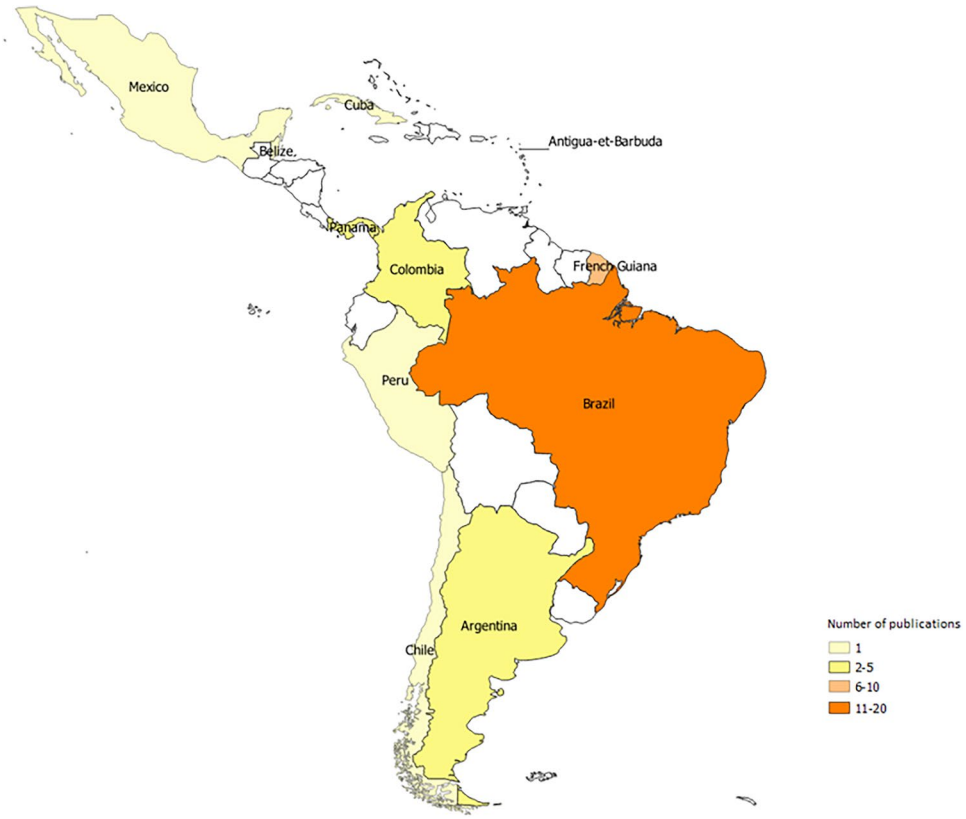

Fig. 5 Map of the publications on *Coxiella burnetii* infection in ticks in Latin America and the Caribbean

of dairy products from infected animals may induce seroconversion but no clinical manifestation [204].

In conclusion, *C. burnetii* infection in Brazil has been reported in different domestic and wild animal species. Although the pathogen seems widespread in the country, studies are concentrated in only six states. Hence, the prevalence of *C. burnetii* in animals is spatially biased. More studies are needed, especially in states without data, to better understand Q fever epidemiology in Brazil and its implications for animal and human health. Increasing Q fever knowledge would benefit preventive and control measures, reducing the risk of human infection and economic losses in livestock.

Argentina

Coxiella burnetii is a pathogen understudied in Argentina, with few or no publications in the second half of the twentieth century and early twenty-first. Serological studies have covered farm animals, pets, and humans, although the diversity of techniques and cutting-edge titles used make their comparison difficult. Only two publications use diagnosis through molecular biology, and they are also the only ones that studied ticks. Q fever is currently subject to compulsory notification.

The description of the first human cases of Q fever by serology in Argentina was carried out in 1957 in Córdoba [205] and in 1959 by a truck driver traveling through the provinces of Chaco, Formosa, Corrientes, and Missions [206]. The first human case in Buenos Aires City (BAC) was reported in 1962 (Ruggiero et al. 1962, unpublished data). Numerous serological studies were carried out in the 1950s and 1960s on different animal species, finding different seropositivities (Table 1) [68–71].

Notably, after these pioneering studies, there were no publications on the subject until 1997, when the suspicion of Q fever was reported in goats of Entre Ríos (although animals imported from Uruguay) from compatible signs by serology and was also detected in people related to the farm [207, 208]. In 1999, *C. burnetii* was detected in two imported cattle that were in quarantine and were then euthanized [208, 209].

Recently, clinically healthy dogs from poor neighborhoods of BAC were seropositive by indirect immunofluorescence [129], but not by IFI in cats [124, 125, 203, 205] or by molecular biology techniques in *Rhipicephalus sanguineus* sensu lato ticks [210]. Also, in BAC, 1/99 human sera were positive by indirect immunofluorescence [211].

In samples collected in 2004, Trezeguet et al. carried out a serological test using ELISA (phases I and II) as a screening test and FC as a confirmatory test in 840 goats of 56 farms covering practically the whole country; although only 9/840 (1,1%) were positive through FC, all belonged to the

province of Buenos Aires (9/186; 4.8%) [212]. In 2005, in a sampling of 30 establishments in the province of Buenos Aires, 41 goats were detected with positive serology [208]. In a new study in 2007 covering goats from almost the entire country, Trezeguet et al. detected 11.6% (33/285) positive in goats from Buenos Aires, Catamarca, Mendoza, Río Negro, Santa Fe, and Santiago del Estero [70].

Pacheco et al. reported the detection of *C. burnetii* by PCR and its isolation by cell culture in *Amblyomma tigrinum* and *Amblyomma parvum* ticks from Córdoba [167].

Finally, in 2022, there was an outbreak of Q fever in slaughterhouse workers from Entre Ríos and Santa Fé [213, 214].

In conclusion, *C. burnetii* is a pathogen little studied in Argentina, with few or no publications in the last decade. Serological studies have covered farm animals, companion animals, and humans, although the diversity of techniques and threshold titles used makes their comparison difficult. On the other hand, only two publications use diagnosis through molecular biology, and they are also the only ones that studied ticks. It is necessary to study this neglected pathogen in depth in Argentina.

Chile

Information on *C. burnetii* in vertebrates and ticks in Chile is scarce. Moreover, its potential presence and distribution started to be investigated only recently. The first study analyzing a Chilean animal was published in late 2013. Archived blood samples of 30 endangered Darwin's foxes (*Lycalopex fulvipes*) captured between 2009 and 2012 were analyzed by qPCR. All samples turned out to be negative [149]. Serum samples of 47 individuals of this same specie captured between 2013 and 2018 were later analyzed by means of a commercial ELISA kit, again with negative results [148]. Although this kit is not validated for this species, the combination of both negative PCR and serological results strongly suggests that this species has no regular contact with this bacterium. The cold environments of southern Chile where this fox survives, are unsuitable for most of the ixodid ticks, which partially explains the absence of this bacterium. A more spatially broad survey was performed using free-ranging dogs and the three species of fox present in Chile (Darwin's fox, the Andean fox, *Lycalopex culpaeus*, and the South American grey fox, *Lycalopex griseus*) as sentinels. Again, none of the 358 dogs and 32 foxes surveyed from 5 different bioregions was seropositive according to the IFA test [133]. On the other hand, the analysis of blood samples from 55 bats belonging to five different species, collected opportunistically in three different Chilean regions, resulted in five positive samples by qPCR. All five samples belonged to any of the nine Brazilian free-tailed bats (*T. brasiliensis*) from the Metropolitan area included in the study. Although the sample size was small, the observed occurrence of this particular species in this region was remarkable [147•].

Regarding livestock, an investigation following a Q fever outbreak that took place in 2017 among dairy farm workers resulted in the presence of the bacteria in two out of 105 raw milk samples [91]. Lastly, an unpublished report mentioned that 13 alpacas imported from Chile to China were found to be seropositive for *C. burnetii* during quarantine [90].

No study has yet systematically analyzed potential arthropod vectors for the presence of *C. burnetii* in Chile. Only a single study reported the presence of a *C. burnetii*-like endosymbiont in an *Ornithodoros amblus* female, collected from the soil near a Humboldt penguin (*Spheniscus humbolti*) nesting area in Isla Grande de Atacama, Chile [176].

In summary, Chile can be considered a country with a low endemicity of *C. burnetii*. Nevertheless, cases in humans seem to have been underestimated [215], and the bacterium is present in domestic and wild animals in the country, as confirmed in bat and cow milk samples. In consequence, veterinarians and public health authorities must be aware of potential cases of Q fever. More extensive studies on domestic animals, wildlife, and ticks are necessary in Chile to know the actual distribution and impact of Q fever in Chile.

Colombia

Until the early 2010s, publications on human Q fever in Colombia were almost nonexistent [216]. In 2006, a seroprevalence of 23.6% of antibodies against *C. burnetii* was reported for the first time in rural field workers in the departments of Córdoba and Sucre [217]. In 2012, two cases of Q fever were identified in Colombia; one associated with endocarditis in Medellín, Colombia, and another case in a patient with pneumonia in Cali [218, 219]. Some seroprevalence studies in cattle from several regions of Colombia were conducted between 1961 and 1981 [92, 93, 95, 125], and then in the 2010s [71, 96, 97, 99], with regard to animal infections caused by *C. burnetii*. The carriage of anti-*C. burnetii* antibodies in cattle was generally high, around 20–25% and around 5% for sheep. Colombia performed one of the rare studies by PCR in goats and sheep in Latin America in milk and vaginal swabs, sowing 6% of positivity in sheep and 0.6% in goats [98]. It is important to note that the strain found had a 100% identity with the strain CbuK Q 154 and a 99% identity with the strain Guiana Cb175. A Colombian team also published one of the rare publications in 2022 of *C. burnetii* in bats from Macaregua caves in the Department of Santander with 5 to 7% positivity in the bats according to the species [150•]. Finally, four studies from Colombia have been published in search of *C. burnetii* in ticks such as *Amblyomma variegatum*, *Rhipicephalus microplus*, and *Rhipicephalus sanguineus*, leading to the evidence of *Coxiella*-like endosymbiont [97, 156, 181–183]. Thus, *C. burnetii* is

Table 5 Studies on *Coxiella burnetii* in ticks and ectoparasites in Latin America

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Robinson [166]	2000	2009	English	Antigua and Barbuda	city of St. Johns abattoir, Antigua	qPCR (I S1111)	Whole tick	Ticks	0/113	0%	Collected from 7 bovines	Yes
								Amblyomma variegatum	95			
								Rhipicephalus	6			
								Microplus				
								A. variegatum	12			
Pacheco [167]	NA	2013	English	Argentina	Córdoba Province	PCR	Whole tick	Ticks *Amblyomma parvum* and *A. tigrinum*	3/105	2.9%	Collected from the common yellow-toothed cavy (*Galea musteloides*) Isolation in Vero cells of *C. burnetii* strain *At12*	Yes
Duron [168]	NA	2017	English	Argentina	Salta Chaco	16S rRNA PCR	Whole tick	Ticks			No *Cb* only CLE	Yes
								Ornithodoros rostratus (Salta)	1/4	CLE		
								Argas monachus (Chaco)	1/3	CLE		
Mioni [86]	NA	2019	English	Argentina	Córdoba Province	PCR	Whole tick	*Amblyomma tigrinum*	1/1	100%	MST73	Yes
Cline [169]	2014–2015	2016	English	Belize	Cayo District	qPCR	Half tick	Ticks*	0/272	0%	Unpublished data (thesis)	No
Machado-Ferreira [170]	2007–2008	2011	English	Brazil	Rio de Janeiro, Minas Gerais	16S rRNA PCR	Whole tick	Ixodidae ticks			CLE	Yes
								Amblyomma cajennense	0/39	0%		
								Dermacentor nitens	0/8	0%		
								Rhipicephalus microplus	0/6	0%		
Labruna [171]		2014	English	Brazil	6 municipalities in 4 states: Minas Gerais, Goiás, Pernambuco, and Rio Grande do Norte	PCR (no precision)	Whole tick	Ticks	0/20	0%	Collected in human houses on opossums	Yes
								Ornithodoros mimon				
Mares-Guia [77]	2011 and 2012	2015	Portuguese	Brazil	Rio de Janeiro	PCR (htpAB)	*Whole*	Fleas	0/21	0%	Fleas collected from feline puppies	No
						PCR	–	Ticks	9/283	3.2%	Ticks collected on dogs	
								R sanguineus	8/266			
								A. sculptum	1/8		Unpublished thesis	
								D. nitens	0/7			
								Fleas				
								Ctenocephalides canis	0/2			

Table 5 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Machado-Ferreira [156]	2010–2012	2016	English	Brazil	Goiás, São Paulo, Ceara, Tocantins, Rio de Janeiro	16S rDNA PCR	Whole tick	Ixodidae ticks*	0/285	0%	~61% of *Rhipicephalus sanguineus* and ~37% of *R. microplus* DNA samples were positive for *Coxiella*-like symbionts	Yes
Guimarães [78]	2013	2017	Portugues	Brazil	Parque Nacional da Serra das Confusões, Caatinga biome, Piauí	IFA	Serum	Ticks *Rhipicephalus microplus*	0/56	0%	Collected on sheep	Yes
Dall'Agnol [172]	2014–2016	2017	English	Brazil	Viamão and Sanatana di Livramento Municipalities Rio Grande do Sul State	16S rRNA metagenomic sequencing	Whole tick	Ticks	0/16	0%	Ticks obtained from crab-eating fox (*Cerdocyon thous*)	Yes
								Amblyomma aureolatum	0%		Microbiota studies of *O. brasiliensis* predominant bacterial genera were *Coxiella* (87.71%)	
								Ornithodoros brasiliensis	87.71% *Coxiella* genera			
Duron [168]	2013	2017	English	Brazil	Sao Francisco de Paula Chapada Gaucha	16S rRNA PCR	Whole tick	Ticks			No *Cb* only CLE	Yes
								Ornithodoros brasiliensis (Sao Francisco de Paula)	1/3	CLE		
								Amblyomma ovale	1/5	CLE		
								Amblyomma cajennense (Chapada Gaucha)	1/3	CLE		
Mares-Guia [173]	2013–2015	2018	English	Brazil	Not specified	PCR (IS1111)	Whole tick	Ticks *Rhipicephalus sanguineus Amblyomma sculptum*	2/180	1.1%	Technique validation. A nested PCR assay for the diagnosis of *C. burnetii* infection	Yes
Ogrzewalska [174]	2016–2018	2019	English	Brazil	Rio de Janeiro City	PCR	Whole tick	*Amblyomma dissimile*	0/60	0%	Ticks collected from snakes	Yes
								Amblyomma rotundatum	0/55	0%		
Jacinavicius [175]	NA	2019	English	Brazil	São Paulo City	PCR 16S RNA	Whole chigger mites	Chigger mites*	0/317	0%	Collected from rodents and marsupials	Yes
Barboza de Oliveira [131]	NA	2020	English	Brazil	Ceara and Pernambuco (Caatinga biome)	PCR *cap* gene	Whole tick	Ticks*	0/196	0%	Collected from rodents, wild canids, and marsupials	Yes

Table 5 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Mendoza-Roldan [143]	2015–2018	2020	English	Brazil	States: Acre, Espirito Santo, Mato Grosso, Mato Grosso do Sul, Minas Gerais, Pará, Rio de Janeiro, and São Paulo	Conventional PCR (*Coxiella* spp.—capsular polysaccharide biosynthesis protein I-like gene (cap))	Ectoparasites from reptiles and amphibians	113 mites 26 ticks* 48 blood samples from live animals and 12 samples of liver from euthanized animals	0/139	0%	Collected from reptiles and amphibians	Yes
Ikeda [144]	2017–201	2021	English	Brazil	Campo Grande city, Mato Grosso do Sul state	qPCR (*IS1111*)	Ectoparasites from nonhematophagous bats	64 bat flies 46 Spinturnicidae mites 21 Macronyssidae mites 19 tick larvae (*Ornithodoros hasei*)	0/150	0%	Collected from nonhematophagous bats	Yes
Duron [168]	2010–2013	2017	English	Brazil	Pan de Azucar	16S rRNA PCR	Whole tick	Ticks			Collected on common vampire bat (*Desmodus rotundus*)	Yes
								Ornithodoros peruvianus	2/3	CLE	Humboldt penguin (*Spheniscus humboldti*)	
								Ornithodoros spheniscus (Pan de Azucar)	1/3	CLE	No *Cb* only CLE	
Brenner [176]	NA	2021	English	Chile	Isla Grande de Atacama	NGS	Whole tick	Ticks *Ornithodoros amblus*	CLE is present but not *Cb*		Collected from seabirds *Spheniscus humbolti* (Humboldt penguin)	Yes
Lima-duarte [177]	2017	2021	English	Brazil	Municipality of Formiga, Minas Gerais State	Nested cPCR mitochondrial 16S rRNA gene	Whole tick	Ticks *Rhipicephalus microplus*	~0/100	0%		Yes
Luzzi [178]	NA	2021	English	Brazil	Jaboticabal, São Paulo State and Porto Alegre, Rio Grande do Sul State	PCR 16S rRNA	Whole tick	Ticks *Rhipicephalus sanguineus*	0/5	0%	Collected from dogs CLE	Yes

Table 5 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Santana [145]	2018–2020	2022	English	Brazil	Municipalitiesof Barretos, Colina, Guaraci, Jaboticabal, Monte Alto, Monte Azul Paulista,Morro Agudo, Olímpia, and Torrinha, São Paulo State	qPCR (*IS1111*)	Whole tick	Ticks *Amblyomma sculptum*	0/184	0%	Collected from 97 free-living wild boars (*Sus scrofa*)	Yes
Guizzo [179]	NA	2022	English	Brazil	Rural area of Porto Alegre (Rio Grande do Sul	qPCR	Whole tick	Ticks *Rhipicephalus microplus*	Several colonies	0% *Cb* 100% CLE		Yes
Lima-Duarte [180]	NA	2022	English	Brazil	Piracicaba, São Paulo State	PCR (16S rRNA gene)	Whole tick	Ticks *Amblyomma sculptum*	0/80	0%	Collected from free-living capybaras	Yes
Faccini-Martínez [97]	2011	2017	English	Colombia	Villeta	Conventional and nested PCR	Whole tick	Ixodidae ticks*	0/1287	0%	Collected from domestic animals, wild mammals, and vegetation	Yes
Machado-Ferreira [156]	2010–2012	2018	English	Colombia	Barranquilla	16S rDNA PCR	Whole tick	Ticks *Amblyomma variegatum*	0/1	0%		Yes
Cotes-Perdomo [181]	2016–2018	2020	English	Colombia	Localities of Bonda, Calabazo, Guachaca, Minca and Aracataca, Magdalena regions	Nested PCR *rpoB* (607 pb) *rpoB* (539 pb)	Whole tick	Ticks*	 0/526 55/526	 0% *Cb* 52.9% CLE	Collected from 18 dogs, 1 donkey (*Equus asinus*), 9 horses 12 cows, 2 mules (*Equus asinus*×*E. caballus*), and 1 turkey	Yes
Segura [182]	2017	2020	English	Colombia	Northern and Middle Magdalena regions, Antioquia	16S rRNA NGS	Pooled ticks	Ticks *Rhipicephalus microplus*	*N*=25	Detected: CLE	Collected from cattle	Yes
Cabrera [183]	2018–2020	2022	English	Colombia	Puerto Berrio, Puerto Triunfo, Puerto Nare, Caracolí, San Roque, Maceo, and San José del Nus. Magdalena Medio region, and Antioquia	BLASTn Analysis and molecular phylogenetic analysis of 16 s rRNA sequences		Ticks *Rhipicephalus* sanguineus	0/169 20/169	0% *Cb* 11.8% CLE	Collected from dogs and bovines in the households [15] or workplaces [1] of 271 patients with acute febrile illness. *C. burnetii* antibodies were detected in 39.5% of the patients and 33.6% by real-time PCR	Yes
Noda [184]	2014	2015	English	Cuba	Candelaria, Artemisa province	PCR (IS1111)	Whole tick	Ticks*	6/468	2 tick pools (4 males and 2 females collected from a horse)	Collected from horses, dogs, and humans All positives were *Amblyomma mixtum*	Yes

Table 5 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Debin [108]	2007	2007	French	French Guiana	Macouria, Kourou, and Cayenne area	PCR	Whole tick	Ticks (species not available)	0/133	0%	Unpublished thesis Collected on dogs and horses	No
Davoust [109]	2014	2014	English	French Guiana	Montagne du Tigre (Cayenne)	qPCR (IS1111)	Whole tick	Tick *Amblyomma geayi*	14/16	88%	Found on a 3-toed sloth (female) (*Bradypus tridactylus*) positive for *C. burnetii.* with serotype MST17	Yes
Pommier de Santi [152]	NA	2014	French	French Guiana	Montagne du tigre (Cayenne) and Macouria Sloths Rescue Center	qPCR (IS1111)	Whole tick	Ticks (species not available)	0/85	0%	Collected on 16 3-toed sloths (*Bradypus tridactylus*)	Yes
Tahir [185]	2013	2016	English	French Guiana	Saint-Jean-du-Maroni	Real-time PCR (IS30A) Positive results confirmed by standard PCR		Ticks *Ornithodoros hasei*	0/107	0%	Collected from 12 bats (*Noctilio albiventris*)	Yes
Duron [168]	2015	2017	English	French Guiana	Cayenne	16S rRNA PCR	Whole tick	Ticks			Collected from unidentified lizard species	Yes
								Amblyomma sp.	1/5	CLE	No *Cb* only CLE	
Binetruy [186]	2017	2019	English	French Guiana	Piste de Lamirande, Matoury	16S rRNA metabarcoding	Whole-tick and tick-organ sequences (guts and carcasses)	Ticks *Amblyomma cajennense* (sensu stricto)	0/100	0%	Study of the impact of different sterilization methods on the internal microbial diversity hosted by the Cayenne tick	Yes
Binetruy [187]	NA	2020	English	French Guiana	Various locations, mainly along the coastline	Metabarcoding	Whole tick	Ticks (18 species belonging to the *Amblyomma* genus*)	0/109	0%	Study on CLE	Yes
Grostieta [188]	2018–2020	2022	English	Mexico	99 localities of the State of Veracruz	PCR	Whole tick	6/888 *Amblyomma mixtum*	0.7%		Collected from cattle and horses	Yes
						16S-rDNA		5/25 in Castán				
								1/5 I Los Angeles			CLE (negative for *Cb*)	
De Rodaniche[189]	NA	1947	English	Panama	City of Panama	NA	NA	Tick *Amblyomma cajennense*	NA	NA	Shown to transmit Q fever in the author's laboratory	Yes
Kueneman [190]	2012–2014	2020	English	Panama	18 sites in Central Panama (lowland tropical rainforest)	PCR 16S rRNA gene	Whole tick	Ticks*	64/733	8.7% *Coxiella* sp. (species not available)	Collected from 179 individual small mammals of 8 species	Yes

Table 5 (continued)

Author	Year of the study	Year of publication	Language	Country	State	Methodology	Sample type	Species	Number of samples	Result	Comments	Published
Duron [168]	2009	2017	English	Peru	Lobos de Tierra Island	16S rRNA PCR	Whole tick	Ticks			Collected from Peruvian pelican (*Pelecanus thagus*), Peruvian booby (*Sula variegata*)	Yes
								Ornithodoros amblus	1/3	CLE	No *Cb* only CLE	

CFT, complement fixation test; *MA*, microagglutination test; *ELISA*, enzyme-linked immunosorbent assay; *IFA*, immunofluorescence assay; *PCR*, qualitative polymerase chain reaction; *qPCR*, quantitative real-time polymerase chain reaction; *MLVA*, multilocus variable number tandem repeats analysis; *MST*, multispacer sequence type; *IHC*, immunohistochemistry; *NA*, data not available; *NGS*, next-generation sequencing; *CLE*, *Coxiella*-like endosymbiont

Details of collected ticks and ectoparasites

*Ticks species from the Cline et al.'s study [169], unpublished: *A. mixtum*, *A. maculatum*, *A. oblongoguttatum*, *A. ovale*, *D. nitens*, *I. affinis*, *R. sanguineus*, *R. microplus*. Ticks species from Machado-Ferreira et al. [156]: *Amblyomma coelebs* ($n=2$), *Amblyomma calcaratum* ($n=2$), *Amblyomma oblongoguttatum* ($n=11$), *Amblyomma ovale* ($n=22$), *Amblyomma parvum* ($n=3$), *Rhipicephalus sanguineus* ($n=90$), *Rhipicephalus microplus* ($n=47$), *Dermacentor nitens* ($n=108$). Chigger mites species from Jacinavicius et al. [175]: *Herpetacarus hertigi, Eutrombicula tinami, Kymocta* sp., *Quadraseta brasiliensis*, *Quadraseta falconensis*, *Quadraseta flochi*, *Quadraseta mackenziei*, *Quadraseta pazca*, *Quadraseta trapezoides*, *Quadraseta* sp., *Serratacarus* sp., and *Trombewingia bakeri*. Ticks species from Barboza de Oliveira et al. [131]: ticks and tick-borne diseases (2020): *Ixodes loricatus*, *Amblyomma auricularium*, *Ornithodoros rietcorreai*, *A. parvum*, and *Rhipicephalus sanguineus*. Fleas: *Polyplax* sp., *Gyropus* sp., *Ctenocephalides felis felis*, *Pulex* sp., and *Haemaphysalis* sp. Ectoparasites and ticks species from Ikeda et al. [144]. Bat flies: *Paratrichobius longicrus*, *Megistopoda aranea*, *Glossophaga soricina*, *Trichobius parasiticus* (complex), *Trichobius dugesii* (complex), *Trichobius joblingi*, *Trichobius costalimai*, and *Strebla hertigi.* Macronyssidae mite: *Steatonyssus*. Ticks: *Ornithodoros hasei.* Ticks and mites species from Mendoza-Roldan et al. [143]: Ticks: *Amblyomma rotundatum*, *Ornithodoros* sp., and *Amblyomm sculptum*. Mites: *Eutrombicula alfreddugesi*, *Chironobius* sp., *Zeterohercon oudemansi*, *Ophionyssus natricis*, *Geckobia hemidactyli*, *Ophiogongylus rotundus*, Geckobiella harrisi. Ticks species from Faccini-Martínez et al. [97]: *Amblyomma cajennense*, *Amblyomma ovale*, *Amblyomma* sp., *Dermacentor nitens*, *Dermacentor* sp., *Ixodes luciae*, *Ixodes* sp., *Rhipicephalus microplus*, and *Rhipicephalus sanguineus.* Ticks species from Cotes-Perdomo [181]: *Amblyomma mixtum* [21], 1 *A. dissimile* [1], *Amblyomma* sp. [2], 22 *Rhipicepalus microplus* [22], *Dermacentor nitens* [20] and 38 *R. sanguineus* [38]. Positive for Coxiella endosymbiont from *R. sanguineus* (34/38), 3 *R. microplus* (3/22), 14 *A. cajennense*, and *D. nitens* (4/20). Tick species from Noda et al. [184]: *Amblyomma mixtum* (67%), *R. Sanguineus* (27%), and *D. Nitens* (6%). Tick species from Binetruy et al. [186]: *Amblyomma dissimile*, *A. rotundatum*, *A. romitii*, *A. humerale*, *A. coelebs*, *A. calcaratum*, *A. pacae*, *A. goeldii*, *A. geayi*, *A. longirostre*, *A. varium*, *A. ovale*, *A. latepunctatum*, *A. scalpturatum*, *A. naponense*, *A. naponense-like*, *A. americanum*, *A. oblongoguttatum*, *A. cajennense*, *A. sculptum*, and *Hyalomma truncatum*. Species from Kueneman [190]: tick species and number of positive for *Coxiella* sp.: *Amblyomma auricularium* (0/71), *A. dissimile* (0/27), *A. geayi* (0/25), *A. mixtum* (33/39), *A. naponense* (3/5), *A. ovale* (3/103), *A. pacae* (0/44), *A. sabanerae* (1/232), *A. varium* (0/9), *Haemaphysalis juxtakochi* (2/150), and *Ornithodorus puertoricensis* (22/28); host species: Didelphimorphia: *Didelphis marsupialis* ($n=55$), *Marmosa robinsoni* ($n=3$), *Metachirus nudicaudatus* ($n=5$), and *Philander opossum* ($n=12$); rodentia: *Hoplomys gymnurus* ($n=23$), *Melanomys caliginosus* ($n=1$), *Oryzomys talamancae* ($n=5$), and *Proechimys semispinosus* ($n=75$)

circulating in Colombia, in livestock as well as in wildlife, especially bats, and deserves the implementation of studies in various animal taxa, both in animals and humans.

Conclusions and Perspectives

It is interesting to note that the literature reviews that follow one another from one decade to the next repeat tirelessly that Q fever is ubiquitous and that it is found everywhere in the world except in New Zealand [2, 68, 69, 207]. It is difficult to know where the claim that *C. burnetii* has been described in every country in the world has its roots. Recently, it was shown that numerous African countries have no trace of publication on *C. burnetii* in humans [208]. In 2016, we published a literature review on human Q fever in South America that showed that seven countries had never reported any cases of human Q fever or seroprevalence studies according to the available literature (Belize, Costa Rica, Guatemala, Guyana, Honduras, Paraguay, Suriname) [63]. The present literature review highlights the fact that there are no available data on *C. burnetii* infection in animals in many countries of Latin America. Thus, among the 21 countries or territories in continental Latin America, five (24%) have no publication related to *C. burnetii* detection in animals (Guyana, Suriname, Honduras, Bolivia, Paraguay), and 17 (65%) among the 26 Caribbean countries and territories, among which populated islands with livestock farms such as Jamaica, Haiti, and the Dominican Republic. There is thus an urgent need for studies on *C. burnetii* infection in animals in Latin America and the Caribbean, as well as in humans, to better understand the dynamic of this infection in the neotropical area.

While seroprevalence studies on *C. burnetii* in livestock exist in various countries, studies on wildlife and domestic animals are rare. Finally, studies on ticks seem to rule out this taxon as a contributor to *C. burnetii* transmission, although many *Coxiella*-LE have been found. Pets may be particularly valuable sentinel indicators for "one health" epidemiological studies because they share human environmental exposures. A significant effort has been made in recent years, particularly in Brazil and French Guiana, but most other Latin American countries, probably due to the low reporting of human cases, do not focus their research in this direction. In order to explain the contagion cycles in hyperendemic areas, it seems important to multiply studies on domestic and wild animals in terms of descriptive epidemiology and molecular epidemiology, considering the surveillance of particular strains. It would be interesting to see if the wild reservoirs are perhaps at the origin of this hyperendemicity, on the one hand, while the domestic ones would rather be at the origin of localized epidemics. There is also a need to study synanthropic species that are neither wildlife nor domesticated, such as mice and the two *Rattus* species. Nevertheless, it is important to address the question of cross-border spread through wildlife and imported domestic animals. Finally, this study demonstrates the need to include *C. burnetii* infection in the public health surveillance systems, considering its wide spectrum of clinical manifestations, and in animal health programs, especially for animals with reproductive disorders," and the need for better surveillance systems. The environmental aspects of the disease (reservoir and source of contamination through feces, dust, etc.) may be considered to introduce a One Health approach to this infection.

Funding This article was supported by the European Union and the Collectivité territoriale de Guyane of French Guiana as part of the call for projects FlashCovid-19 and the AMAZCOV'N FEVERS project (FEDER, SYNERGIE GY0028034).

Data Availability Most of the data that support the findings of this study are openly available consulting PubMed (National Institutes of Health's National Library of Medicine), ScienceDirect (Elsevier), SciELO (Scientific Electronic Library Online) and LILACS. The unpublished data and "grey literature" that support the findings of this study are available from the corresponding author, LE, upon reasonable request.

Declarations

Conflict of Interest The authors declare no competing interests.

Human and Animal Rights and Informed Consent All reported studies/experiments with human or animal subjects performed by the authors were performed in accordance with all applicable ethical standards, including the Helsinki Declaration and its amendments, institutional/national research committee standards, and international/national/institutional guidelines.

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•• Of major importance

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Authors and Affiliations

Loïc Epelboin[1,2] · Mateus De Souza Ribeiro Mioni[3] · Aurelie Couesnon[4] · Mona Saout[5] · Edith Guilloton[2] · Salma Omar[2] · Vincent Pommier De Santi[6] · Bernard Davoust[7,8] · Jean Lou Marié[7,9] · Anne Lavergne[10] · Damien Donato[10] · Alexandro Guterres[11] · Sebastien Rabier[2] · Justin Destoop[12] · Felix Djossou[1] · Xavier Baudrimont[13] · Antoine Roch[13] · Gabriel Leonardo Cicuttin[14] · Tatiana Rozental[11,15] · Mathieu Nacher[2] · Javier Millán[16,17,18] · Elba R. Sampaio De Lemos[11] · Jorlan Fernandes[11] · Olivier Duron[19] · Benoit De Thoisy[10,20] · Elodie Rousset[4]

✉ Loïc Epelboin
epelboincrh@hotmail.fr

[1] Unité Des Maladies Infectieuses Et Tropicales, Centre Hospitalier de Cayenne Andrée Rosemon, Avenue des Flamboyants, Cayenne F-97300, French Guiana

[2] Centre d'Investigation Clinique Inserm 1424, Centre Hospitalier de Cayenne Andrée Rosemon, Cayenne F-97300, French Guiana

[3] Instituto de Biotecnologia (IBTEC), Universidade Estadual Paulista Júlio de Mesquita Filho, Botucatu, Brazil

[4] French Agency for Food, Environmental and Occupational Health and Safety (ANSES), Laboratory of Sophia Antipolis, Animal Q Fever Unit, Sophia Antipolis, France

[5] UMR TBIP 1019 Tropical Biomes and Immunophysiopathology, University of French Guiana, Cayenne, French Guiana

[6] French Military Center for Epidemiology and Public Health, Marseille, France

[7] Animal Epidemiology Expert Group, French Military Health Service, Tours, France

[8] Aix Marseille Univ, IRD, AP-HM, MEPHI, IHU Méditerranée Infection, Marseille, France

[9] Institut de Recherche Biomédicale Des Armées (IRBA), Brétigny-Sur-Orge, France

[10] Laboratoire Des Interactions Virus-Hôtes, Institut Pasteur de La Guyane, Cayenne F-97300, French Guiana

[11] Laboratory of Hantaviroses and Rickettsiosis, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Rio de Janeiro 21040-900, Brazil

[12] Service de Dermatologie, Centre Hospitalier de Cayenne Andrée Rosemon, Cayenne F-97300, French Guiana

[13] Direction Générale des Territoires Et de La Mer de La Guyane, Cayenne, French Guiana

[14] Instituto de Zoonosis Luis Pasteur, Av. Díaz Vélez 4821, Ciudad Autónoma de Buenos Aires, Argentina

[15] Kimron Veterinary Institute (Bacteriology Department), Ministry of Agriculture and Rural Development, 5025001 Bayit Dagan, Israel

[16] Instituto Agroalimentario de Aragón-IA2 (Universidad de Zaragoza-CITA), Miguel Servet 177, 50013 Zaragoza, Spain

[17] Fundación ARAID, Avda. de Ranillas, 50018 Zaragoza, Spain

[18] Facultad de Ciencias de La Vida, Universidad Andres Bello, República 440, Santiago, Chile

[19] MIVEGEC, IRD, CNRS, Université de Montpellier, Montpellier, France

[20] Collection JAGUARS, Association Kwata, Cayenne, French Guiana