

Diversity and distribution of *Bartonella* spp. in domestic animals, wildlife, and ectoparasites in Brazil: a comprehensive review

Diversidade e distribuição de *Bartonella* spp. in animais domésticos, fauna selvagem e ectoparasitos no Brasil: uma revisão abrangente

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Abstract

Bartonella are intracellular Gram-negative blood-borne bacteria capable of infecting a wide range of hosts, primarily mammals and birds. They are responsible for emerging and re-emerging infectious diseases characterized by persistent intraerythrocytic bacteremia in mammals. Out of 49 species described, 13 presents zoonotic potential. This review aimed to update the current knowledge on the occurrence, distribution, and genetic diversity of *Bartonella* in domestic animals, wild mammals and birds, and ectoparasites in Brazil. A total of 72 scientific articles published between 2007 and 2026 were included. The available information indicates that the Southeastern and Central-Western regions of Brazil account for most reports of *Bartonella* in animals and ectoparasites, whereas the Northern and Northeastern regions remain comparatively understudied. Overall, studies investigating *Bartonella* in Brazil have become increasingly frequent and geographically widespread over the years. Although some investigations rely on single-gene analyses, most employ multi-locus sequence analysis and phylogenetic reconstruction, providing stronger evidence for species identification and diversity. In contrast, relatively few studies have incorporated whole-genome sequencing or comprehensive phenotypic and biochemical characterization through bacterial isolation and blood culture. Future research should prioritize advanced genomic approaches and bacterial isolation to improve our understanding of the diversity, evolution, and epidemiology of *Bartonella* circulating in Brazil.

Keywords: Bartonellaceae, genetic diversity, wild mammals, pets, livestock, wild birds.

Resumo

Bartonella são bactérias Gram-negativas intracelulares e hemotrópicas, capazes de infectar uma ampla variedade de hospedeiros, principalmente mamíferos e aves. Estão associadas a doenças infecciosas emergentes e reemergentes, caracterizadas por bacteremia intraeritrocitária persistente em mamíferos, sendo que, das 49 espécies descritas, 13 apresentam potencial zoonótico. Esta revisão teve como objetivo atualizar o conhecimento sobre a ocorrência, distribuição e diversidade genética de *Bartonella* spp. em animais domésticos, mamíferos silvestres, aves e ectoparasitos no Brasil. Foram incluídos 72 artigos científicos publicados entre 2007 e 2026. As evidências disponíveis demonstram que as regiões Sudeste e Centro-Oeste concentram a maior parte dos registros da ocorrência de *Bartonella* em animais e ectoparasitos, enquanto as regiões Norte e Nordeste permanecem relativamente pouco investigadas. De modo geral, os estudos sobre *Bartonella* spp. no Brasil

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tornaram-se mais frequentes e abrangentes ao longo dos anos. Embora algumas pesquisas utilizem a análise de um único gene, a maioria emprega abordagens multilocus e reconstruções filogenéticas, fornecendo evidências mais robustas para a identificação das espécies e avaliação da diversidade genética. Em contrapartida, ainda são escassos os estudos que utilizam sequenciamento genômico completo, isolamento bacteriano e caracterização fenotípica e bioquímica. Dessa forma, futuras investigações devem priorizar abordagens genômicas avançadas e o isolamento bacteriano, a fim de ampliar o conhecimento sobre a diversidade, evolução e epidemiologia das espécies de *Bartonella* circulantes no Brasil.

Palavras-chave: Bartonellaceae, diversidade genética, mamíferos selvagens, animais de companhia, animais de produção, aves selvagens.

Introduction

The genus *Bartonella* (Hyphomicrobiales: Bartonellaceae) comprises Gram-negative facultative intracellular α -proteobacteria that primarily infect erythrocytes and endothelial cells of a wide range of vertebrate hosts, including humans, domestic and mammals, and wild birds (Morse et al., 2012; Harms & Dehio, 2012). Transmission occurs primarily through hematophagous arthropod vectors, such as fleas, lice, sand flies, bat flies, and ticks, which play a pivotal role in the maintenance and dissemination of *Bartonella* spp. in natural and urban environments (Breitschwerdt, 2014; C). Over recent decades, the increasing description of novel *Bartonella* species, genotypes, host species, and associated vectors has revealed a considerably more complex epidemiological scenario than previously recognized, particularly at the interface among wildlife, domestic animals, and humans. Currently, 50 *Bartonella* species are formally recognized, while additional provisional 'Candidatus' taxa have been detected, particularly in wildlife and arthropod vectors (Freese et al., 2026). Many of these remain poorly characterized or have been only sporadically reported, highlighting the still largely unexplored diversity of the genus.

Among domestic animals, cats are considered the main reservoirs of zoonotic *Bartonella* species, namely *Bartonella henselae*, *Bartonella clarridgeiae*, and *Bartonella koehlerae*. The cat flea, *Ctenocephalides felis felis*, plays a crucial role in the maintenance and transmission of *B. henselae* among feline populations, with transmission to humans occurring mainly through flea feces contaminating the skin and claws of infected cats (Guptill, 2010). Experimental studies demonstrated that transmission between cats does not occur efficiently through bites, scratches, or fomites in the absence of fleas (Abbott et al., 1997; Guptill et al., 1997, 1998), reinforcing the epidemiological importance of ectoparasites in feline bartonellosis. Although alternative transmission routes, such as saliva contamination or regurgitation during flea feeding, have been proposed, these mechanisms remain unconfirmed (Moore et al., 2024). In dogs, however, the transmission dynamics of *Bartonella* spp. are still not fully understood.

Beyond companion animals, increasing evidence indicates that wildlife species also play important role in the maintenance and circulation of *Bartonella* spp. in Brazil. Molecular detection of *Bartonella* DNA has already been reported in fleas collected from both domestic and wild animals in different Brazilian regions (Sousa et al., 2018; Raimundo et al., 2022), reinforcing the existence of interconnected transmission networks involving wild mammals, domestic animals, ectoparasites, and humans. In wildlife, *Bartonella* infections have been reported in numerous mammalian taxa, including rodents, carnivores, marsupials, xenarthrans, bats, and wild birds. These hosts may contribute to the maintenance and dispersion of genetically diverse *Bartonella* lineages in natural ecosystems, particularly in biodiverse countries such as Brazil, where anthropogenic environmental changes may favor pathogen spillover among wildlife, domestic animals, and humans. Among wildlife hosts, bats have attracted particular attention due to their ecological diversity, gregarious behavior, long-distance dispersal capacity, and close associations with hematophagous ectoparasites such as bat flies, which may facilitate the maintenance and circulation of highly diverse *Bartonella* genotypes (Morse et al., 2012; Sándor et al., 2018).

The diagnosis of bartonellosis remains challenging because infected hosts frequently exhibit low, cyclic, or intermittent bacteremia (Breitschwerdt et al., 2010). The isolation of *B. henselae* in 1992 from domestic cats favored the subsequent detection and description of novel *Bartonella* species or subspecies in a plethora of domestic and wild carnivores (Chomel et al., 2004). In recent years, the diagnosis of the infection relies on a workflow combining polymerase chain reaction (PCR), mainly quantitative real-time, microfluidic, and digital PCR assays (André et al., 2016; Alabí Córdova et al., 2025; Calchi et al., 2025) and bacterial isolation from blood samples. Such methods improved the detection of *Bartonella* spp. in both domestic and wild animals. Studies employing liquid pre-enrichment culture using *Bartonella* Alpha Proteobacteria Growth Medium (BAPGM) prior to DNA extraction

and isolation onto blood/chocolate agar demonstrated increased sensitivity for bacterial detection (Furquim et al., 2021; Amaral et al., 2022a, b; Dias et al., 2023; Neves et al., 2025). Additionally, successful bacterial isolation from naturally infected animals has been associated with the use of fresh blood samples or samples stored at ultra-low temperatures, such as -70°C or liquid nitrogen, in order to preserve bacterial viability until culturing is performed (Tea et al., 2004; Amaral et al., 2022a, b).

Despite the growing number of reports involving domestic and wild hosts in Brazil, no updated review has comprehensively summarized the occurrence and diversity of *Bartonella* spp. in animals and associated ectoparasites from Brazil. Therefore, the present review aims to provide an updated overview of the occurrence of *Bartonella* spp. in domestic and wild hosts in Brazil, as well as in associated ectoparasites, emphasizing host diversity, molecular detection methods, geographic distribution, and epidemiological aspects associated with these bacteria.

Material and Methods

Publications were retrieved from PubMed, SciELO, and Google Scholar using the following search strategy: ("*Bartonella**" OR "Bartonellaceae*") AND ("wild*" OR "wildlife" OR "domestic" OR "ectoparasites" OR "arthropods" OR "free-living" OR "captive") AND "Brazil". The review included original studies published between 2007 and 2025 that reported the molecular detection or characterization of *Bartonella* spp. in animals, ectoparasites, or arthropods from Brazil. Special attention was given to the biome and state of origin of each report to assess potential eco-epidemiological patterns. Figures were created using QGIS 3.28 software (QGIS Development Team, 2022) and Canva Pro (Canva, 2026).

Results

To facilitate the visualization of *Bartonella* distribution across Brazil, a supplementary table summarizing host species, *Bartonella* species, molecular targets, and geographic origin is provided (Supplementary File 1). Additionally, distribution maps were generated to illustrate reports of *Bartonella* detection in wild animals from Northern and Central-Western Brazil (Figure 1), Northeastern Brazil (Figure 2), and Southeastern and Southern Brazil (Figure 3). Separate maps depicting the occurrence of *Bartonella* in domestic animals (Figure 4) and arthropods (Figure 5) are also presented. A map showing the geographical division of Brazilian states is available in Supplementary File 2.

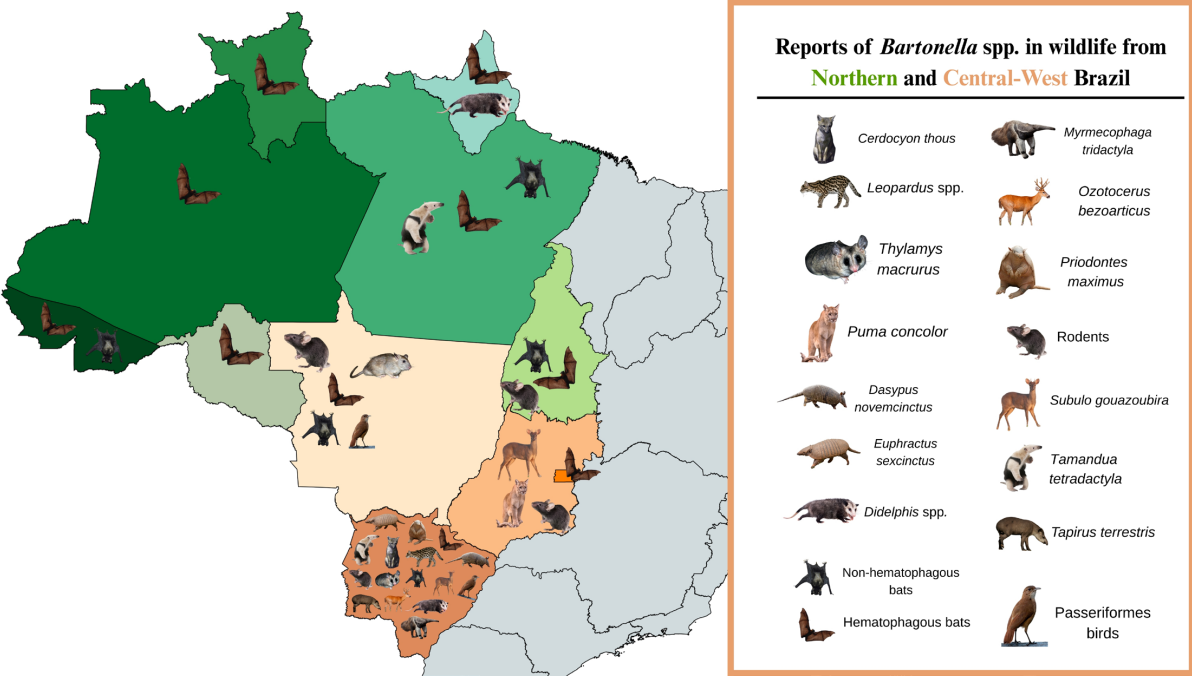


Figure 1. Reports of *Bartonella* spp. in wild animals from Northern and Central-Western Brazil.

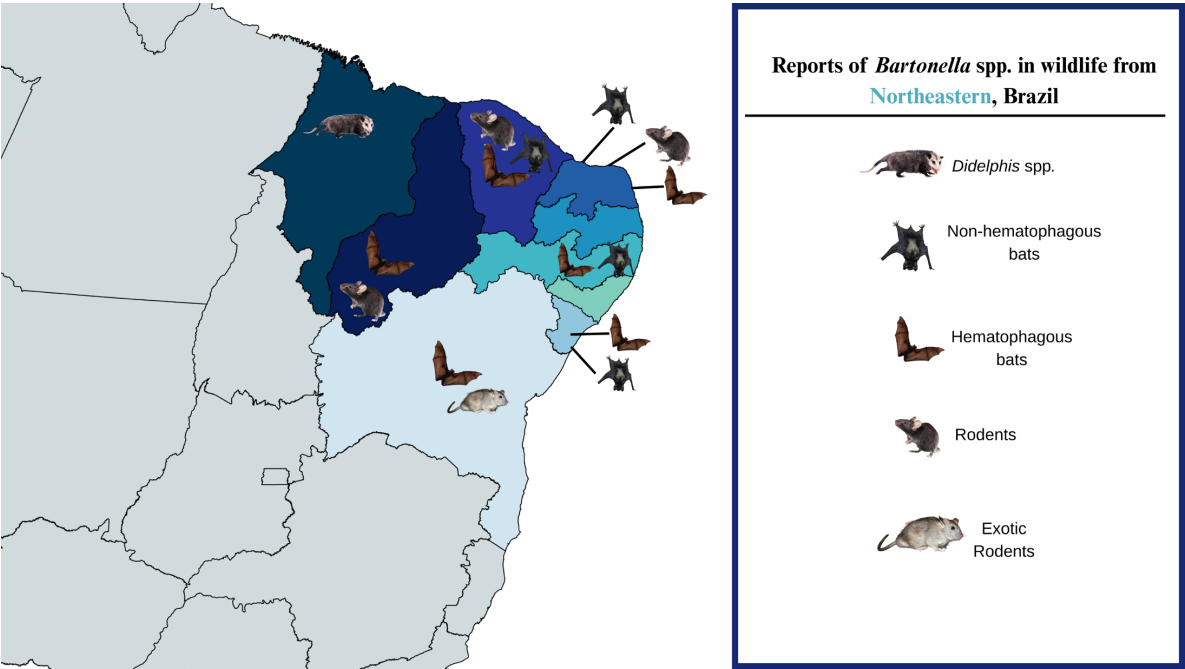


Figure 2. Reports of *Bartonella* spp. in wild animals from Northeastern Brazil.

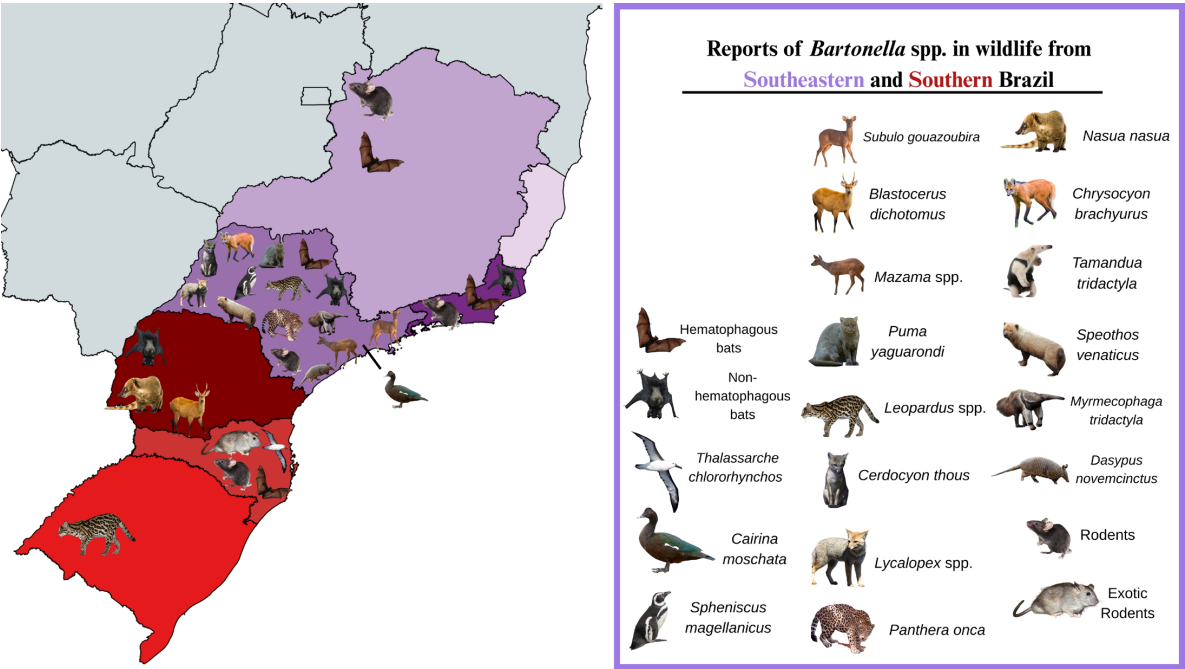


Figure 3. Reports of *Bartonella* spp. in wild animals from Southeastern and Southern, Brazil.

Bartonella spp. in domestic animals from Brazil

Order Carnivora

Dogs (*Canis lupus familiaris*)

Among domestic animals, dogs and cats play important epidemiological roles in the maintenance and transmission of zoonotic *Bartonella* species. The most relevant *Bartonella* species infecting companion animals include *B. henselae*, *B. clarridgeiae*, *B. koehlerae*, *B. quintana*, *B. rochalimae*, and *B. vinsonii berkhoffii* (Chomel & Kasten, 2010; Breitschwerdt,

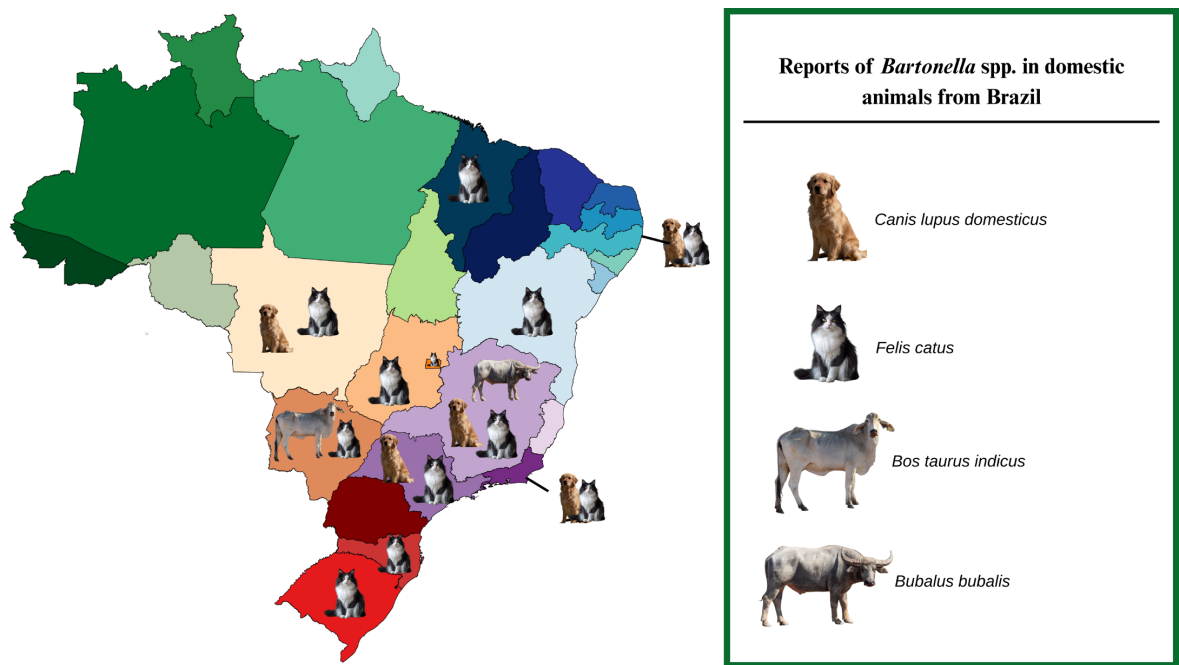


Figure 4. Reports of *Bartonella* spp. in domestic animals from Brazil.

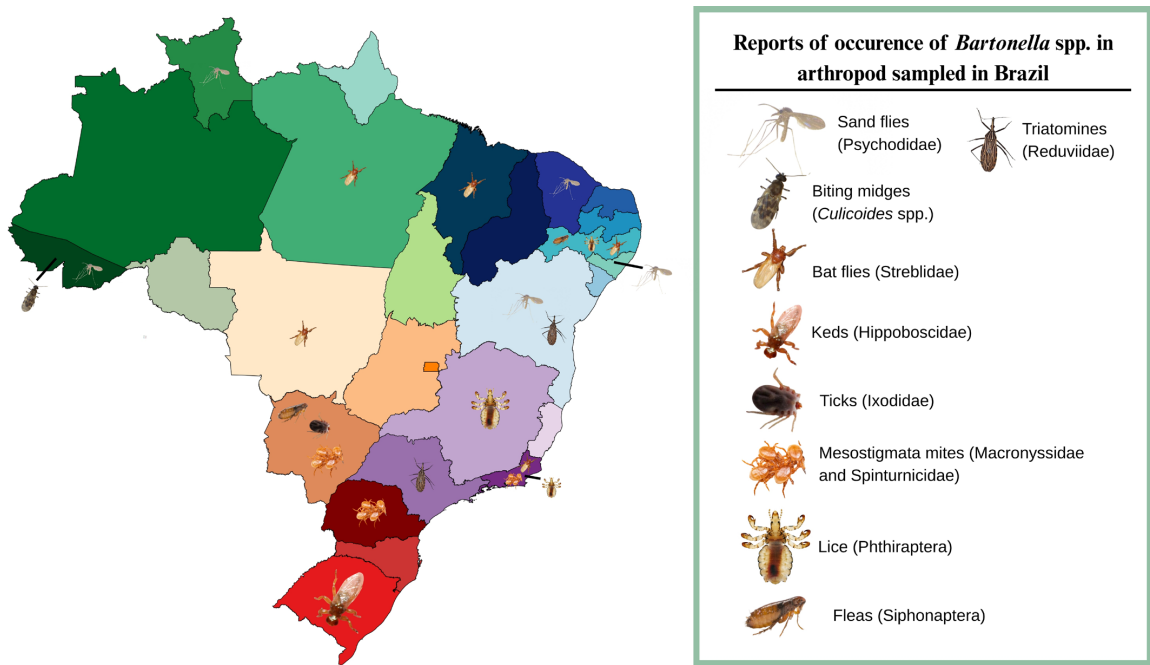


Figure 5. Reports of *Bartonella* spp. in arthropods from Brazil.

2017; Álvarez-Fernández et al., 2018). The epidemiological role of dogs has increasingly gained attention, especially considering their close contact with humans and shared exposure to arthropod vectors (Chomel et al., 2006; Lashnits et al., 2019), although the transmission of *B. henselae* from dogs to humans remains unclear.

Canine bartonellosis is commonly associated to endocarditis, myocarditis, cardiac arrhythmias, heart murmurs, fever, respiratory abnormalities, granulomatous or lymphocytic hepatitis, peliosis hepatis, lethargy, anemia, thrombocytopenia, leukocytosis, hypoalbuminemia, elevated liver enzymes, azotemia, weight loss, splenomegaly, epistaxis, uveitis, choroiditis, lameness, and polyarthritis (MacDonald et al., 2004; Chomel et al., 2006). *Bartonella*-associated endocarditis, particularly involving the aortic valve, represents one of the most severe clinical presentations described in dogs (André et al., 2019a).

In Brazil, studies investigating *Bartonella* spp. in dogs remain relatively scarce. The first molecular and serological investigation was performed by Diniz et al. (2007) in the State of São Paulo, where 198 dogs with clinical and/or laboratory findings resembling tick-borne diseases were analyzed. A total of 4/198 (2%) and 3/198 (1.5%) dogs were seropositive in the indirect immunofluorescence assays (IFA) to *B. henselae* and *B. vinsonii* subsp. *berkhoffii* antigens, respectively. Furthermore, one of the seropositive samples was positive for *Bartonella* sp. in a conventional (c)PCR targeting the ITS (16S-23S rRNA) intergenic region. Molecular assays based on distinct molecular markers (*pap*-31 and *rpoB*) showed the occurrence of *B. henselae* and *B. vinsonii* subsp. *berkhoffii* from the blood and/or isolates (BAPGM pre-enrichment growth medium and BAPGM blood-agar plates).

Subsequent epidemiological studies demonstrated variable exposure and infection rates among canine populations from different Brazilian regions. In Pernambuco state, Fontalvo et al. (2017) detected IgG antibodies anti-*Bartonella* spp. in 24.8% (27/109) of dogs from rural dwellings. The same study identified DNA of *B. rochalimae* and *B. vinsonii* subsp. *berkhoffii* in *Pulex irritans* fleas collected from dogs, while *B. henselae* and *B. clarridgeiae* were detected in *Ctenocephalides felis felis* fleas collected from cats, reinforcing the role of fleas in *Bartonella* transmission dynamics.

Later, André et al. (2019a) described a case of aortic valve endocarditis caused by *B. clarridgeiae* in a mixed-breed dog presenting hyperthermia, anorexia, and severe systolic and diastolic murmurs, reinforcing the pathogenic potential of *Bartonella* infections in dogs. Conversely, da Silva et al. (2019), evaluating dogs and cats from Rio de Janeiro state, detected *Bartonella* DNA exclusively in cats, whereas all sampled dogs were PCR-negative.

Also in São Paulo state, Gonçalves et al. (2022) reported anti-*Bartonella* spp. IgG antibodies in 8.3% (28/335) of sampled dogs. In Rio de Janeiro, Gonçalves-Oliveira et al. (2023) reported a seropositive dog whose owner had been diagnosed with infective endocarditis caused by *B. henselae*, further supporting the epidemiological link between companion animals and human bartonellosis.

The close environmental overlap between dogs and humans has raised interest in the use of dogs as sentinels for *Bartonella* exposure. Lashnits et al. (2019) proposed that seroreactivity to *B. henselae* in dogs may reflect the risk of human exposure in shared environments.

The potential risk of *Bartonella* transmission through blood transfusion has become an additional concern for both human and veterinary medicine. Although da Silva et al. (2025) reported all blood donor dogs sampled in central-western Brazil were negative for *Bartonella* spp., based on microbiological and qPCR assays, studies conducted in the United States and Canada identified *Bartonella* DNA in apparently healthy canine blood donors, reinforcing the possibility of occult bacteremia in clinically normal animals (Balakrishnan et al., 2014; Nury et al., 2021).

More recently, Miranda et al. (2026) investigated dogs suspected of visceral leishmaniasis in Mato Grosso state and detected *B. henselae* DNA in 53.75% (43/80) of sampled animals using a qPCR targeting the *gltA* gene and blood cultures. Additionally, *Leishmania* spp. DNA was detected in 65.11% (28/43) of the dogs, suggesting frequent exposure to multiple vector-borne pathogens in endemic areas. The high occurrence of *B. henselae* among dogs with clinical suspicion of visceral leishmaniasis highlights the need for further studies to better understand the clinical and epidemiological significance of *Bartonella* infection in dogs from endemic regions, regardless of confirmed *Leishmania* infection.

In contrast to previous Brazilian studies reporting low molecular occurrence of *Bartonella* spp. in dogs, Castillo et al. (2026) detected *Bartonella* DNA in 70.8% (34/48) of domiciled dogs belonging to COVID-19-positive households in Minas Gerais states.

Overall, current evidence suggests that dogs may act as incidental hosts, sentinels, or potentially secondary reservoirs for zoonotic *Bartonella* species. Although bacteremia appears to occur less frequently in dogs than in cats, canine bartonellosis is often associated with clinically significant disease, particularly cardiovascular manifestations such as endocarditis. Together, these findings reinforce the importance of investigating *Bartonella* infections in dogs within a One Health perspective, considering the close relationship between dogs, humans, and arthropod vectors.

Cats (*Felis catus*)

Bartonella infections have been reported in domestic cats worldwide, mostly *B. henselae*, *B. clarridgeiae*, and *B. koehlerae*, which are considered the main feline-associated *Bartonella* agents. Evidence suggests a long-standing association between cats and *Bartonella* spp., since *B. henselae* DNA was identified in the dental pulp of cats from French burial sites dating from the 13th to 16th centuries (La et al., 2004). Domestic cats play a central role in the maintenance and transmission of *Bartonella* species in urban environments (Álvarez-Fernández et al., 2018).

Naturally infected cats are frequently asymptomatic, even during persistent bacteremia. Nevertheless, *Bartonella*-positive cats may develop lymphadenitis, gingivitis, stomatitis, urological disorders, uveitis, and endocarditis (Boulouis et al., 2005; Lappin et al., 2000; Chomel et al., 2003). Establishing a direct causal relationship between *Bartonella* infection and clinical manifestations remains challenging due to the multifactorial nature of these disorders and the high prevalence of *Bartonella* infection among healthy cats (Guptill, 2010). Hematological and biochemical abnormalities are generally mild or absent, although anemia, neutropenia, thrombocytopenia, hyperglobulinemia, and hyperproteinemia have occasionally been reported (Guptill, 2010; Silva et al., 2019; Whittemore et al., 2012; Williams et al., 2022).

In Brazil, *Bartonella* spp. have been detected in domestic cats across multiple geographic regions. In the Southern region, Rio Grande do Sul, positivity rates ranging from 17% to 25.5% using PCR assays targeting the *ribC*, *gltA*, and *nuoG* genes (Staggemeier et al., 2010, 2014; Malheiros et al., 2016). The detected species were predominantly *B. henselae* and *B. clarridgeiae*. In Santa Catarina state, Pedrassani et al. (2019) detected *Bartonella* spp. (including *B. henselae*, *B. clarridgeiae*, and *B. koehlerae*) in 13.3% (4/30) of sampled cats.

The Southeast region concentrates most Brazilian studies, with positivity rates ranging from 4.3% to 90.2% (Crissiuma et al., 2011; Bortoli et al., 2012; André et al., 2014; Drummond et al., 2018; Raimundo et al., 2019; Silva et al., 2019; Furquim et al., 2021). In São Paulo state, Bortoli et al. (2012) and André et al. (2014) reported molecular detection of *B. henselae* and *B. clarridgeiae* using PCR assays targeting the ITS region, *ribC*, *pap-31*, *gltA*, and *rpoB* genes, with positivity rates of 4.3% and 30%, respectively. Later, Drummond et al. (2018) demonstrated markedly high positivity rates when combining BAPGM pre-enrichment culture with PCR and bacterial isolation methods. Using this combined approach, *Bartonella* DNA was detected in 90.2% (101/112) of sampled cats, while bacterial isolation yielded 11 *B. henselae* isolates. Similarly, Furquim et al. (2021), using BAPGM enrichment associated with qPCR targeting the *nuoG* gene, reported positivity rates of 33.1% (50/151) and 57.4% (89/155) in cats from São Paulo and Minas Gerais state, respectively. In addition, 17 *B. henselae* isolates were obtained through bacterial culture.

In Rio de Janeiro state, Crissiuma et al. (2011) reported 42% (17/40) positivity by PCR targeting the *hrtA* gene, while serological reactivity reached 47% (19/40) by IFA. Additionally, Kitada et al. (2014) reported that 64.3% (72/112) of cats with sporotrichosis and 45.5% (35/77) of healthy cats tested seropositive for *Bartonella* species in the state of Rio de Janeiro. Subsequently, Souza et al. (2017), Silva et al. (2018), and Raimundo et al. (2019) confirmed the circulation of *B. henselae*, *B. clarridgeiae*, and *B. koehlerae* among domestic cats using PCR assays targeting the *gltA* gene and ITS region, with positivity ranging from 24.7% to 74.85%. Raimundo et al. (2019) additionally identified coinfections involving *B. henselae*, *B. clarridgeiae*, and *B. koehlerae*, reinforcing the complexity of *Bartonella* epidemiology and the possibility of simultaneous exposure to multiple species in feline hosts.

Recently, Castillo et al. (2026) investigated the occurrence of *Bartonella* spp. in 38 domiciled cats living with COVID-19-positive owners in Minas Gerais states. Molecular analysis detected *Bartonella* DNA in 15.8% (6/38) of the cats. Sequencing of representative amplicons identified *B. clarridgeiae*, reinforcing the circulation of this zoonotic species in companion cats from Brazil.

Studies from the Northeast region reported positivity rates ranging from 4.5% to 20.7% (Braga et al., 2012; Fontalvo et al., 2017; Cruz et al., 2022). In Maranhão state, Braga et al. (2012) detected *B. henselae* and *B. clarridgeiae* in 4.5% (9/200) of sampled cats. In Pernambuco, although all cats were PCR-negative for *ribC* gene, Fontalvo et al. (2017) detected serological reactivity to *Bartonella* spp. in 15% (6/40) of animals by IFA, suggesting previous exposure to these bacteria. Cruz et al. (2022), investigating cats from Bahia state, detected *Bartonella* DNA both in blood and claw samples. Interestingly, 23% (9/39) of claw samples were positive, whereas qPCR targeting the *nuoG* gene detected positivity in 20.7% (39/188) of blood samples, with *B. henselae* and *B. koehlerae* identified among the sequenced amplicons. The detection of *Bartonella* DNA in claws reinforces the importance of cats in the transmission of *Bartonella* spp. to humans, considering the role of scratches in pathogen transmission.

In the Midwest region, positivity rates ranged from 1.6% to 46% (Miceli et al., 2013; Braga et al., 2015; André et al., 2015; Dias et al., 2023; Neves et al., 2025). In Mato Grosso state, Miceli et al. (2013) and Braga et al. (2015) reported relatively low positivity rates of 2.24% (4/178) and 1.6% (3/182), respectively, mainly associated with *B. henselae* and *B. clarridgeiae*. In contrast, André et al. (2015) detected *Bartonella* spp. DNA in 30.46% (46/151) of cats from Mato Grosso do Sul, demonstrating substantially higher exposure in this region.

More recently, studies employing BAPGM pre-enrichment associated with molecular assays and isolation on chocolate agar reported markedly higher detection rates. In Goiás state, Dias et al. (2023) identified *Bartonella* DNA in 42% (42/100) of sampled cats using qPCR targeting the *nuoG* gene and obtained 12 *B. henselae* isolates through bacterial culture. Similarly, Neves et al. (2025) detected *Bartonella* spp. DNA in 32% (32/100) of cats from the Federal

District by qPCR, while serological reactivity by IFA reached 60.75% (96/158). In addition, bacterial isolation yielded three *B. henselae* isolates. Notably, 46% (46/100) of feline blood donors tested positive for *Bartonella* spp., highlighting the potential epidemiological relevance of asymptomatic bacteremic cats in transfusional medicine. This finding is particularly important considering that experimental studies demonstrated the viability of *B. henselae* in stored red blood cell units for up to 35 days, suggesting that infected donor cats may represent a potential source of transfusion-mediated infection (Magalhães et al., 2008). The zoonotic risk posed by these asymptomatic reservoirs is further underscored by Lamas et al. (2010) in Rio de Janeiro; by screening pets owned by immunocompromised individuals, the authors demonstrated that owning cats was closely associated with human *Bartonella* spp. seropositivity, reinforcing the role of domestic felines as critical sources of infection in urban environments.

Recent advances in molecular epidemiology have allowed a more refined characterization of *B. henselae* strains circulating in cats from Brazil. Using multi-locus sequence type (MLST) based on eight housekeeping genes (*gltA*, *groEL*, *ribC*, *batR*, *nlpD*, *ftsZ*, *rpoB*, and 16S rRNA), Furquim et al. (2021), Dias et al. (2023), and Neves et al. (2025) identified five distinct Sequence Types (STs) in domestic cats from the Southeast (ST9 and ST37) and Midwest (ST1, ST2 and ST5) of Brazil. These STs represent distinct allelic profiles defined by sequence variation across the eight MLST loci, with each unique combination of alleles assigned to a different ST. Notably, ST1, ST2 and ST5 have previously been associated with human infections, reinforcing the zoonotic relevance of feline-associated *B. henselae* strains. While ST1 and ST5 are amongst the most frequently reported sequence types worldwide, ST2 appears to exhibit a more restricted geographic distribution. The successful genotyping of these isolates was achieved following BAPGM pre-enrichment culture and bacterial isolation, highlighting the importance of optimized methodologies for recovering viable *Bartonella* isolates from naturally infected cats.

Overall, molecular surveys have predominantly identified *B. henselae*, *B. clarridgeiae*, and *B. koehlerae* circulating among Brazilian cats, with the former representing the most frequently detected *Bartonella* species. Furthermore, studies combining serological, molecular, and enrichment culture methods have consistently demonstrated superior detection performance compared with PCR alone (Furquim et al., 2021; Dias et al., 2023; das Neves et al., 2025). The absence of complete agreement among diagnostic techniques, as observed by das Neves et al. (2025), reinforces the fastidious nature of *Bartonella* spp., as well as the occurrence of low, cyclic, or intermittent bacteremia in naturally infected cats. Together, these findings highlight the importance of combining complementary diagnostic approaches to improve the accuracy of epidemiological investigations involving feline bartonellosis.

Order Artiodactyla

Family Bovidae

The lineage II of *Bartonella* encompasses species strictly associated to ruminants and their associated hematophagous ectoparasites, such as *B. bovis*, *B. chomelii*, *B. capreoli*, *B. schoenbuchensis* and *B. melophagi* (Wagner & Dehio, 2019). In Brazil, a study performed in the states of Minas Gerais and Mato Grosso, reported the occurrence of *Bartonella* spp. in cattle (*Bos taurus indicus*) and buffaloes (*Bubalus bubalis*) and their associated ectoparasites (Gonçalves et al., 2020b). A total of 75 cattle and 101 buffaloes blood samples were submitted to a screening HRM (High Resolution Melting) qPCR targeting the 16S-23S ITS region and further molecular assays targeting the *ssrA*, *gltA* and *rpoB* genic regions for the detection and characterization of *Bartonella* spp. A total of 21/75 (28%) cattle and 1/101 (1%) buffalo blood samples were positive in the molecular assays. BLAST analyzes based on the four investigated loci, revealed 100% identity with *B. bovis*. Phylogenetic inferences clustered the obtained *gltA* and *rpoB* sequences in the same sub-clade as other *B. bovis* sequences from cattle from France, Malaysia, Thailand and Senegal, buffaloes (*Syncerus caffer*) from Mozambique and moose (*Alces alces*) from Sweden. Further genetic diversity analyses revealed the occurrence of six different *gltA* genotypes and seven different *rpoB* genotypes among the analyzed samples.

Bartonella spp. in wild animals from Brazil

Order Carnivora

Family Canidae

IgG antibodies to *Bartonella* spp. were detected in blood samples of captive wild canids in zoos from the states of São Paulo and Mato Grosso, southeastern and midwestern Brazil, respectively (Fleischman et al., 2015). Based on

IFA, IgG antibodies to *B. vinsonii* subsp. *berkhoffii*, *B. clarridgeiae*, *B. henselae* and *B. rochalimae* were detected in 11/97 (11.3%) of the sampled canids, including 5/39 (12.8%) crab-eating foxes (*Cerdocyon thous*), 3/27 (11.1%) bush dogs (*Speothos venaticus*), 2/23 (8.7%) maned wolves (*Chrysocyon brachyurus*) and 1/8 (12.5%) hoary fox (*Lycalopex vetulus*).

Recently, Calchi et al. (2025) compared digital PCR (dPCR) and qPCR for the detection of *Bartonella* spp. in wildlife samples from Brazil, demonstrating a substantially higher sensitivity of dPCR. Using dPCR, *Bartonella* spp. DNA was detected in 3/11 (27.3%) crab-eating foxes (*C. thous*), whereas only one sample was positive by qPCR.

Family Felidae

Blood samples of 57 captive neotropical felids (*Leopardus geoffroyi* n=1; *Leopardus wiedii* n=17; *Leopardus tigrinus* n=22; *Leopardus pardalis* n=14; *Puma yagouaroundi* n=3; and *Panthera onca* n=10) were evaluated for the presence of *Bartonella* spp. infections in a sanctuary located in the state of São Paulo (Guimarães et al., 2010). A total of 10/67 (14.9%) (3/22 [13.6%] *L. tigrinus*; 3/17 [17.6%] *L. wiedii*; 1/1 [100%] *L. geoffroyi*; 1/3 [33%] *P. yagouaroundi*; 1/14 [7.14%] *L. pardalis*; 1/10 [10%] *P. onca*) blood samples were positive for *Bartonella* spp. in a conventional (c) PCR based on the 16S-23S rRNA (ITS) intergenic region. The ten sequences obtained showed 100% similarity to *B. henselae*.

In the Pampa biome, Rio Grande do Sul state, southern Brazil, Souza et al. (2021) detected the presence of IgG antibodies to *Bartonella* spp. and bartonellae DNA in free-ranging wild felids. Blood samples were collected from a total of 53 free-ranging wild felids, including 39 *L. geoffroyi* and 14 *L. wiedii* and were submitted to IFA for the detection of IgG antibodies anti-*Bartonella* and cPCR assays (*ribC* and *gltA*) for the detection of bacterial DNA. Out of the 42 analyzed serum samples, 9/27 (33%) *L. geoffroyi* and 2/11 (18%) *L. wiedii* were seropositive for *Bartonella* spp. *B. henselae* DNA was detected in 2/39 (5.1%) of *L. geoffroyi* blood samples (Souza et al., 2021). Moreover, Calchi et al. (2025) reported 6/35 (17.1%) wild felids positive for *Bartonella* spp. by dPCR (16S-23S ITS genic region), including *L. pardalis* (1/12), *P. onca* (4/21), and *P. concolor* (1/2). Also, one *P. onca* sample tested positive by qPCR (16S-23S ITS genic region),

Family Procyonidae

A study performed in the state of Paraná, southern Brazil, investigated the occurrence of blood-borne parasites, including *Bartonella* spp., in free-living ring-tailed coatis (*Nasua nasua*) (Perles et al., 2023). A total of 12/49 (24.5%) blood samples were positive for *Bartonella* spp. in a qPCR assay targeting the *nuoG* gene and, out of those, *Bartonella* sp. sequences were obtained for the *pap-31*, *gltA* and *ftsZ* genic regions. BLAST analyses based on those molecular markers revealed an identity ranging between 99-100% with *Bartonella machadoae* previously isolated from wild rodents in Brazil. Phylogenetic inferences based on the *gltA* and *ftsZ* molecular markers clustered the obtained sequences in the same clade as *B. machadoae*.

Order Artiodactyla

Bartonella spp. infection in Neotropical deer from Brazil was recently reported by Calchi et al. (2025), when evaluating blood samples from free-ranging deer using both qPCR and dPCR assays for the 16S-23S ITS genic region, *Bartonella* DNA was detected by dPCR in 56/174 (32.2%) samples, whereas only 12 animals tested positive by qPCR, highlighting the substantially higher sensitivity of dPCR for detecting low-level *Bartonella* bacteremia. Positive animals included *Blastocercus dichotomus* (45/139), *Subulo gouazoubira* (6/22), *Ozotocercus bezoarticus* (3/6), and *Mazama juncunda* (2/4). These findings represent the first molecular evidence of *Bartonella* infection in deer from Brazil and suggest that the occurrence of this bacterium in deer populations may have been previously underestimated due to the limited sensitivity of conventional molecular assays. The study further reinforced the expanding host range of *Bartonella* spp. among free-ranging wildlife in Brazil and highlighted the usefulness of dPCR as a promising tool for epidemiological investigations in wildlife hosts.

Order Didelphimorphia

Family Didelphidae

Among marsupials from Brazil, *Bartonella* sp. was first reported in the Pantanal wetland, state of Mato Grosso do Sul (Amaral et al., 2022a). *Bartonella* spp. DNA was detected in blood samples (submitted to pre-enrichment liquid

BAPGM) from 4/8 (50%) marsupials (2/4 *Thylamys macrurus* and 2/4 *Monodelphis domestica*). Multilocus analysis based on distinct molecular markers (16S rRNA, *gltA*, *ftsZ*, *rpoB*, *groEL* and ITS) revealed a close identity to *B. machadoae* and *Bartonella* spp. previously detected in rodent-associated ectoparasites from Brazil. Based on Whole Genome Sequencing, phylogenomic inferences, biochemical and scanning electronic microscopy, a novel species, namely *Bartonella harrusi*, was described based on one isolate found on a specimen of *T. macrurus*.

More recently, *Bartonella* spp. were detected in blood samples of 2/45 (4.4%) *D. marsupialis* (common opossum) sampled in forested areas of the Maranhão state, northeastern Brazil (Braga et al., 2023). Although they were positive in the screening qPCR protocol based on the *nuoG* gene, those samples were negative in all cPCR protocols (*gltA*, *ftsZ*, *groEL*, *nuoG*, *pap31*, *ribC*, ITS), possibly due to the low number of DNA copies and precluding additional molecular characterization.

Chagas-de-Souza et al. (2025) investigated the occurrence of *Bartonella* sp. in blood samples of 27 different marsupials (*D. marsupialis* n = 16; *D. imperfecta* n = 1; *Marmosa murina* n = 7; *M. demerarae* n = 1; *Philander opossum* n = 2) captured in the Amazon Rainforest biome, northern region of Brazil. Only 1/27 (3.7%) sample (belonging to *D. marsupialis*) was positive for *Bartonella* sp. in a qPCR assay based on the *nuoG* gene. The sample was negative for *Bartonella* sp. in further molecular assays targeting the *gltA*, *rpoB*, *ribC*, *groEL* and the 16S-23S ITS genic regions, likely due to the low *Bartonella* DNA copy numbers in the sample.

Order Perissodactyla

Family Tapiridae

Bartonella DNA was detected in lowland tapirs (*Tapirus terrestris*) from Brazilian Cerrado and Pantanal biomes in the Mato Grosso do Sul state (Mongruel et al., 2023). A total of 8/99 (8%) blood samples were positive in qPCR for *Bartonella* spp. based on the *nuoG* gene; after molecular characterization, 5/99 (5%) *ribC* sequences clustered together with *B. henselae*.

Order Rodentia

Rodents act as the most critical and globally widespread natural reservoirs of *Bartonella* agents, exhibiting high infection rates and a remarkable genetic diversity across wild and synanthropic species (Yao et al., 2022). The persistent reservoir state (caused by the bacteria capability of maintaining a persistent intraerythrocytic bacteremia), associated with the presence of blood-feeding arthropods, such as fleas, presents a continuous spillover risk to other species and humans, especially in rural and urban areas where rodents and other animals cohabitate (Deng et al., 2012; Lei & Olival, 2014; Moreno Salas et al., 2019; Krügel et al., 2022). Furthermore, phylogenetic evidence suggests that while *Bartonella* originally spread from bats before jumping to other mammalian orders millions of years ago, the modern global dissemination of these strains was heavily accelerated by human shipping routes, with synanthropic rats (*Rattus* spp.) acting as highly mobile vehicles of spread into new ecosystems worldwide (Kosoy et al., 2012; McKee et al., 2021).

Among the *Bartonella* species that infect small mammals, *B. grahamii*, *B. elizabethae*, *B. tribocorum*, and *B. vinsonii* subsp. *arupensis* stand out as the most widely documented and important pathogens circulating globally within wild and synanthropic rodent populations (Buffet et al., 2013; Favacho et al., 2015; Jian et al., 2022). Those species show significant zoonotic potential, as they frequently cross the species barrier from their rodent reservoirs to humans, leading to serious public health concerns (Yao et al., 2022). These rodent-borne pathogens can induce severe clinical manifestations in humans, including neuroretinitis, bacteremia, and life-threatening culture-negative endocarditis (Favacho et al., 2015; Jian et al., 2022).

Family Cricetidae

A study conducted in five Brazilian biomes (Amazon Forest, Atlantic Forest, Caatinga, Cerrado, and Pantanal) analyzed spleen samples of 296 individual rodents, belonging to over 29 species of Cricetidae synanthropic rodents, collected in 15 different states (Gonçalves et al., 2016). A total of 105/296 (35.5%) were positive in a qPCR assay for the *nuoG* genic region (*Akodon montensis* [5/16], *Akodon* sp. [16/27], *Calomys cerqueirai* [1/3], *Delomys dorsalis* [4/9], *Euryoryzomys russatus* [6/12], *Holochilus* sp. [4/6], *Hylaeamys* sp. [6/9], *Juliomys* sp. [1/1], *Necomys lasiurus* [22/42], *Necomys rattus* [6/8], *N. squamipes* [4/6], *Oligoryzomys flavescens* [2/3], *O. nigripes* [4/26], *Oryzomys megacephalus* [1/2],

Oxymycterus dasytrichus [3/3], *Oxymycterus* sp. [3/3], *Rhipidomys macrurus* [2/3], *Rhipidomys* sp. [8/15], *Sooretamys angouya* [1/2]). Further molecular characterization based on obtained *gltA* sequences revealed the occurrence of 15 different genotypes and, along with *ftsZ* and *groEL* sequences, revealed a close relationship to the *B. vinsonii* complex.

A study conducted in the Cerrado biome from central-western Brazil (Mato Grosso do Sul state) detected *Bartonella* sp. in seven different species of rodents (Favacho et al., 2015). DNA was extracted from the heart tissue of 41 rodents (*Calomys callosus* n = 19; *N. lasiurus* n = 13; *Cerradomys maracajuensis* n = 4; *Oecomys catherinae* n = 2; *Oxymycterus delator* n = 1; *Nectomys aquanipes* n = 1; *O. megacephalus* n = 1) and submitted to PCR assays targeting the ITS locus and *gltA* genic region of *Bartonella* spp. Overall, 19/43 (46.3%) rodents were positive to *Bartonella* spp.: *Calomys callosus* (4/19; 21%), *N. lasiurus* (6/13; 46.1%), *C. maracajuensis* (4/4; 100%), *O. catherinae* (1/2; 50%), *O. delator* 1/1; 100%), *N. aquanipes* (1/1; 100%), and *O. megacephalus* (1/1; 100%). All the obtained *gltA* and ITS sequences showed 98% identity with *B. vinsonii* subsp. *arupensis*.

A study conducted in the Atlantic Forest biome of Rio de Janeiro, southeastern Brazil, investigated the occurrence of *Bartonella* spp. in free-ranging rodents captured in forest areas or near human dwellings across eight different municipalities (Rozental et al., 2017). Spleen samples were collected from a total of 102 individuals belonging to 15 different Cricetidae species: *Akodon cursor* (n = 32), *A. lindberghi* (n = 5), *A. montensis* (n = 3), *Bucepattersonius iheringi* (n = 1), *Calomys tener* (n = 1), *Delomys dorsalis* (n = 14), *Euryoryzomys russatus* (n = 7), *Necomys lasiurus* (n = 1), *Nectomys squamipes* (n = 5), *Oecomys catherinae* (n = 1), *Oligoryzomys flavescens* (n = 2), *O. nigripes* (n = 16), *Oxymycterus dasytrichus* (n = 12), *O. delator* (n = 1), and *Rhipidomys itoan* (n = 1). These samples were then submitted to molecular assays for the detection and characterization of *Bartonella* spp. based on different molecular markers (*gltA* and *rpoB*). A total of 23/102 (22.5%) spleen samples were positive for *Bartonella* spp.: 8/32 (26.8%) *A. cursor*; 2/3 (66.6%) *A. montensis*; 3/14 (21.4%) *D. dorsalis*; 6/7 (86%) *E. russatus*. 1/5 (20%) *N. squamipes*; 3/12 (25%) *O. dasytrichus*. Phylogenetic analyses of each genic region (*gltA* and *rpoB*) and concatenated phylogenetic analyses revealed that the sequences obtained in the study clustered together in a monophyletic clade, which was sister to the *B. vinsonii* complex clade. Another study conducted in the Atlantic Forest from the Rio de Janeiro State, also detected the occurrence of *Bartonella* spp. in free-ranging rodents from peri urban and rural areas (Gonçalves-Oliveira et al., 2020). A total of 86 rodents were sampled for spleen and liver: *A. cursor* (n = 44), *N. squamipes* (n = 27), *O. nigripes* (n = 6), *C. cerqueirai* (n = 4), *C. tener* (n = 3) and *O. dasytrichus* (n = 2). Out of those, a total of 8/86 (9.3%) individuals (5/44 [11.3%] *A. cursor* and 3/27 [11.1%] *N. squamipes*) were positive for *Bartonella* spp. using cPCR assays based on the *gltA* (7/8; 87.5%), *ftsZ* (8/8; 100%) and *groEL* (7/8; 87.5%) genic regions. Phylogenetic analyzes revealed the occurrence of new *Bartonella* genotypes in *A. cursor* and *N. squamipes*, as well as genotypes closely related to *B. rochalimae* and *B. vinsonii* complex and *Bartonella* sp. previously detected in rodents from Brazil.

In the Amazon Rainforest biome, in the states of Amapá and Pará, Chagas-de-Souza et al. (2025) detected *Bartonella* spp., through a qPCR based on the *nuoG* genic region, in a blood sample collected from a free-living *N. rattus*. Other blood samples from rodents analyzed in the study (*Mesomys hispidus* n = 4; *Mus musculus* n = 1; *N. rattus* n = 1; *O. bicolor* n = 1; *Proechimys guyannensis* n = 1) tested all negative for *Bartonella* spp.

Family Echimyidae

A total of 87 spleen samples, belonging to Echimyidae rodents (*Clyomys laticeps* n=8, *Proechimys gouldii* n=7, *P. gr. cuvieri* n=2, *P. roberti* n=2, *P. sp.* n=6, *Thrichomys apereoides* n=10, *T. fosteri* n=18, *T. inermis* n=7, *T. laurentius* n=20, *Thrichomys* sp. n=3, *Trinomys dimidiatus* n=1, *T. iheringi* n=3) sampled in eight Brazilian states across five different biomes (Gonçalves et al., 2016). Out of those, 11/87 (12.6%) (*T. apereoides* 1/10, *T. laurentius* 3/20 and *T. fosteri* 7/18) were positive in a qPCR based on the *nuoG* gene. Further molecular characterizations and phylogenetic analyzes based on three molecular markers (*gltA*, *ftsZ* and *groEL*) positioned the obtained sequences in the same sub-clade as *B. vinsonii* complex.

A study conducted in the Mato Grosso do Sul state detected the occurrence of *Bartonella* spp. in free-ranging rodents from Pantanal wetland areas (Sousa et al., 2018). A total of 102 spleen samples (*Thrichomys fosteri* n = 77; *Oligoryzomys marmora* n = 25) were submitted to a molecular screening using a qPCR based on the *nuoG* gene of *Bartonella* spp. and further assays based on different genic regions (*gltA*, *ftsZ*, *rpoB*, *ribC* and *nuoG*) for positive samples. A total of 35/102 (34.3%) rodents were positive for *Bartonella* spp., comprising 30/77 (38.9%) *T. fosteri* and 5/25 (20%) *O. marmora*. The obtained *Bartonella* sp. sequences were submitted to BLASTn analyzes: four *O. marmora* *gltA* sequences showed 96% identity with *Bartonella* sp. sequences previously detected in rodents from France; three *T. fosteri* and four *O. marmora* *ftsZ* sequences showed an identity of 91% and 94-96% to *B. vinsonii*

subsp. *berkhoffii* and *B. alsatica*, respectively; nine *T. fosteri nuoG* sequences showed 95-95% identity with *B. alsatica*. Phylogenetic inferences of the concatenated *gltA* and *ftsZ* genic regions positioned the obtained rodent sequences in a monophyletic clade, which was sister to the *B. vinsonii* complex clade. On the other hand, phylogenetic inferences of the concatenated *nuoG* and *ftsZ* genes positioned these sequences in a monophyletic clade, sister to a sub-clade containing *Bartonella* species from rodents: *B. acomydis*, *B. birtlesii*, and *B. pachyuromydis*.

Another study conducted in the Pantanal wetland, state of Mato Grosso do Sul, central-western Brazil, isolated a novel species, namely *B. machadoae*, from rodents captured in that area (Amaral et al., 2022b). Among Cricetidae rodents, a total of 83 individuals were sampled (n=79 [95.1%] *Thrichomys fosteri*; n= 4 [4.9%] *Clyomys laticeps*), with blood samples from 57 *T. fosteri* and 4 *C. laticeps* and spleen samples from 22 *T. fosteri*. *Bartonella* spp. DNA, detected through a qPCR based on the *nuoG* genic region, was detected in blood samples (submitted to pre-enrichment liquid BAPGM) from 5/83 (6%) of the samples, all belonging to *T. fosteri*. Multilocus analysis based on distinct molecular markers (16S rRNA, *gltA*, *ftsZ*, *rpoB*, *groEL* and ITS) revealed a close identity to *B. vinsonii* complex and *Bartonella* spp. previously detected in rodents and rodent-associated fleas from Brazil and Peru. Further Whole Genome Sequencing, phylogenomic, biochemical, and microscopical analyzes of an isolate obtained from a *T. fosteri* rodent's blood sample supported the description of *B. machadoae* (Amaral et al., 2022b).

In the Brazilian Cerrado, state of Mato Grosso, Anjos Pacheco et al. (2024) detected the occurrence of *Bartonella* sp. in a free-ranging rodent. Among the 83 rodent spleen samples analyzed (*Cerradomys* sp. n = 1; *Oecomys* sp. n = 1; *T. pachyurus* n = 80 and *T. karimii* n = 1), only one *T. pachyurus* (1/83; 1.2%) was positive for *Bartonella* sp. in a qPCR targeting the *nuoG* gene. The sample was negative for further characterization protocols, precluding additional phylogenetic inferences.

Family Muridae

Spleen samples from 43 Muridae rodents (*Rattus rattus* n=29 and *Mus musculus* n= 14), captured in the Amazon Rainforest, Atlantic Forest, Caatinga and Cerrado biomes, were analyzed for the presence of *Bartonella* spp. DNA. A single sample from a *Rattus rattus* specimen, captured in the state of Mato Grosso, Cerrado biome, was positive in a qPCR based on the *nuoG* gene. However, the authors did not obtain DNA sequences to further perform phylogenetic analyzes (Gonçalves et al., 2016). Another study involving 55 individuals of *R. rattus* was conducted in the state of Santa Catarina, southern Brazil (Gonçalves et al., 2020a). The spleen samples were analyzed for the occurrence of *Bartonella* spp. using a qPCR assay targeting the *nuoG* gene, in which 2/55 (3.6%) rats were positive for *Bartonella* spp. BLASTn analysis based on the ITS revealed that the sequences shared 99.6% identity to *B. coopersplainsensis*, while the analysis of the 16S rRNA sequence revealed identity of 100% with both *B. coopersplainsensis* and *Bartonella* sp. previously detected in a Muridae (*Rattus tanezumii*) from China.

A study conducted in an urban slum in the state of Bahia, northeastern Brazil, detected the occurrence of *Bartonella* in brown rats (*Rattus norvegicus*) (Costa et al., 2014). *Bartonella* spp. were isolated from 5/26 (19.2%) of the analyzed rats, through blood culture. Out of those, four *R. norvegicus* were infected with *B. queenslandensis* and only one was infected with *B. tribocorum*. A more recent study, conducted in an urban slum in the same locality, reinforced previous results by detecting the presence of *Bartonella* spp. in *R. norvegicus* (Zeppelini et al., 2023). DNA was extracted from blood clots of 79 individuals and submitted to a cPCR assay based on the *gltA* genic region for *Bartonella* spp. detection. A total of 9/79 (11.3%) samples were positive for *Bartonella* spp. All nine sequences showed 100% identity with a *Bartonella* sp. sequence previously detected in a brown rat (*R. norvegicus*) from USA, while six of them showed 99.5% identity to *B. queenslandensis* and the other three 99.7% to *B. tribocorum*.

Order Chiroptera

Chiropterans are highly specialized natural reservoirs for *Bartonella* spp., harboring diverse genotypes across more than 100 species of bats globally (Veikkolainen et al., 2014; Wang et al., 2025). Due to exclusive biological features, such as high-density colonial roosting and the unique ability to fly long distances, these mammals are recognized as the second main reservoir for *Bartonella* worldwide, surpassed only by rodents (André et al, 2023; Han et al., 2017). While many bat-associated genotypes are strictly host-specific, certain strains carry undeniable zoonotic importance; most notably, '*Candidatus Bartonella mayotimonensis*' (isolated from *Myotis* spp. bats) has been definitively identified as an emerging human pathogen capable of causing severe, culture-negative endocarditis (Veikkolainen et al., 2014). Likewise, '*Candidatus Bartonella rousetii*', a novel species isolated from *Rousettus aegyptiacus* bats and their associated Streblidae flies (*Eucampsipoda Africana*) from Nigeria, has also been

implicated as a zoonotic agent. This conclusion is supported by the detection of antibodies against '*Candidatus Bartonella rousetii*' in humans living near caves inhabited by these bats, suggesting spillover exposure from the bat reservoir (Bai et al., 2018).

In the Brazilian states of Paraná, Pará, and Tocantins, Ikeda et al. (2017) detected *Bartonella* DNA in 17/322 (5.28%) biological samples (blood, spleen, liver, and heart tissues) collected from Neotropical bats using a qPCR assay targeting the *nuoG* gene. Positive samples were obtained from *Sturnira lilium* (4/24; 16.7%), *Carollia perspicillata* (6/31; 19.4%), *Glossophaga soricina* (5/25; 20.0%), *Phyllostomus discolor* (1/1; 100%), and *Natalus espirotosantensis* (1/1; 100%). Phylogenetic analyses based on *gltA*, *nuoG*, *rpoB*, *ftsZ*, and 16S rRNA positioned the sequences obtained in the same sub-clade as other *Bartonella* sequences derived from New World bats. The authors also observed that when present, *Bartonella* sequences obtained from Old World bats clustered separately from the obtained sequences. Subsequently, Ikeda et al. (2020) evaluated the genetic diversity of *Bartonella* spp. in non-hematophagous bats in the state of Mato Grosso do Sul. The qPCR assay targeting the *nuoG* gene revealed positivity rates of 13.5% (18/133) in bat blood samples, represented by *Platyrrhinus lineatus* (12/78; 15.4%), *Artibeus planirostris* (3/22; 13.6%), *Artibeus lituratus* (2/25; 8.0%), and *Carollia perspicillata* (1/8; 12.5%). In that study, at least two distinct *Bartonella* genotypes were identified in each bat blood sample, with a total of 13 genotypes occurring for the *gltA* genic region, revealing a high diversity among bat hosts. Additionally, a higher diversity of *gltA* sequences was observed in bat blood samples compared to those obtained from their associated bat flies. Phylogenetic analyzes based on different molecular markers (*gltA*, *rpoB*, *nuoG* and *ftsZ*) clustered each of the genotypes on their own sub-clades, with the sequences obtained in the study being phylogenetically close to *Bartonella* sp. previously detected in bats (hematophagous and non-hematophagous) and their associated ectoparasites (flies) from Brazil, Guatemala, Peru, Thailand and USA and other *Bartonella* species previously detected in rodents.

Ferreira et al. (2018) investigated the occurrence of *Bartonella* spp. in 119 spleen samples from 21 species of bats captured in three regions of the Brazilian Atlantic Forest, in the states of Rio de Janeiro, Bahia, and Santa Catarina. *Bartonella* spp. DNA was detected in 22 (18.5%) of the bats analyzed (5/34 [14.7%] *C. perspicillata*; 1/7 [14.2%] *Rhinophylla pumilio*; 6/15 [40%] *D. rotundus*; 1/4 [25%] *P. discolor*; 1/7 [14.2%] *A. fimbriatus*; 1/14 [7.1%] *A. lituratus* 1/2 [50%] *A. obscurus*). Phylogenetic analysis based on the *gltA* gene identified at least two independent clusters, indicating the occurrence of novel *Bartonella* genotypes. One of the sub-clades (containing sequences from *A. fimbriatus*, *A. obscurus*, *P. discolor* and *S. lilium*) was closely related to *Bartonella* sp. sequences previously detected in non-hematophagous bats from Costa Rica, forming a sister clade to the ruminant-associated *Bartonella* spp., while the other sub-clade (containing sequences from *C. perspicillata*, *D. rotundus* and *S. lilium*) was closely related to *Bartonella* sp. sequences previously detected in rodents.

Bartonella DNA was detected in 51 (24.51%) liver samples of 208 vampire bats sampled across 15 Brazilian states, by qPCR targeting the 16S–23S rRNA intergenic spacer (ITS). Positive samples included 40 (78.4%) samples from *Desmodus rotundus* and 11 (21.6%) from *Diphylla ecaudata*. The ITS sequences obtained showed 80%–96% identity with *B. bacilliformis* and *B. ancashensis*. Genotype analysis based on the *gltA* and *rpoB* genic regions revealed the occurrence of 11 different genotypes (for each genic region) among hematophagous bats. Phylogenetic inference based on the *gltA* gene positioned the sequences into six distinct clades, which were related to *Bartonella* genotypes previously detected in *D. rotundus* and in bat-associated flies in Latin America (André et al., 2019b). Phylogenetic analyzes based on the *rpoB* gene clustered all the obtained sequences in the same sub-clade, with specific branches for each genotype detected, closely related to the ruminant-associated *Bartonella* lineage.

Gonçalves-Oliveira et al. (2020) collected 110 spleen samples from bats in the state of Rio de Janeiro, of which 4/110 (3.6%) were positive for *Bartonella* spp., using cPCR assays for the *gltA*, *ftsZ* and *groEL* genes, including *Artibeus lituratus* (3/58; 5.17%) and *Carollia perspicillata* (1/15; 6.67%). Phylogenetic inference based on the *ftsZ* gene positioned the sequences obtained from bats into three distinct clades, which clustered with *Bartonella* genotypes previously described in bats and their ectoparasites, as well as with lineages detected in Neotropical rodents, suggesting possible evolutionary and/or ecological sharing among these hosts. In addition, *groEL* and *ftsZ* genotypes of *Bartonella* detected in *C. perspicillata* indicated the presence of novel variants of the agent in the sampled bats.

Bernal et al. (2022) investigated the occurrence of *Bartonella* spp. in bats from the Atlantic Forest biome in the state of São Paulo, analyzing 341 liver samples from 12 Neotropical species belonging to the families Phyllostomidae (n = 224; 65.7%), Molossidae (n = 85; 24.9%), and Vespertilionidae (n = 32; 9.4%). Molecular analyses revealed 2 (0.6%) samples positive for the *gltA* gene, both belonging to *Glossophaga soricina* from the municipality of São Roque. The obtained sequences clustered phylogenetically with *Bartonella* spp. genotypes previously described in *G. soricina* from the Cerrado biome in the state of Tocantins (Ikeda et al., 2017).

André et al. (2023) characterized the bacterial microbiome of non-hematophagous bats, in the state of Mato Grosso do Sul, central-western Brazil. Oral and rectal swabs from 30 bats (13/30 [43.3%] *A. lituratus*, 9/30 [30%] *A. planirostris*, 5/30 [16.6%] *Eptesicus furinalis*, 2/30 [6.6%] *C. perspicillata*, and 1/30 [3.3%] *P. lineatus*) were analyzed. Among them, only two bat swabs, one rectal and one oral (from *E. furinalis*), had the presence of *Bartonella* spp. Despite the associated ectoparasites (Streblidae flies) having a higher abundance of *Bartonella* spp. in their microbiome (77%), the low occurrence in bats can be associated with the type of sample analyzed, which does not reflect the intraerythrocytic behavior of *Bartonella* species, which are more prevalent in blood-related samples.

Franco et al. (2024) investigated the presence of *Bartonella* spp. in spleen samples from bats belonging to 30 species from the Amazon biome in the state of Acre. Of the 208 samples submitted to qPCR targeting the *nuoG* gene, 21/208 (10.1%) were positive for *Bartonella* spp., including 14/69 (20.3%) *C. perspicillata*, 3/54 (5.6%) *A. planirostris*, 1/9 (11.1%) *P. elongatus*, and 1/3 (33.3%) *L. silvicolium*. Phylogenetic analyses of the two *gltA* genotypes obtained showed that they clustered with *Bartonella* genotypes previously detected in bats from other regions of Brazil.

Anjos Pacheco et al. (2024) investigated the presence of *Bartonella* spp. DNA in 139 bats from central-western Brazil, of which 23 (16.54%) tested positive by qPCR targeting the *nuoG* gene, including *Artibeus lituratus* (9/49; 18.37%), *Carollia perspicillata* (6/32; 18.75%), *Glossophaga soricina* (4/21; 19.05%), *Phyllostomus discolor* (2/18; 11.11%), and *Lophostoma silvicolium* (2/19; 10.53%). Phylogenetic analyses based on the *gltA* and *ftsZ* genes positioned the *Bartonella* sequences detected in bats with genotypes previously reported in other bat species and bat-associated flies in Brazil and in other countries of Latin America and Georgia. In addition, the *rpoB* sequence detected in *L. silvicolium* clustered with a *Bartonella* sp. sequence detected in *Noctilio albiventris* from French Guiana.

In the study by Franco et al. (2025), the occurrence and genetic diversity of *Bartonella* spp. were investigated in vampire bats, with emphasis on *Desmodus rotundus*, in the Brazilian Amazon, sampled in the states of Amapá, Amazonas, Pará and Roraima, northern region of Brazil. Molecular screening by qPCR targeting the *nuoG* gene identified positive samples in 73/228 (31.9%) of the analyzed bat spleens. Characterization using the *gltA* and *rpoB* genes revealed high genetic diversity, with the samples distributed in six and 11 genotypes, respectively. Phylogenetic inferences demonstrated the presence of multiple genotypes, some of which clustered with lineages previously described in bats from different regions, while others formed distinct groups, suggesting possible local ecological structuring. Later, *Bartonella* spp. DNA was detected by dPCR in 46/51 (90.2%) samples from vampire bats (*D. rotundus*), whereas qPCR detected positivity in only 17/51 (33.3%) samples, highlighting the superior sensitivity of dPCR for *Bartonella* detection in wildlife samples (Calchi et al., 2025).

Recently, Barbier et al. (2026) investigated the occurrence, genetic diversity, and ecological drivers of *Bartonella* spp. infection in cave-dwelling bats from northeastern Brazil. Of the 203 blood samples screened for *Bartonella* spp. using a qPCR assay targeting the 16S–23S ITS region, 113/203 (55.7%) were positive. Positivity rates varied among bat species, with 101/160 (63.1%) in *P. gymnonotus*, 10/17 (58.8%) in *D. rotundus*, 8/15 (53.3%) in *G. soricina*, 2/4 (50.0%) in *N. macrourus*, 8/17 (47.1%) in *C. perspicillata*, and 2/5 (40.0%) in *P. personatus*, whereas no positive individuals were detected in *A. geoffroyi* (0/10) or *L. aurita* (0/4). Molecular characterization based on the *ftsZ*, *gltA*, *ribC*, and *rpoB* genes revealed high genetic diversity, including 12 *ftsZ* genotypes, 17 short-fragment *gltA* genotypes, and 19 large-fragment *gltA* genotypes. Most sequences showed highest similarity to *Bartonella* genotypes previously reported in bats and bat-associated ectoparasites from Neotropical regions, and phylogenetic analyses clustered the majority of the obtained sequences within bat-associated *Bartonella* clades. The detected genotypes detected in bats (and associated Streblidae flies) belonging to the same family tended to group together. Some *ftsZ* genotypes were phylogenetically related to ruminant-associated *Bartonella* lineages, reinforcing previous observations suggesting an evolutionary relationship between bat-associated *Bartonella* and strains infecting other mammalian hosts. The study also demonstrated broad spatial circulation of *Bartonella* genotypes among caves and bat species, with several genotypes shared across geographically distant roosts.

Superorder Xenarthra

Few studies have been performed regarding the molecular occurrence of *Bartonella* spp. in xenarthran mammals (armadillos, anteaters and sloths) worldwide. In Brazil, a study performed by Calchi et al. (2020), detected the occurrence of a putative novel *Bartonella* species in xenarthrans sampled in different states of Brazil. The authors analyzed a total of 330 mammalian samples: 96 spleen samples from anteaters (*Myrmecophaga tridactyla* n = 53; *Tamandua tetradactyla* n = 23) and armadillos (*Euphractus sexlineatus* n = 8; *Dasypus novemcinctus* n = 9; *Cabassous unicinctus* n = 2; *Priodontes maximus* n = 1) collected in the states of Mato Grosso do Sul and São Paulo, plus 242 blood samples from sloths (*Bradypus variegatus* n = 194; *Choloepus* sp. n = 31; *Choloepus didactylus* n = 5; *Bradypus* sp. n = 3),

anteaters (*T. tetradactyla* n = 7) and armadillos (*D. novemcinctus* n = 1; *C. unincinctus* n = 1) from the states of Pará and Rondônia, northern Brazil. The DNA obtained from the samples was submitted to a qPCR based on the *nuoG* genic region of *Bartonella* spp., and five samples (5/338; 1.5%) came out positive: four *E. sextinctus* spleen samples from Mato Grosso do Sul and one *T. tetradactyla* blood sample from Pará. Using different molecular markers (*gltA*, *ftsZ* and *rpoB*) the BLAST analyzes revealed 93-100% identicalness with *B. washoensis* previously detected in a ground squirrel (*Spermophilus dauricus*) from Japan. Phylogenetic inferences based on the *gltA* and *ftsZ* genes positioned the obtained sequences in a monophyletic clade, closely related to *B. washoensis* previously detected in humans and Prairie dogs (*Cynomys lucavana*) from USA and *S. dauricus* from Japan. Furthermore, based on genotypic analyses that revealed the occurrence of genotypes exclusive to xenarthrans and to Brazil, the authors proposed that the detected organism represented a novel *Candidatus* taxon, which they named '*Candidatus* Bartonella washoensis subsp. brasiliensis'.

A more recent study conducted in the states of Mato Grosso do Sul and São Paulo also investigated the molecular occurrence of *Bartonella* spp. in xenarthrans (Sada et al., 2024). A total of 167 biological samples (139 blood and 28 spleen) from armadillos (*E. sextinctus* n = 48; *P. maximus* n = 29; *D. novemcinctus* n = 4; *C. tatouay* n = 1) and anteaters (*M. tridactyla* n = 79; *T. tetradactyla* n = 6) were submitted to a qPCR targeting the 16S-23S intergenic spacer region of *Bartonella* spp. A total of 58/167 (34.7%) samples were positive in the screening assay: 23/48 (47.9%) *E. sextinctus*; ¼ (25%) *D. novemcinctus*; 9/29 (31%) *P. maximus*; 21/77 (27.3%) *M. tridactyla*; 3/6 (50%) *T. tetradactyla*. Phylogenetic inferences based on the *ftsZ* mgene positioned the sequences obtained from *E. sextinctus* in the same sub-clade as '*Candidatus* Bartonella washoensis subsp. brasiliensis' previously detected in *E. sextinctus* from Mato Grosso do Sul, reinforcing the occurrence of a novel *Bartonella* species in Xenarthra mammals from Brazil.

Another study detected *Bartonella* spp. DNA by both dPCR and qPCR in 6/44 (13.6%) xenarthran samples. Positive animals included *T. tetradactyla* (1/9), *E. sextinctus* (3/5), and *D. novemcinctus* (2/7) (Calchi et al., 2025).

Order Passeriformes

Although the main hosts of *Bartonella* comprises mammals, there are a few studies worldwide and in Brazil that sought to investigate the occurrence of these bacteria in birds. The first study to detect the presence of *Bartonella* spp. in wild birds in Brazil was conducted in the Pantanal biome, in the states of Mato Grosso and Mato Grosso do Sul (Alabí Córdova et al., 2024). The authors collected and extracted DNA from a total of 500 blood samples, belonging to 13 different orders of birds, and submitted them to a qPCR assay based on the *nuoG* genic region, which resulted in a total of 19/500 (3.8%) positive samples (*Cantorchilus leucotis* n = 1/5 [20%]; *Chloroceryle americana* n = 1/5 [20%]; *Formicivora rufa* n = 1/1 [100%]; *Furnarius leucopus* n = 1/10 [10%]; *Furnarius rufus* n = 1/16 [6.2%]; *Hemitriccus striaticollis* n = 1/5 [20%]; *Leptotila verreauxi* n = 1/10 [10%]; *Paroaria capitata* n = 2/26 [7.7%]; *Progne tapera* n = 1/2 [50%]; *Ramphocelus carbo* n = 6/108 [5.5%]; *Thamnophilus doliatus* n = 1/1 [100%]; *Tyrannus melancholicus* n = 2/5 [40%]). The positivity was later confirmed by a qPCR based on the 16S-23S genic region, resulting in a total of 12/19 (63.15%) positive samples. The authors obtained DNA sequences for four genic regions: 16S rRNA (*Formicivora rufa*) which showed 100% identity with *B. machadoae*; *nuoG* (*Progne tapera*) which showed 100% identity with *B. henselae*; *ribC* (*Furnarius rufus*, *Paroaria capitata* and *Progne tapera*) that showed 100% identity with *B. henselae*; ITS (*P. capitata*, *Thamnophilus doliatus* and *Tyrannus melancholicus*) which showed 97.6-98.8% identity with *B. machadoae* and 98.8-99.5% identity with *B. henselae*. Another study also conducted in the Pantanal, state of Mato Grosso do Sul, detected *Bartonella* spp. in a single blood sample (1/275; 0.36%) from a *F. rufa* through a high-throughput microfluidic real-time PCR based on the *ssrA* genic region (Alabí Córdova et al., 2025).

Calchi et al. (2025) performed a new study, using the same samples collected by Alabí Córdova et al. (2024), in which they tested 18 bird samples for *Bartonella* using a dPCR based on the 16S rRNA genic region. A total of 4/18 (22.2%) samples were positive for *Bartonella* sp.: *Saltator coerulescens* n = 2; *Turdus leucomelas* n = 1; *Cyamocorax chrysops* n = 1. The study demonstrated that dPCR had a much higher sensitivity when compared to qPCR assays targeting the *nuoG* gene of *Bartonella* spp.

Order Anseriformes

Blood samples collected from ducks in São Paulo State revealed a remarkably high molecular occurrence, with *Bartonella* DNA detected in 9/10 (90%) animals by nested PCR targeting the *ftsZ* gene. Sequencing of representative amplicons showed 100% nucleotide identity with *B. henselae* strain Houston-1. Duck blood samples were also subjected to liquid enrichment and solid culture for the isolation of *Bartonella* spp.; however, no viable bacteria were

recovered. Although the detection of bacterial DNA alone does not confirm active infection or reservoir competence, the authors suggested that Muscovy ducks may participate in an ecological interface involving hematophagous arthropods, domestic animals, and wildlife, highlighting the need for further investigations into the epidemiological role of avian hosts in the maintenance of *Bartonella* spp. (Santos et al., 2026).

***Bartonella* spp. in exotic animals in Brazil**

Order Sphenisciformes

Family Spheniscidae

A study conducted in the southern, state of Santa Catarina, and southeastern, state of São Paulo, coast of Brazil, detected the presence of *Bartonella* DNA in rescued Procellariiformes and Sphenisciformes birds (Lee et al., 2025). A total of 52 blood samples belonging to 12 different species of Procellariiformes and 200 blood and spleen samples (164 spleen, 24 blood and 6 for both) from individual *Spheniscus magellanicus* penguins were submitted to a molecular screening for *Bartonella* spp. using a qPCR based on a 243-bp fragment of the 16S-23S ribosomal DNA internal transcribed spacer (ITS). Among the 56/252 (22.2%) positive samples, 5/56 (8.9%) were represented by blood samples of Procellariiformes (*Thalassarche melanophoris* n=3 and *Thalassarche chlororhynchos* n=2) and 51/56 (91.1%) were *S. magellanicus* samples (including 42 spleen and 9 blood samples). In the molecular characterization, the authors obtained DNA sequences from eight Magellanic penguins: seven *nuoG* sequences, five 16S-23S (ITS) sequences and one *rpoB* sequence. The sequences obtained in the study (*nuoG*, ITS and *rpoB*) showed an identity of 100% with *B. henselae* sequences previously detected in humans from Switzerland, South Korea and USA and Passeriformes-associated ticks (*Hyalomma marginatum*, *H. concinna*, *Ixodes ricinus* and *I. frontalis*) from Turkey. Phylogenetic inferences based on the *nuoG* gene positioned the obtained sequences in the same sub-clade as *Bartonella* sp. previously detected in Passeriformes and mongooses (*Urva aropunctuata*) and *B. henselae* previously detected in Passeriformes-associated *Ixodes frontalis* ticks and *Dermanyssus galinae* mites from Turkey. For the 16S-23S (ITS), the obtained sequences were phylogenetically positioned in the same sub-clade as *Bartonella* sp. previously detected in mongooses and cats and *B. henselae* previously detected in humans and cats.

***Bartonella* spp. in ectoparasites from Brazil**

Order Diptera

Suborder Nematocera

Family Ceratopogonidae

A study conducted in the Brazilian Amazon Rainforest (state of Pará) investigated the presence of *Bartonella* DNA in 299 specimens, namely *Culicoides hylas* (192/299, 64.2%), *C. foxi* (88/299, 29.4%), and *C. leopoldoi* (19/299, 6.3%) (Arantes et al., 2025a). Overall, 72/299 (24%) tested positive in a qPCR for *Bartonella* spp. based on the 16S-23S rRNA intergenic spacer region, including 37/88 (42%) *C. foxi*, 29/192 (15.1%) *C. hylas*, and 6/19 (31.6%) *C. leopoldoi*. The *gltA* sequences obtained from both *C. hylas* and *C. foxi* showed an identity of 99.7-100% with *B. bovis* while the *pap31* sequences obtained from both species showed an identity of 88.5-90.7% with *Bartonella* sp. previously detected in non-hematophagous bats (*Carollia perspicillata*) from Brazil. One *ribC* sequence obtained from a *C. foxi* specimen showed an identity of 100% with *B. henselae*. Phylogenetic inferences positioned the *gltA* sequences within a sub-clade containing *B. bovis* sequences and within the same sub-clade as *Bartonella* species that infect ruminants and their associated ectoparasites (*B. chomellii*, *B. melophagi*, *B. capreoli*, *B. schoenbuchensis*). Phylogenetic inferences positioned the single *ribC* sequence in the same sub-clade as *B. henselae*, *B. koehlerae* and *B. quintana*.

Family Psychodidae

Lee et al. (2024) analyzed 634 phlebotomine specimens, belonging to 44 different species, captured in different states from the North and Northeastern regions of Brazil. A total of 55/634 (8.7%) specimens were positive for *Bartonella* spp. in

a screening qPCR based on the 16S-23S rRNA region: 48 from Acre (*Nyssomyia antunesi* [n = 18/76; 23.6%], *Evandromyia walkeri* [n = 7/43; 16.2%], *Trichophoromyia* sp. [n = 5/40; 12.5%], *L. sherlocki* [n = 4/19; 21%], *Nyssomyia shawi* [n = 3/15; 20%]; *Psychodopygus llanosmartinsi* [n = 2/11; 18.1%]; *Psychodopygus davis* [n = 2/30; 6.6%]; *Bichromomyia flaviscutellata* [n = 1/4; 25%]; *Evandromyia saulensis* [n = 1/14; 7.1%]; *Nyssomyia* sp. [n = 1/1; 100%]; *N. whitmani* [n = 1/12; 8.3%]; *P. nevesi* [n = 1/5; 20%]; *Pintomyia serrana* [n = 1/6; 16.6%]; *Viannamyia furcata* [n = 1/2; 50%]; 2 from Alagoas (*Trichophoromyia viannamartinsi* [n = 2/65; 3%]; 2 from Roraima (*Psychodopygus squamiventris* [n = 1/1; 100%]; *Psychodopygus ayrozai* [n = 1/40; 2.5%]); 1 from Bahia (*Trichopygomyia longispina* [n = 1/55; 1.8%]); 1 from Ceará (*Lutzomyia longipalpis* [n = 1/27; 3.7%]); and 1 from Pará (*Psychodopygus paraensis* [n = 1/17; 5.9%]). BLASTn analyzes revealed an identity of >96% between a *gltA* sequence obtained from a *L. longipalpis* with *B. ancashensis* sequences previously detected in humans and 94-94.7% between a *nuoG* sequence obtained from a *N. antunesi* and *Bartonella* sp. sequences previously detected in *Pteronotus davis* bats from Guatemala. Phylogenetic analyzes positioned the obtained *gltA* sequence from a *L. longipalpis* in the same sub-clade as *B. ancashensis* sequences previously detected in humans from Peru and a sand fly (*Dampfomyia beltrani*) from Mexico.

Another study performed in the Amazon Rainforest biome investigated the presence of *Bartonella* sp. DNA in 297 sand flies from 25 different species in the state of Pará (Arantes et al., 2025b). Out of the 253 analyzed specimens, 32/253 (12.6%) were positive in a screening qPCR based on the 16S-23S rRNA genic region: 7/32 (21.87%) *Psychodopygus* series Chagasi, 5/32 (15.62%) *Psychodopygus* series Guyanensis, 3/32 (9.3%) *Psychodopygus carrerai*, 4/32 (12.5%) *Psychodopygus ayrozai*, 2/32 (6.25%) *Psychodopygus paraensis*, 2/32 (6.25%) *Psychodopygus davis*, 1/32 (3.12%) *Psychodopygus bispinosus*, 1/32 (3.12%) *Psychodopygus llanosmartinsi*, 1/32 (3.12%) *Psychodopygus amazonensis*, 2/32 (6.25%) *Nyssomyia richardwardi*, 1/32 (3.12%) *Nyssomyia shawi*, 1/32 (3.12%) *Nyssomyia anduzei*, 1/32 (3.12%) *Trichophoromyia* sp., and 1/32 (3.12%) *Trichopygomyia* sp. BLASTn analyzes revealed that two 16S-23S rRNA sequences (detected in *P. series* Guyanensis and *N. anduzei*) had an identity of 98.5% and 98.7% with *Bartonella* sp. previously detected in bats (*Miniopterus schreibersii* and *Myotis emarginatus*) from Georgia; two *gltA* sequences (*P. llanosmartinsi* and *P. series* Chagasi) had an identity of 90.9% and 93.4% with *B. bovis* and *Bartonella* sp. sequences previously detected in Brazilian cattle and a *H. quadripertusus* lice from Israel; two *nuoG* sequences (*Trychophoromyia* sp. and *P. davis*) had an identity of 94% and 93.1% with *B. bacilliformis*; one *pap-31* sequence (*P. series* Guyanensis) had an identity of 91% with *Bartonella* sp. previously detected in bats (*C. perspicillata*) from Brazil. Phylogenetic inferences based on the *gltA* gene clustered the two sequences (detected in *P. series* chagasi and *P. llanosmartinsi*) in the same sub-clade as *B. bacilliformis* and *Bartonella* sp. previously detected in sand flies (*Brumptomyia mesai* and *Psathyromyia shannoni*) from Mexico, which was a sister clade to the *B. ancashensis* and *Bartonella* sp. previously detected in Brazilian sand flies (Lee et al., 2024) sub-clade.

Subordem Brachycera – Infraordem Muscomorpha

Family Hippoboscidae

A study conducted in the southern region of Brazil, in the Pampa biome of the Rio Grande do Sul state, molecularly detected and characterized *Bartonella* spp. in louse flies (Souza et al., 2017). The authors collected a total of 429 adult *Lipoptena mazamae* flies from 11 road-killed gray brocket deer (*Mazama gouazoubira*). All the collected flies (429/429; 100%) were positive in a cPCR targeting the *ribC* genic region and the same *Bartonella* sp. sequence was detected among the positive samples. Phylogenetic inferences positioned the obtained genotype together with *Bartonella* sp. previously detected in *Neolipoptena* sp. flies from USA. Although the role of deer keds in the transmission of *Bartonella* is not yet elucidated, the occurrence of genotypes in deer and associated flies reinforces the importance of these infections, since species from the same lineage (ruminant-lineage or lineage 2) are known to have pathogenic potential.

Family Streblidae

A total of 202 Streblidae flies belonging to eight different species were collected from five different species of non-hematophagous bats (*Artibeus fimbriatus*, *A. lituratus*, *A. obscurus*, *C. perspicillata* and *Sturnia lilium*) in the state of Rio de Janeiro, southeastern Brazil, and submitted to a qPCR based on the *nuoG* gene. As a result, 40/202 [19.8%] were positive for *Bartonella* spp.: 6/32 (18%) *Paratrachobius longicrus*, 7/24 (29%) *Strebla guajiro*, 2/5 (40%) *Aspidoptera phyllostomatis*, 5/43 (11%) *Aspidoptera falcata*, 1/10 (10%) *Trichobius anducei*, 1/4 (25%) *Megistopoda aranea*, 18/55 (32%) *Trichobius joblingi* and 0/29 (0%) *Megistopoda proxima*. A total of six sequences were obtained: two *nuoG*

sequences (*S. guajiro* and *M. aranea*), two *gltA* (*S. guajiro*), one *ribC* (*S. guajiro*) and one *rpoB* (*S. guajiro*). The obtained *gltA* sequences were phylogenetically related to *Bartonella* sp. sequences previously detected in a *Trichobius* sp. fly from Dominican Republic and bats from Mexico, Brazil and Costa Rica; the *nuoG* sequences clustered together in a single clade; the *rpoB* sequence was phylogenetically related to *Bartonella* sp. previously detected in a bat from Brazil; the *ribC* sequence was phylogenetically close to *B. taylorii* (Amaral et al., 2018).

In the state of Maranhão, northeastern Brazil, *Bartonella* genotypes, phylogenetically related to *Bartonella* sp. previously detected in bats and/or bat flies from Costa Rica and Brazil, were detected in Streblidae flies (Braga et al., 2020). The genotypes were detected in *Trichobius* spp. flies, which were positive for *Bartonella* in a screening qPCR for the *nuoG* gene (3/15, 20%). The *gltA* sequences positioned in the same sub clade as *Bartonella* sp. sequences previously detected in a non-hematophagous bat (*C. perspicillata*) and Streblidae flies (*Glossophaga soricina* and *Speiseria ambigua*) from Costa Rica and *Desmodus rotundus* bats from Brazil. Similarly, the obtained *rpoB* sequence was phylogenetically close to *Bartonella* sp. sequences previously detected in *D. rotundus* from Brazil.

In the state of Mato Grosso, bat-associated flies were also investigated for the presence of *Bartonella* DNA (Ikeda et al., 2020). A total of 11/64 (17.1%) Streblidae flies (6/10 *Trichobius dugesii* complex; 4/29 *T. costalimai*; 1/18 *M. aranea*), collected from *Artibeus lituratus*, *A. planirostris*, *Platyrrhinus lineatus*, *Glossophaga soricina*, *Eptesicus furinalis*, *Molossus molossus*, *M. temminckii*, *Phyllostomus discolor* and *Carollia perspicillata* bats, were positive for *Bartonella* spp. in qPCR assays based on the *nuoG* gene. This study reinforced the importance of bats and their associated ectoparasites in the maintenance of *Bartonella* sp. in wild environments, by showing a high genotypic diversity (13 different genotypes) among the *gltA* sequences obtained in the ectoparasites and blood samples of the bats. Phylogenetic inferences using this molecular marker revealed that each genotype clustered within a single sub-clade, with some of them being close to each other and to *Bartonella* sp. sequences previously detected in non-hematophagous (*Platyrrhinus lineatus*, *Sturnira lilium*, *Carollia perspicillata*, *Diphylla ecaudata*) and hematophagous (*Desmodus rotundus*) bats and associated flies (*Strebla guajiro*) from Brazil. Genotypic and phylogenetic analyzes of the *nuoG*, *rpoB* and *ftsZ* molecular markers also revealed the occurrence of different genotypes (eight, five and three, respectively), reinforcing the broad genetic diversity of *Bartonella* among bats and their associated hematophagous ectoparasites.

In the Brazilian Amazon Rainforest, state of Pará, Streblidae flies were collected from bat carcasses and investigated for the occurrence of *Bartonella* spp. (Franco et al., 2024). Among the total of 142 flies (118 *Trichobius parasiticus* and 23 *Strebla wiedemanni* collected from *Desmodus rotundus* and 1 *Trichobius diaemi* collected from *Diaemus youngii*), 90/142 (63.4%) were submitted to a screening qPCR based on the *nuoG* gene of *Bartonella* spp., in which 45/90 (50%) were positive. Positivity rates for *Bartonella* spp. of 8/23 (34.8%) were obtained for *S. wiedemanni*, 36/118 (30.5%) for *T. parasiticus* and 1/1 (100%) for *T. diaemi*. Phylogenetic inferences based on the *gltA* and *rpoB* genic regions revealed that the sequences obtained in Streblidae flies were closely related to *Bartonella* sp. sequences previously detected in *D. rotundus* bats from Belize, Mexico, Guatemala and Peru.

Similarly, a more recent study revealed high genotypic diversity among Streblidae bat flies from the Amazon Rainforest biome, in streblid fly species associated with cave-dwelling bats (Lopes et al., 2026). The study analyzed Streblidae specimens collected from non-hematophagous bats (21 species) captured in caves and remnants of humid forest in the states of Pernambuco (northeastern Brazil, Caatinga biome) and Pará (northern Brazil, Amazon Rainforest biome). Using a qPCR assay based on the intergenic 16S-23S ITS region of *Bartonella* sp., the authors detected a total of 45/120 (37.5%) positive specimens (25/56 *T. joblingi*, 11/22 *M. proxima*, 5/8 *A. falcata*, 2/10 *Trichobius longipes*, 1/10 *Trichobius tiptoni*, and 1/11 *P. longicrus*), which did not retrieve any sequences for further characterization protocols. On the other hand, a total of 144/565 (25.4%) flies, collected from cave dwelling bats from the state of Pará, were qPCR positive for *Bartonella* spp.: 3/10 *Exastinions clovisi*, 2/2 *M. minuta*, 1/3 *Nycterophilina fairchildi*, 47/173 *Nycterophilina parnelli*, 2/5 *S. ambigua*, 1/1 *S. guajiro*, 39/157 *Trichobius caecus*, 1/2 *Trichobius dugesii*, 3/9 *Trichobius flagellatus*, 36/151 *Trichobius galei*, 6/19 *T. joblingi*, and 3/27 *Trichobius johnsonae*. Genotypic analyzes revealed the occurrence of 11 distinct genotypes among the 19 *gltA* sequences obtained, four distinct genotypes among the nine *rpoB* sequences obtained, and six distinct genotypes among the nine *ftsZ* sequences obtained. Phylogenetic analyzes revealed that the *gltA* sequences clustered in two different sub clades: one closely related to other *Bartonella* sp. sequences previously obtained in non-hematophagous bats and their associated ectoparasites from Brazil, sister to rodent-associated clades (*B. vinsonii* complex and *B. harrusi* and *B. machadoae* sub-clade); the other closely related to other *Bartonella* sp. sequences previously obtained in non-hematophagous bats and their associated ectoparasites from Brazil, Costa Rica, Mexico, Spain and USA, sister to ruminant-associated clades (*B. chomelii*, *B. schoenbuchensis*, *B. bovis*).

Studies regarding the microbiome composition of Streblidae flies have also identified the occurrence of *Bartonella* spp. in these dipterans. Speer et al. (2022) characterized the bacterial microbiome of 222 obligate bat flies (84.7% (188/222) Streblidae and 15.3% (34/222) Nycteribiidae) collected from 155 bats, including *Artibeus lituratus* (n = 45), *Carollia perspicillata* (n = 34), *Desmodus rotundus* (n = 22), *Glossophaga soricina* (n = 19), *Sturnira lilium* (n = 18), and *Trachops cirrhosus* (n = 17), sampled across ten Atlantic Forest fragments in southeastern Brazil. The authors demonstrated that parasite species identity was the main factor shaping microbiome composition. Although Streblidae microbiomes were predominantly composed of *Arsenophonus* (>70% relative abundance), *Bartonella* was consistently detected at low relative abundance (<10%) in several streblid species. In contrast, Nycteribiidae flies exhibited microbiomes dominated by *Bartonella* and *Wolbachia*, which together accounted for more than 75% of the bacterial community. Furthermore, habitat loss altered the structure of ectoparasite-associated bacterial communities, increasing the connectivity and centrality of bacterial association networks in smaller forest fragments, suggesting that environmental disturbance may indirectly influence the ecology and circulation of vector-associated bacteria, including *Bartonella* (Speer et al., 2022). Similarly, in the state of Mato Grosso do Sul, André et al. (2023) detected the occurrence of *Bartonella* in the microbiome of 37/48 (77%) Streblidae flies (*M. araneae* 10/18; *T. costalimai* 13/14; *T. dugesii* 8/9; *T. joblingi* 1/2; *T. parasiticus* 2/2; *S. hertigi* 2/2), which were collected from non-hematophagous bats (*A. planirostris*, *A. lituratus*, *C. perspicillata*, *Eptesicus furinalis*, *G. soricina*, *P. lineatus* and *P. discolor*).

More recently, a total of 1017 Streblidae flies were collected from bats sampled in six caves in northeastern Brazil, of which 912 were screened for *Bartonella* spp. using a qPCR assay targeting the 16S-23S ITS region. Overall, 521/912 (57.1%) flies tested positive, representing a remarkably high *Bartonella* detection rate among bat flies reported in Brazil. Positivity varied among fly species (*N. fairchildi* 361/559; *N. parnelli* 15/40; *Strebla curvata* 3/5; *T. caecus* 3/12; *T. dugesii* 19/35; *T. galei* 2/3; *T. joblingi* 3/5; *T. johnsonae* 27/124; *T. parasiticus* 85/116; *Trichobius uniformis* 3/9). Molecular characterization revealed high genetic diversity of *Bartonella* spp. among cave-dwelling bats and their associated streblid flies. Interestingly, ecological analyses revealed no significant association between *Bartonella* infection and streblid fly infestation intensity, bat colony size, or bat species richness, suggesting that *Bartonella* transmission dynamics in cave systems are influenced by complex ecological interactions rather than simple host or ectoparasite abundance patterns. These findings reinforce the role of cave-dwelling bats as important reservoirs of highly diverse *Bartonella* lineages and highlight the importance of ecological and host-parasite interaction networks in shaping *Bartonella* circulation in natural environments.

Order Ixodida

Family Ixodidae

Gonçalves et al. (2020b) detected the occurrence of *Bartonella* spp. in ticks associated with cattle (*Bos taurus*) in the state of Mato Grosso do Sul, midwestern Brazil. Based on a HRM real-time PCR based on the ITS (16S-23S rRNA) intergenic region, the authors detected the presence of *Bartonella* sp. DNA, phylogenetically related to *B. bovis*, in 13/125 (10.4%) engorged females of *Rhipicephalus microplus* ticks. A further HRM assay based on the *ssrA* gene detected *B. bovis* in 9/13 (69.2%) of the screening-positive ticks. One tick (1/13; 7.7%) was positive in a cPCR assay based on the *gltA* gene, and the sequence obtained was phylogenetically related to *Bartonella* sp. previously detected in lice (*H. quadripertusus*) from Israel and Thailand.

Order Mesostigmata

Families Macronyssidae and Spinturnicidae

A study conducted with mites collected from bats in the states of Minas Gerais and Rio de Janeiro, southeastern Brazil, and Paraná, southern Brazil, detected the occurrence of *Bartonella* spp. in those ectoparasites (Chagas et al., 2024). The authors analyzed macronyssid specimens, collected from 14 different bat species, for the presence of *Bartonella* sp. using a real-time PCR based on the *nuoG* gene and cPCR assays for seven different molecular markers (16S rRNA, *nuoG*, *rpoB*, *pap31*, *gltA*, *groEL* and *ftsZ*). Out of 165 mites analyzed, 8/165 (4.8%) were positive in the qPCR and only three sequences were obtained: two *nuoG* sequences obtained from *Parichoronyssus bakeri* and *Macronyssoides kochi*, collected from *Artibeus* sp. and *Phyllostomus hasatus*, respectively, and one 16S rRNA sequence obtained from a *Steatonyssus* sp. collected from a *Eptesicus* sp. bat. The *nuoG* sequences were phylogenetically related to *Bartonella* sp. previously detected in Streblidae flies (*T. dugesii*, *T. costalimai* and *M. aranea*) and vampire

bats (*Desmodus rotundus* and *Diphylla ecaudata*) from Brazil. The single 16S rRNA sequence was phylogenetically close to *Bartonella* sp. previously detected in bats from Thailand, feces of bats from China and an *Anopheles gigas* specimen from Vietnam.

Bartonella spp. were detected in Macronyssidae pool mites (23.8%; 5/21) collected from bats sampled in Campo Grande, state of Mato Grosso do Sul. The positive pools were represented by *Steatonyssus* spp. (Ikeda et al., 2020). The bacterial microbiome of bats and their associated ectoparasites also revealed the occurrence of *Bartonella* spp. in Macronyssidae and Spinturnicidae mites collected from non-hematophagous bats (*Artibeus lituratus*, *Artibeus planirostris*, *Eptesicus furinalis* and *Phyllostomus discolor*) in the state of Mato Grosso do Sul. From 58 pooled mites, *Bartonella* spp. were detected in the microbiome of 7/42 (16.6%) of Spinturnicidae mites (1/4 [25%] *Periglischrus acutisternus*; 1/5 [20%] *Periglischrus* sp.; 4/29 [13.8%] *Periglischrus iheringi*; 1/4 [25%] *Periglischrus torrealbai*) and 3/15 (20%) of Macronyssidae mites (3/15 [20%] *Steatonyssus* sp.) (André et al., 2023).

Order Psocoptera

Suborder Anoplura

Family Haematopinidae

Bartonella genotypes, with 100% identity to *Bartonella* sp. genotypes previously isolated from *Haematopinus quadripertusus* from Israel and closely related to a genotype detected in *H. quadripertusus* from Thailand, were detected in *H. tuberculatus* lice associated with water buffaloes (*Bubalus bubalis*) from Minas Gerais, southeastern Brazil (Gonçalves et al., 2020b). A total of 4/95 (4.2%) specimens were positive in a HRM real-time PCR based on the ITS (16S-23S rRNA) intergenic region and cPCR protocols based on the *gltA* and *rpoB* genes.

Family Polyplacidae

Fontalvo et al. (2017) detected *Bartonella* sp. in a *Polyplax* sp. louse (1/1; 100%) collected from a common punaré (*Thrichomys apereoides*) captured in the Caatinga biome of the Pernambuco state, northeastern Brazil. The specimen was positive in molecular assays targeting the *gltA* and *ribC* genes of *Bartonella* spp., but no sequences were obtained.

Suborders Amblycera and Ischnocera

Families Menoponidae and Philopteridae

Two different *Bartonella* sp. genotypes (*nuoG* genic region) were detected in *Austromenopon echinatum* (Amblycera: Menoponidae) and *Halipeurus abnormis* (Ischnocera: Philopteridae) collected from a Cory's Shearwater (*Calonectris borealis*) specimen stranded in the coast of Rio de Janeiro, southeastern Brazil (Bassini-Silva et al., 2025). From the total 33 analyzed ectoparasites, 15/33 (45.4%) were positive to *Bartonella* spp. in a qPCR based on the *nuoG* gene (7 females and 1 female of *H. abnormis* and 6 females and 1 male of *A. echinatum*). The *nuoG* sequences, obtained in cPCR protocols, from each species, *H. abnormis* and *A. echinatum*, were identical to each other and showed the highest similarity to *B. vinsonii* subsp. *berkhoffii* isolated from domestic dogs and *Bartonella* sp. previously detected in blood samples of *Glossophaga soricina* from Guatemala, respectively.

Order Siphonaptera

Family Pulicidae

A study conducted in the state of Pernambuco, northeastern Brazil, detected the presence of *Bartonella* spp. in fleas associated with wild crab-eating foxes (*C. thous*) and domestic dogs and cats (Fontalvo et al., 2017). Among the specimens analyzed, a total of 9/9 (100%) *Pulex irritans*, collected from *C. thous*, 1/43 (2.3%) and 35/61 (57.3%) *C. felis felis* and *P. irritans* collected from domestic dogs, and 24/45 (53.3%) *Ctenocephalides felis felis* fleas, collected from domestic cats, were positive for *Bartonella* spp. in conventional cPCR assays targeting the *gltA* and *ribC* genic regions. BLASTn analyses revealed that the *gltA* sequences obtained in fleas (*P. irritans*) associated with *C.*

thous had an identity 100% with *B. rochalimae*; those detected in *C. felis felis* associated with domestic cats had an identity 100% with *B. clarridgeiae* and *B. henselae*. Among dogs' ectoparasites, the authors only obtained sequences from the *P. irritans* specimens, which had an identity of 100% with *B. rochalimae* and *B. vinsonii* subsp. *berkhoffii*.

A study conducted in the Mato Grosso do Sul state detected the occurrence of *Bartonella* spp. in ectoparasites associated with wild animals in Pantanal wetland areas (Sousa et al., 2018). A total of 75 *Polygenis* (*P.*) *bohlsi bohlsi* fleas (associated with *T. fosteri* rodents) were pooled into 38 groups and submitted to a molecular screening using a qPCR based on the *nuoG* gene of *Bartonella* spp. and further assays based on different genic regions (*gltA*, *ftsZ*, *rpoB*, *ribC* and *nuoG*) for positive samples. A total of 3/38 (7.8%) flea pools were positive for *Bartonella* spp. The *Bartonella* sp. sequences obtained in two *Polygenis* (*P.*) *bohlsi bohlsi* *gltA* sequences showed 95% identity with *Bartonella* sp. sequences previously detected in rodents from Brazil; three *ftsZ* sequences detected in *Polygenis* (*P.*) *bohlsi bohlsi* showed an identity of 96% to *Bartonella* spp. from a wild rodent in Brazil. Phylogenetic inferences of the concatenated *gltA* and *ftsZ* genic regions positioned the *Bartonella* sequences obtained in fleas in a monophyletic clade, along with *Bartonella* sp. sequences previously detected in rodents from Brazil.

Order Hemiptera

Expanding the diversity of hematophagous arthropods harboring *Bartonella* spp., these alphaproteobacteria have been recently detected in field-collected *Triatoma sordida* from peridomestic environments in the state of Bahia, northeastern (Santos et al., 2024). The bacterial DNA was detected in 23/81 (28.4%) specimens by qPCR targeting the *gltA* gene, with all sequenced amplicons showing 100% identity to *B. henselae*.

More recently, Santos et al. (2026) provided the first molecular evidence of *B. henselae* DNA in *Rhodnius prolixus*. Among 84 triatomines maintained in an insectary from São Paulo state, 4/84 (4.76%) were positive by nested PCR, and sequencing confirmed 100% identity with *B. henselae* strain Houston-1. These findings complement previous reports of *Bartonella* detection in *Triatoma rubrofasciata* from China (Zhang et al., 2023), and *Eratyrus mucronatus* from French Guiana (Laroche et al., 2017), suggesting that triatomines may become exposed to *Bartonella* under natural or laboratory conditions. However, the authors emphasized that the detection of bacterial DNA should not be interpreted as evidence of vector competence or biological transmission, and that additional experimental studies are required to determine whether triatomines are capable of maintaining and transmitting *Bartonella* spp. within natural transmission cycles.

Bartonella spp. in humans in Brazil: A One Health framework

In Brazil, human infections caused by *Bartonella* spp. have been increasingly recognized across diverse clinical and epidemiological settings, reinforcing their importance within a One Health framework. The main species reported in humans include *B. henselae*, *B. quintana*, and, less frequently, atypical or genetically diverse *Bartonella* lineages detected through molecular diagnostic approaches (Drummond et al., 2023). Worldwide, human bartonellosis is mainly associated with three pathogenic species: *B. bacilliformis*, the agent of Carrion's disease (encompassing Oroya fever and *verruca peruana*) transmitted by *Lutzomyia verrucarum* sandflies in Andean regions; *B. henselae*, the causative agent of Cat-Scratch Disease (CSD) transmitted among felines and to humans via *C. felis felis* flea feces; and *B. quintana*, the louse (*Pediculus humanus*)-borne agent of Trench Fever associated with socioeconomic vulnerability (Alexander, 1995; Foucault et al., 2006; Gupta, 2010).

Among human bartonellosis, CSD represents the most common clinical manifestation, whose principal reservoir are represented by domestic cats. Transmission to humans usually occurs following scratches or bites contaminated with flea feces harboring the bacterium. CSD is generally a self-limiting disease characterized by papules at the inoculation site, regional lymphadenopathy, and fever; however, atypical manifestations, including endocarditis, neuroretinitis, hepatosplenic disease, and bacillary angiomatosis, may occur, particularly in immunocompromised individuals (Regnery et al., 1992; Anderson et al., 1994; Boulouis et al., 2005; Chomel et al., 2009; Breitschwerdt et al., 2010).

Although CSD is usually self-limiting, severe *Bartonella* infections have been most frequently documented in immunocompromised patients, particularly individuals living with HIV, in whom *B. quintana* and *B. henselae* are associated with bacillary angiomatosis, chronic bacteremia, and endocarditis (Breitschwerdt et al., 2008; Boodman et al., 2023). In Brazil, a high seropositivity rate for *Bartonella* spp. (38.4%) was detected among HIV-positive patients, with cat ownership being closely associated with seropositivity in this vulnerable cohort (Lamas et al., 2010). In addition, *B. henselae* remains the predominant species implicated in cases of infective endocarditis in

immunocompetent patients in Brazil; however, this condition is widely recognized as underdiagnosed due to the bacterium's fastidious growth requirements and the limited sensitivity of conventional blood cultures, often requiring specialized molecular diagnostic techniques (Lamas et al., 2007; Boodman et al., 2023). Considering that domestic cats are the primary reservoirs of *B. henselae* and that *Bartonella* spp. have been detected in a wide range of domestic and wild mammalian hosts throughout Brazil, the occurrence of human infections underscores the interconnected roles of animal reservoirs, arthropod vectors, and humans in the maintenance of *Bartonella* transmission cycles.

The growing recognition of companion animals as hosts for multiple pathogens further emphasizes the importance of a One Health perspective for *Bartonella* surveillance. Beyond their well-established role as reservoirs of zoonotic *Bartonella* species, dogs and cats may simultaneously harbor other vector-borne pathogens of veterinary and public health importance (André et al., 2015).

Increasing evidence suggests that *Bartonella* spp. may establish asymptomatic or persistent bacteremia in humans. Recent molecular and serological studies have reported *Bartonella* DNA and/or antibodies in blood donors and asymptomatic individuals, supporting the hypothesis of subclinical or persistent bacteremia in human population and highlighting potential transfusion-related and occult transmission risks (Drummond et al., 2023; Breitschwerdt et al., 2008). In Rio de Janeiro, Lamas et al. (2010) reported a 34% *Bartonella* spp. seroprevalence among healthy blood donors. More extensively, Pitassi et al. (2015) evaluated *Bartonella* spp. bacteremia in 500 human blood donors from Campinas, São Paulo, revealing that 16 donors (3.2%) were positive by PCR and/or isolation (15 positive for *B. henselae* and one for *B. clarridgeiae*). IgG antibodies against *B. henselae* and *B. quintana* were detected in 16% and 32% of these donors, respectively, although serology showed no correlation with culture positivity. Within this context, Vieira-Damiani et al. (2015) reported the first detection of *B. clarridgeiae* in an asymptomatic human blood donor in Brazil using liquid enrichment culture, PCR, and DNA sequencing, reinforcing the challenges of occult infections in transfusional medicine.

Epidemiological analyses indicate that contact with cats and a history of tick bites are significant risk factors for *Bartonella* spp. infection among blood donors in southeastern Brazil (Pitassi et al., 2015). Consequently, implementing comprehensive preventive measures, such as strict ectoparasite control, keeping domestic animals indoors, and educating the public to avoid cat scratches or bites, is essential to reduce the transmission risk of these pathogens to human populations and mitigate urban zoonotic cycles (Diniz et al., 2016; Drummond et al., 2023). Additionally, a study performed in the state of São Paulo, southeastern Brazil, reported the occurrence of *Bartonella* spp. in persons experiencing homelessness (Faccini-Martínez et al., 2023). A total of 79/109 (72.5%) serum samples were seropositive for *Bartonella* spp. using IFA. Furthermore, blood samples and lice (*Pediculus humanus humanus*) were subjected to DNA extraction and further molecular identification of *Bartonella*. A total of 1/114 (0.9%) blood samples and 14/82 (17%) louse pools were positive in molecular assays for the *gltA* and *rpoB* genes. Sequencing and BLASTn analysis identified *B. quintana* as the circulating agent. The authors suggested that persons experiencing homelessness may be predisposed to bartonellosis and other vector-borne infections due to the increased exposure to ectoparasites. Overall, these findings highlight the importance of integrated surveillance involving human, animal, and vector populations, as well as improved diagnostic capacity, to better understand the epidemiology of *Bartonella* spp. in Brazil within a One Health perspective.

Future Perspectives

Despite advances in understanding the epidemiology of *Bartonella* in Brazil, there is still a lack of important information regarding diagnostic approaches, bacterial isolation, genomic characterization, and elucidation of transmission dynamics. Future research should prioritize the integration of sensitive diagnostic methods with bacterial isolation, comparative genomics, and vector ecology to improve the understanding of the diversity, evolution, and epidemiological importance of *Bartonella* species within One Health. (Regier et al., 2016).

Digital PCR (dPCR) is a highly sensitive tool for the detection and quantification of *Bartonella* DNA, demonstrating superior sensitivity compared to conventional and qPCR assays, especially in samples with low bacterial load (Maggi et al., 2020, 2021). Recently, Calchi et al. (2025) demonstrated the superior performance of dPCR compared to conventional molecular assays for the detection of *Bartonella* DNA in free-living wild animals in Brazil, highlighting its potential for epidemiological investigations involving hosts with low-level bacteremia. Based on these advances, future studies should integrate dPCR with *Bartonella* alpha-proteobacterial growth medium (BAPGM) and bacterial isolation, aiming to improve the sensitivity of detection of this group of bacteria. Since *Bartonella* infections are

characterized by low bacteremia, and the fastidious nature of these bacteria makes laboratory diagnosis difficult, the combination of bacterial enrichment with high-sensitivity molecular detection can improve diagnostic performance. Furthermore, bacterial isolation is indispensable for phenotypic characterization, antimicrobial susceptibility testing, and the generation of reference strains for comparative genomic analyses. Thus, the integration of dPCR, BAPGM enrichment, and bacterial isolation is an excellent strategy to improve the diagnosis of *Bartonella* infections, while simultaneously expanding the availability of isolates for genomic studies.

Expanding the isolation of *Bartonella* strains from domestic and wild animal hosts across Brazil should also be considered a research priority. To date, most Brazilian studies have relied primarily on molecular detection, limiting the availability of cultured isolates for downstream genomic investigations. Increasing the number of isolates would facilitate whole-genome sequencing and pan-genome analyses, enabling the identification of accessory genes, host-adaptation mechanisms, virulence-associated factors, and genomic recombination events, while also contributing to the discovery and taxonomic characterization of novel *Bartonella* species circulating in the country (Deng et al., 2012; Wagner & Dehio, 2019).

Another important line of research involves applying microbiome based approaches to investigate the representation of the genus *Bartonella* in ectoparasite microbial communities. Metagenomic and 16S rRNA sequencing can provide a broader understanding of microbial diversity and reveal differential abundance and interactions between *Bartonella* and endosymbiotic bacteria such as *Wolbachia*, *Coxiella*-like, *Francisella*-like, and *Rickettsiella* endosymbionts. These microorganisms have been shown to influence vector physiology, immune responses, and pathogen colonization, potentially affecting the acquisition, persistence, and transmission of vector-borne pathogens (Wang et al., 2023). Characterizing these microbial interactions may reveal ecological mechanisms that influence *Bartonella* maintenance and transmission within arthropod populations.

Future studies should also focus on determining the vector competence of ectoparasites found in Brazil for *Bartonella* spp. Although *Bartonella* DNA has been detected in several arthropod taxa, including fleas, ticks, lice, mites, and hippoboscids flies, molecular detection alone does not demonstrate biological vector competence. Experimental studies are required to determine whether these ectoparasites are capable of acquiring *Bartonella* during blood feeding, maintaining viable bacteria, supporting bacterial persistence or replication, and successfully transmitting the pathogen to susceptible vertebrate hosts (Tsai et al., 2011; Regier et al., 2016). Such investigations are essential to distinguish incidental bacterial carriage from true biological transmission and to improve our understanding of the epidemiology of bartonellosis in Brazil.

Finally, future investigations should prioritize under-sampled Brazilian biomes, including the Amazon, Caatinga, Cerrado, Pantanal, Pampa, and coastal and marine ecosystems, as well as neglected wildlife hosts and their associated ectoparasites. Although Brazil harbors one of the world's greatest biodiversity, significant geographic and taxonomic gaps remain in the current knowledge of *Bartonella* diversity. Expanding surveillance to these poorly explored ecosystems will improve our understanding of the geographic distribution, host range, evolutionary history, and emergence of novel *Bartonella* species, ultimately contributing to more accurate assessments of zoonotic risk and pathogen transmission dynamics within the Brazilian One Health context (Regier et al., 2016; Álvarez-Fernández et al., 2018).

In general, the integration of highly sensitive diagnostics, bacterial isolation, comparative genomics, microbiome analyses, standardized molecular methodologies, and experimental studies of vector competence will advance the understanding of the ecology, evolution, and transmission of *Bartonella* spp. in Brazil. These efforts will strengthen epidemiological surveillance, enhance the understanding of host-pathogen-vector interactions, and provide a scientific basis for the development of prevention and control strategies within the framework of One Health.

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Data availability

Data is contained within the article.

Ethics declaration

This literature review was based solely on publicly available secondary sources. Since no primary data was collected from humans or animals, approval from a research ethics committee was not required. All information was obtained in an ethical and responsible manner.

Conflict of interest

The authors declare no conflict of interest.

Author contributions

Marcos Rogério André: conceptualization, data curation, formal analysis, investigation, methodology, project administration, visualization, writing – original draft, writing – review and editing. Daniel Antônio Braga Lee: investigation, project administration, writing – original draft, writing – review and editing. Lorena Freitas das Neves: investigation, project administration, writing – original draft, writing – review and editing. Eliz Oliveira Franco: investigation, project administration, writing – original draft, writing – review and editing. Rosangela Zacarias Machado: funding acquisition, investigation, project administration, writing – original draft, writing – review and editing.

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Supplementary Material

Supplementary material accompanies this paper.

Supplementary File 1- Table 1. Studies conducted in Brazil on the detection and occurrence of *Bartonella* spp. in domestic, wild animals and arthropods in the country.

Supplementary File 2 - A map showing the geographical division of Brazilian states.

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