



Article

Molecular Detection of a *Bartonella* sp. in Fleas and Mites Collected from Wild Rodents (Cricetidae: Sigmodontinae) in the Northeast of Argentine Patagonia

Winter Marina ^{1,2,†}, Acosta Diana Belén ^{3,†} , Abate Sergio Damián ¹ and Sanchez Juliana Patricia ^{2,4,*}

¹ Centro de Investigaciones y Transferencia de Río Negro (CONICET-UNRN), Universidad Nacional de Río Negro-Sede Atlántica, Viedma 8500, Argentina; mwinter@unrn.edu.ar (W.M.); sabate@unrn.edu.ar (A.S.D.)

² Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Ciudad Autónoma de Buenos Aires C1425FQB, Argentina

³ Centro de Bioinvestigaciones-CeBio, Centro de Investigaciones y Transferencia del Noroeste de la Provincia de Buenos Aires-CIT NOBA (CONICET-UNNOBAUNSA), Pergamino 2700, Argentina; dbacosta@comunidad.unnoba.edu.ar

⁴ Instituto Nacional de Parasitología (INP)—ANLIS-Malbrán, Ciudad Autónoma de Buenos Aires C1282AFF, Argentina

* Correspondence: jpsanchez@anlis.gob.ar

† These authors contributed equally to this work.

Simple Summary

This study investigated fleas and mites from wild mice in Argentine Patagonia, detecting *Bartonella* DNA. This specific pathogen had not previously been reported in the region. The proximity of these wild hosts to human settlements and workspaces suggests a potential risk of transmission to people and pets. These results contribute to a better understanding of the distribution and epidemiology of ectoparasite-borne zoonotic diseases.

Abstract

Ectoparasite-borne infections have become a global public health problem. This study investigated the diversity of fleas and mites associated with wild rodents in the northeastern region of Argentine Patagonia and analyzed the molecular presence of *Rickettsia* and *Bartonella* within these arthropods. Research was conducted in the Monte Desierto biome, focusing on areas where wildlife, livestock, and human activities overlap. Ectoparasites ($n = 32$) were collected from captured rodents and subjected to PCR amplification and phylogenetic analysis using *gltA* and *rpoB* for *Bartonella* and *OmpA*, *OmpB* and *gltA* for *Rickettsia*. *Bartonella* DNA was detected in all studied ectoparasites, with the obtained *gltA* and *rpoB* sequences showing 100% and 99% identity, respectively, to reference sequences of *Bartonella* sp. closely related to *Bartonella quintana*, whereas no *Rickettsia* DNA was detected. Specifically, the pathogen was identified in four flea species (*Craneopsylla minerva wolffhugeli*, *Neotyphloceras crackensis*, *Polygenis rimatus*, and *Ectinorus* sp.) and the mite *Gigantolaelaps wolffsohni*, while *Rickettsia* was not detected in any samples. These findings constitute the first report of *Bartonella* sp. closely related to *B. quintana* in this geographical region as well as the first detection of the bacterium in these specific flea and mite species in South America. Our results suggest an active wild cycle of *Bartonella* sp., emphasizing the importance of the One Health approach in monitoring emerging infectious diseases.

Keywords: *gltA*; *rpoB*; *Neotyphloceras crackensis*; *Craneopsylla minerva wolffhugeli*; *Ectinorus* sp.; *Polygenis rimatus*; *Gigantolaelaps wolffsohni*; zoonoses



Academic Editor: Stephen K. Wikel

Received: 23 June 2026

Revised: 18 July 2026

Accepted: 24 July 2026

Published: 28 July 2026

Copyright: © 2026 by the authors.

Licensee MDPI, Basel, Switzerland.

This article is an open access article distributed under the terms and

conditions of the [Creative Commons](https://creativecommons.org/licenses/by/4.0/)

[Attribution \(CC BY\)](https://creativecommons.org/licenses/by/4.0/) license.

1. Introduction

Sigmodontine rodents (Cricetidae) constitute the most diverse mammalian subfamily and serve as primary hosts for fleas (Siphonaptera) [1]. The high species richness of fleas associated with these rodents suggests a deep coevolutionary history between host and ectoparasite [1,2]. Beyond these evolutionary dynamics, fleas are critical vectors for pathogens; specifically, bartonellosis, rickettsiosis, and yersiniosis represent the primary zoonotic diseases transmitted by these insects [3]. However, while research has predominantly focused on ticks and secondarily on fleas, the role of Mesostigmata mites as rodent ectoparasites and potential pathogen carriers remains comparatively understudied, particularly in South America [4].

Mites and fleas serve as vectors for bacteria of the genus *Bartonella*. This genus comprises a large number of facultative intracellular bacteria. Currently, there are 131 species and candidates of *Bartonella* in the List of Prokaryotic names with Standing in Nomenclature (LPSN) (<https://lpsn.dsmz.de/search?word=bartonella> accessed on 18 June 2026), with at least 17 identified as zoonotic pathogens affecting humans and domestic animals [5,6]. Given its broad impact, bartonellosis is increasingly regarded as a major emerging infectious disease [3]. In Argentina, clinical bartonellosis has been documented in both pediatric and adult patients. Reported cases include cat scratch disease (CSD) caused by *Bartonella henselae* (Hyphomicrobiales; Bartonellaceae) in Buenos Aires and San Luis provinces, as well as *B. quintana*-induced infective endocarditis in an adult from Buenos Aires [7–9]. Moreover, *Bartonella* DNA has been detected in Argentine fleas associated with domestic and wild meso mammals and wild rodent fleas [10–16].

Similarly, the genus *Rickettsia* comprises a diverse group of obligate intracellular bacteria. Currently, 177 species and candidates are listed in LPSN (<https://lpsn.dsmz.de/search?word=Rickettsia> accessed on 18 June 2026). The environmental circulation of rickettsiae depends strictly on vector-host interaction, and recent years have seen a significant rise in reported cases globally [17]. However, according to the Subcommittee on Rickettsiosis to the Tick-Borne Disease Working Group (2022), official figures are likely underestimated due to the lack of rapid diagnostic tests at primary healthcare centers [18]. In Argentina, human rickettsiosis has been primarily linked to *Rickettsia rickettsii* and *R. parkeri*, both transmitted by ticks [17,19,20]. While the growing body of knowledge in Argentina has focused heavily on ticks and ectoparasites associated with domestic animals, studies regarding wild species remain comparatively limited [14–16,21–27].

Over the past decade, arthropod-borne infections have become a global public health problem. These include diseases transmitted by ectoparasites, with outbreaks and emergencies in countries where they have caused serious cases in humans [28]. Anthropogenic pressure, rather than wildlife presence alone, dictates disease emergence risks at the human–animal interface. Activities like forestry, mining, agriculture, and urbanization alter host–vector–pathogen dynamics and increase spatial overlap. Furthermore, climate-driven rodent migrations into human settlements exacerbate zoonotic transmission. Therefore, research into rodent–ectoparasite vector associations is crucial to understanding these shifting dynamics and establishing baseline data [29,30]. The aim of this study was to evaluate the diversity of ectoparasites associated with wild rodents in the extreme northeast of Argentinian Patagonia, and analyze the molecular presence of *Rickettsia* and *Bartonella* in these arthropods.

2. Material and Methods

2.1. Study Area

The study area was located in the northeastern-most part of Argentine Patagonia, on the border between the provinces of Buenos Aires and Rio Negro (Figure 1). The natural

ecosystem corresponds to the Monte Desierto biome [31]. The climate is semi-arid to arid, with high evaporation exacerbated by wind, and average annual precipitation ranges from less than 100 to 450 mm. The vegetation is fairly uniform in terms of appearance and floristic composition [31,32]. Native xerophytic flora alternates with exotic species and areas of semi-extensive livestock farming (mainly cattle) and agriculture. Rodent traps were placed on private properties with a weak or nonexistent biosecurity protocol. Dogs and cats were observed coexisting with livestock and wildlife. Thus, it is common for dogs to travel weekly between rural and urban areas with their owners.

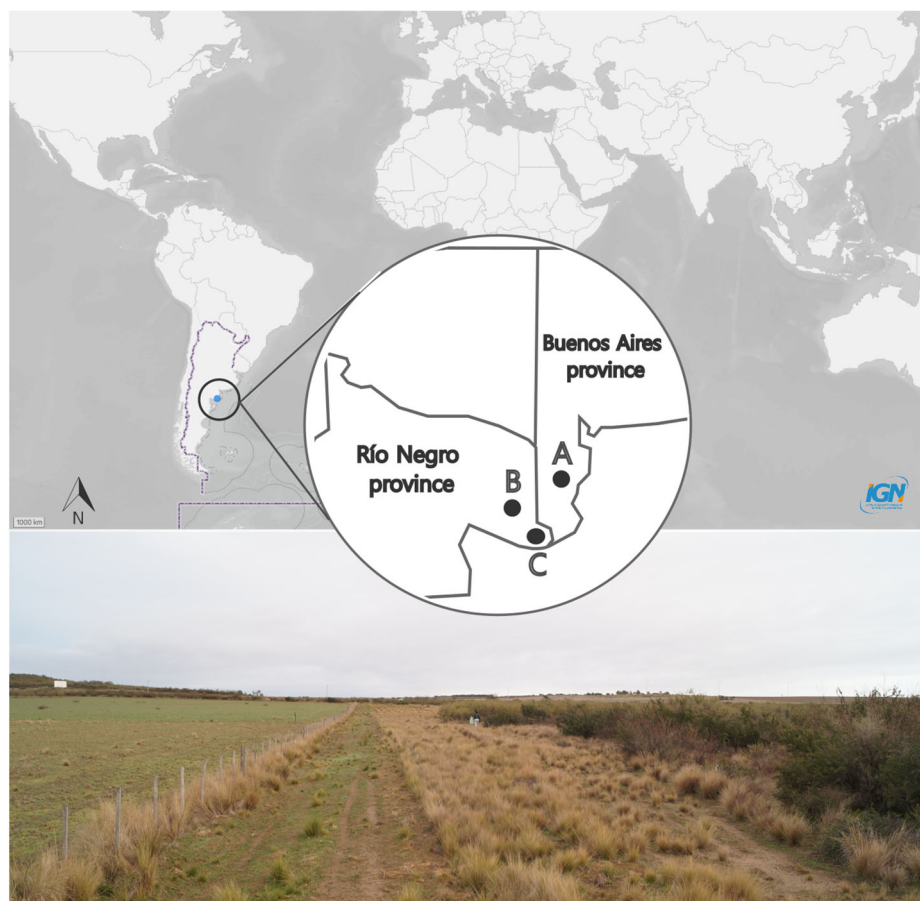


Figure 1. Wild rodent capture points: site A ($-40^{\circ}27'55''/-62^{\circ}47'55''$), site B ($-40^{\circ}43'35''/-63^{\circ}17'56''$) and site C ($-40^{\circ}58'34''/-62^{\circ}53'08''$) in Argentine Patagonia, and a panoramic view of capture site A (below).

2.2. Host and Ectoparasites Collection and Identification

Between June and August of 2017 and 2018, eight rodent trapping sessions were conducted across three sampling sites: Site A (4 trapping sessions; $-40^{\circ}27'55''/-62^{\circ}47'55''$), Site B (2 trapping sessions; $-40^{\circ}43'35''/-63^{\circ}17'56''$), and Site C (2 trapping sessions; $-40^{\circ}58'34''/-62^{\circ}53'08''$) (Figure 1). Rodents were captured using Sherman live traps ($23 \times 8 \times 9 \text{ cm}^3$) baited with oats. Traps were inspected daily in the early morning for three consecutive days. At each site, 40 traps were deployed nightly in two parallel lines of 20, spaced 5 m apart, following the local topography and vegetation. Species identification followed the criteria of Gómez Villafañe et al. [33]. Biosecurity protocols were strictly observed during animal handling, and an open-air field laboratory was established at each site. The study was approved by the Secretary of Environment and Sustainable Development of Río Negro (085206SAYDS/218/2015) and the Office of Flora and Fauna of Buenos Aires (22500-2952). Additionally, protocols were reviewed and authorized by

the Institutional Care and Use Committee (CICUAL) of the Faculty of Veterinary Sciences, University of Buenos Aires (2016/4, dated 16 June 2016).

Ectoparasites were collected by forceps and stored in 96% ethyl alcohol until molecular analyses were carried out in the Centro de Bioinvestigaciones (CeBio—UNNOBA). Details on parasitological examination as well as on flea identification can be found in Sanchez (2013), Sanchez and Lareschi (2019) and for mites in Furman (1972) [34–36].

After DNA extraction, fleas and mites were prepared for morphological study and identification. Fleas were cleared and softened in an aqueous solution of potassium hydroxide 10% (KOH), dehydrated in an increasing series of ethanol (80–100%), further diaphanized in eugenol, and mounted on permanent slides with Canadian balsam and studied under light microscopy. Identification keys used included those of Hopkins and Rothschild (1953), Johnson (1957) and Smit (1987) [37–39]. Mites were cleared in lactophenol and mounted individually in Hoyer's medium for their identification in accordance with the original descriptions and drawings of Furman (1972) [36].

DNA 70 ethanol followed by sterile distilled water to remove external contaminants before processing. For fleas, a small incision was made between the third and fourth abdominal tergites using a sterile scalpel to obtain material for DNA extraction, while preserving the remaining specimen for subsequent morphological identification. For mites, a small incision was made through the body to obtain material for DNA extraction, while maintaining the remaining specimen for morphological examination. The material used to handle the ectoparasites was sterilized between each sample. Genomic DNA extraction was performed from individual ectoparasites per host, using the Chelex®-100 (Bio-Rad Laboratories, Hercules, CA, USA) method described by Acosta et al. [16]. The genomic DNA obtained was stored at -20°C under sterile conditions. Following the DNA extraction, the fleas and mites' exoskeletons were recovered and stored in 96% ethanol and subsequently mounted for species identification.

2.3. Molecular Detection of *Bartonella* spp. and *Rickettsia* spp.

The presence of *Bartonella* was screened using the citrate synthase (*gltA*) and RNA polymerase beta-subunit (*rpoB*) genes, while the presence of *Rickettsia* was screened using the citrate synthase (*gltA*), outer membrane protein A (*ompA*) and outer membrane protein B (*ompB*) genes (Table 1). Using the *gltA* gene, the genus of both bacteria can be confirmed, while the other molecular markers show the specific identity. For the amplification, the polymerase chain reaction (PCR) program started with an initial denaturation for 5 min at 95°C , followed by 40 cycles (95°C for 30 s, gene-specific annealing $^{\circ}\text{C}$ for 30 s, and 72°C for 30 s), and a final extension step at 72°C for 5 min (Table 1). PCR was set to a final volume of 20 μL , containing 1 ng/ μL of template DNA for mite samples and up to 20 ng/ μL for flea samples, according to the DNA yield obtained from individual ectoparasite extractions, 1.5 mM MgCl_2 , 0.2 μM of each primer, 0.2 mM of each dNTP, 1X reaction buffer, 0.5U of Pegasus DNA polymerase and ultrapure sterile water to come to final volume. All amplifications were performed in conjunction with a negative (distilled water) and positive (DNA of *Bartonella* spp. provided by the Servicio Bacteriología Especial, “Dr. Carlos G. Malbrán,” INEI-ANLIS, Buenos Aires, Argentina, and DNA of *Rickettsia* spp. provided by the Instituto Nacional de Enfermedades Virales Humanas “Dr. Julio I. Maiztegui,” INEV-ANLIS, Pergamino, Argentina) controls. Additionally, all PCR setup procedures were performed under sterile conditions in a laminar flow cabinet, using dedicated materials and aerosol-resistant filter tips to minimize the risk of cross-contamination. DNA fragment amplification was confirmed by electrophoresis on 1% m/v agarose gel, stained with ethidium bromide (10 $\mu\text{g}/\mu\text{L}$) and visualized under UV light.

Table 1. Primers used for PCR amplification of *Bartonella* and *Rickettsia* genes.

Specificity	Target Gene	Primer Name	Nucleotide Sequence (5'–3')	Annealing T (°C)	Product Length (bp)	Reference
<i>Bartonella</i>	<i>gltA</i>	BaGltA_F	TCTACGGTACGTCTTGCTGGATCA	56.2	201	[40]
		BaGltA_R	GCCCATAAGGCGGAAAGGATCATT			
	<i>rpoB</i>	BaRpoB_F	CGCGCGATCATGTTGATTGATGG	56.6	159	
		BaRpoB_R	ATGGTGCTTCAGCACGTACAAGAG			
<i>Rickettsia</i>	<i>gltA</i>	CS-239	GCTCTTCTCATCCTATGGCTATTAT	60	834	[41]
		CS-1069	CAGGGTCTTCGTGCATTTCTT			
	<i>ompA</i>	Rr190.70	ATGGCGAATATTTCTCCAAAA	46	632	[42]
		190-701	GTTCCGTTAATGGCAGCATCT			
	<i>ompB</i>	120-M59	CCGCAGGGTTGGTAACTGC	51	820	[43]
		120-807	CCTTTTAGATTACCGCCTAA			

In the samples with positive PCR for the genes analyzed, we proceeded to purification using 10U of Exonuclease I (Thermo Fisher Scientific, Waltham, MA, USA) and 1U of FastAp thermosensible alkaline phosphatase (Thermo Fisher Scientific), incubating at 37 °C for 15 min and a subsequent 15 min at 85 °C to stop the reaction. The purified samples were sequenced by Macrogen® (Seoul, Republic of Korea).

2.4. Data Analysis

The obtained sequences for the genes were analyzed and manually edited using the BioEdit program [44]. To assign identity to each sequence with statistical significance, it was subjected to a homology comparison against the GenBank nucleotide database, making use of the nucleotide BLAST algorithm (<https://blast.ncbi.nlm.nih.gov/Blast.cgi> accessed on 15 May 2026). The sequences have been deposited in the GenBank nucleotide database (<https://www.ncbi.nlm.nih.gov/genbank/> accessed on 15 May 2026) under accession numbers PZ407960 to PZ407968.

To perform the phylogenetic analysis, sequences were taken from the GenBank nucleic acid database. The complete set of gene sequences was employed for a multiple alignment performed with the ClustalW algorithm in MEGA v.11 [45]. The resulting alignment was checked and manually corrected. Moreover, phylogenetic trees were built using the Maximum Likelihood (ML) and Neighbor Joining (NJ) methods of statistical inference, both for individual genes and for concatenated sequences. In the case of the concatenation of genes, the Farris test was initially performed using methods PAUP* based on the inference on parsimony to establish whether these genes could be used [46,47]. Through the Mesquite program, the sequences were concatenated [48]. The evolutionary history was inferred using the ML method based on the Tamura 3-parameter (I + G) model with 10,000 replicates of random-addition taxa and tree bisection and reconnection branch swapping. Branch support was assessed using 1000 bootstrap replicates. All positions were weighted equally.

3. Results

With a total sampling effort of 910 trap-nights, we recorded 127 captures (61 in 2017 and 66 in 2018). Ectoparasites were recovered from 16 rodents: 26 fleas—*Craneopsylla minerva wolffhuegeli* (18), *Neotyphloceras crackensi* (3), *Polygenis rimatus* (4), *Ectinorus* sp. (1)—and 6 *Gigantolaelaps wolffsohni* mites (6). Specific host–parasite associations are detailed in Table 2.

Table 2. Rodent–flea (F) and rodent–mite (M) associations found per year. The number indicates how many times that association was recorded in that year.

Year	Rodent	Ectoparasite	Site
2017	<i>Graomys griseoflavus</i>	<i>Neotyphloceras crackensis</i> (1) F	A
		<i>Craneopsylla minerva wolffhuegeli</i> (1) F	A
2018	<i>Calomys musculus</i>	<i>Craneopsylla minerva wolffhuegeli</i> (1) F	A
	<i>Graomys griseoflavus</i>	<i>Neotyphloceras crackensis</i> (3) F	A
		<i>Craneopsylla minerva wolffhuegeli</i> (4) F	A, C
		<i>Ectinorus</i> sp. (1) F	A
		<i>Polygenis rimatus</i> (2) F	A
	<i>Eligmodontia typus</i>	<i>Craneopsylla minerva wolffhuegeli</i> (1) F	C
	<i>Calomys musculus</i>	<i>Craneopsylla minerva wolffhuegeli</i> (1) F	A
	<i>Oligoryzomys longicaudatus</i>	<i>Gigantolaelaps wolffsohni</i> (3) M	A, C
		<i>Craneopsylla minerva wolffhuegeli</i> (1) F	A

Total genomic DNA was extracted from fleas and mites collected from all infested rodents. The genus *Bartonella* was detected for the *gltA* and *rpoB* genes in all the ectoparasites studied. Both genes were detected in fleas of the species *Neotyphloceras crackensis* (3/3), *Craneopsylla minerva wolffhuegeli* (18/18), *Ectinorus* sp. (1/1) and *Polygenis rimatus* (4/4), and in the mite species *Gigantolaelaps wolffsohni* (6/6). Among the PCR-positive specimens, five individual ectoparasites, representing each positive ectoparasite species, were selected for sequencing and molecular analyses (Supplementary Material Table S1). The resulting sequences were deposited in GenBank under accession numbers PZ407960–PZ407963 (*gltA*) and PZ407964–PZ407968 (*rpoB*).

Sequence analysis revealed genetic variation among the detected *Bartonella* variants. The *rpoB* sequences corresponded to five distinct haplotypes, each showing nucleotide differences among samples (Supplementary Material Table S1). Similarly, the *gltA* marker showed four haplotypes and 29 variable nucleotide positions among the analyzed sequences (Supplementary Material Table S1).

For *gltA*, nBLAST analysis indicated 100% (query cover 100%; e-value = 0.0) identity with *Bartonella* spp. For the *rpoB* gene, the nBLAST analysis indicated 99% (query cover 97%; e-value = $3e^{-159}$) identity with *Bartonella quintana*. When both genes were concatenated, it gave an identity of 98% with *Bartonella quintana* (query cover 100%; e-value = $2e^{-157}$). Phylogenetic analyses through ML and NJ inferences were inferred from the *gltA* and *rpoB*, separately analyzed, as well as by concatenating these genes, resulting in a total length of 309 bp (Figures S1 and S2 in Supplementary Materials). The phylogenetic analysis, both the ML and NJ inferences, showed the same topology; thus, only the ML is shown. These results showed that all sequences obtained in this study are grouped with *B. quintana* (Figure 2; Supplementary Material Figures S1 and S2). Although the amplified *gltA* and *rpoB* fragments were shorter than those proposed by La Scola et al. (2003) for species-level identification, these loci have been widely used in molecular surveys of *Bartonella* because they contain informative polymorphic sites that facilitate preliminary genetic characterization [49,50]. However, given the limited phylogenetic resolution provided by these short fragments, we conservatively refer to the detected bacterium as *Bartonella* sp. closely related to *B. quintana* rather than assigning it unequivocally to that species.

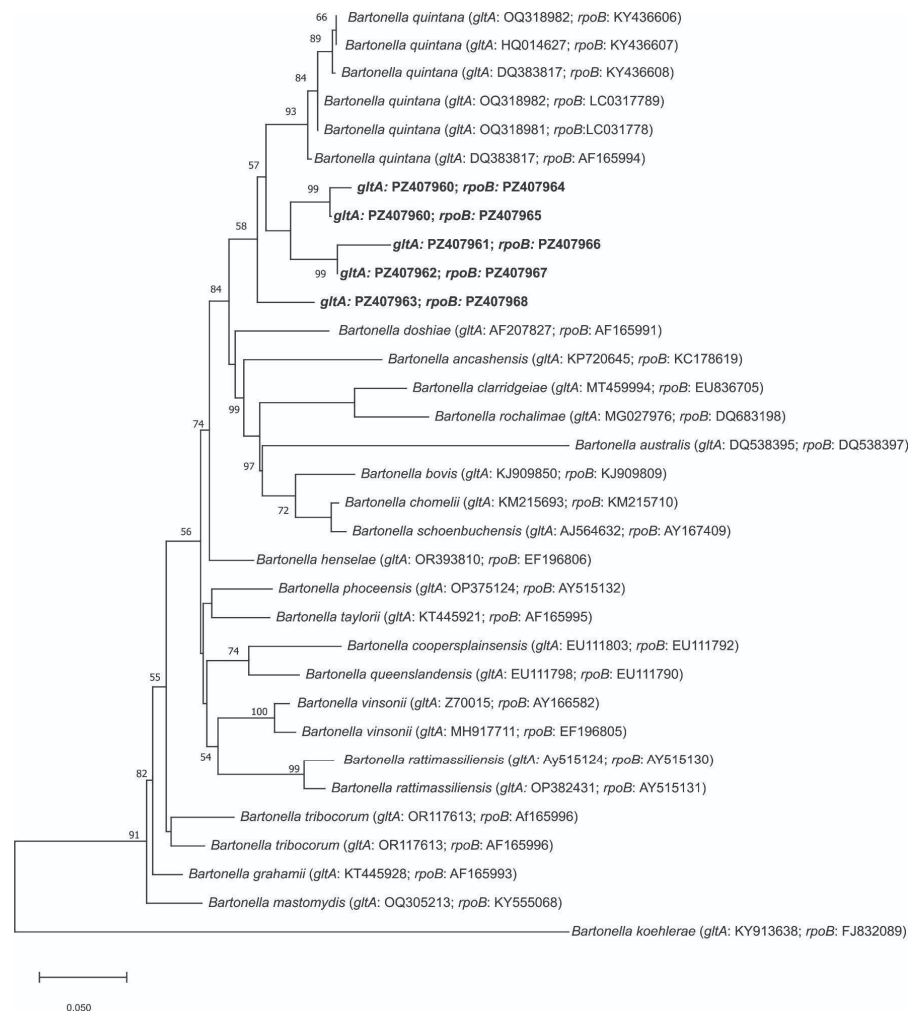


Figure 2. Phylogenetic analysis obtained with the Maximum Likelihood methodology of *Bartonella* spp. found in fleas and mites from Argentine Patagonia. A total of 309 bp were aligned nucleotide sites of the bartonellosis genes *gltA* and *rpoB*, which were concatenated and subjected to analysis by the Maximum Likelihood method. In the nodes, bootstrap values > 50% are shown. The GenBank accession number for each genotype is indicated in parentheses after each *Bartonella* species.

The genus *Rickettsia* was not detected in the ectoparasites studied.

4. Discussion

Some studies have shown that the diversity of ectoparasites remains constant among rodent communities in anthropogenic environments with varying degrees of alteration [51].

Interactions between wild and domestic animals facilitate horizontal transmission and create new niches for pathogen evolution and persistence. Zoonotic agents can spread to humans through any point of contact with wildlife or livestock. In this context, wild rodents often act as silent links; by sharing micro- and macro-environments, they establish epidemiological chains that bridge the gap between species. Most studies of rodent-ectoparasites-pathogen associations have been conducted near natural protected areas [52]. Therefore, the information obtained in this study becomes even more relevant when one considers that the sampling sites are private fields that are the visual essence of the One Health approach. These areas blend wild environments with the presence of domestic production animals: primarily cattle and sheep, and domestic dogs used for fieldwork but living alongside people. The role of dogs, in this case, could be fundamental in linking infections from wild and urban environments. Dogs act as reservoirs for various *Bartonella*

species; notably, high prevalence rates have been reported in clinically asymptomatic individuals [53–56].

Human body lice, *Pediculus humanus humanus*, are considered the main vectors of trench fever caused by *B. quintana* [57]. However, *B. quintana* DNA and other species have been amplified from bed bugs and cosmopolitan fleas including *Ctenocephalides canis*, *Ctenocephalides felis felis*, and *Pulex irritans* (Pulicidae) [58]. Furthermore, *B. quintana* infections have been reported to be one of the major causes of endocarditis. A recent review highlights the lack of data on other arthropods-beyond lice-and a marked geographical asymmetry in research; while some regions have abundant studies on the vectors of this zoonosis, in others the information is practically nonexistent [59].

In southern South America, research has documented the circulation of *Bartonella* among various flea species infesting rodents and other wild mammals. In Brazil, *Bartonella* sp. DNA was identified in *Craneopsylla minerva minerva* from *Oligoryzomys nigripes* (3/6); in *Polygenis occidentalis* from *Oxymycterus nasutus* and *O. nigripes* (2/5); and in *P. platensis* parasitizing *Akodon azarae* and *Scapteromys tumidus* (2/2) [60]. Additionally, *B. clarridgeiae* and *Bartonella* sp. were detected in *Ctenocephalides felis* (2/6) collected from wild felids such as the margay (*Leopardus wiedii*) and jaguarundi (*Herpailurus yagouaroundi*), respectively [61]. In Chile, *B. tribocorum* was found in *Plocopsylla* sp. and *Nosopsyllus* sp. from *Mus musculus* and *Abrothrix* spp. (11/39) [62]. Regional studies in Argentina show diverse findings: in southern Patagonia, *Bartonella* sp. was detected in *Neotyphloceras crackensis* (28/36) from *Phyllotis xanthopygus*, *Eligmodontia morgani* and *Abrothrix hirta*, whereas in northern Argentina, López Berrizbeitia et al. (2024) reported *B. quintana* in *C. m. minerva* (10/22) and *Polygenis acodontis* (6/14) from several wild rodents [13,14]. Most recently, *B. rochalimae* DNA was amplified from *Phthiropsylla agenoris* (1/13) on armadillos (*Chaetophractus villosus*), and from *Pulex irritans* (2/2) on plains vizcachas (*Lagostomus maximus*) and gray foxes (*Lycalopex gymnocercus*) [16]. Research on the presence of *Bartonella* DNA in fleas in southern South America shows wide variability in the apparent prevalences detected, both when analyzing each flea species individually and when evaluating all samples. In the region, reported values range from 8% to 100%, a range consistent with the findings of this study. Notably, sample sizes per species are often relatively small, underscoring the logistical and technical challenges inherent in wildlife field research.

The genus *Gigantolaelaps* is a group of large ectoparasitic mites that infest New World sigmodontine rodents, specifically of the tribe Oryzomyini (such as *O. longicaudatus*) [57]. In this system, males reside exclusively in the host's nest, whereas females live on the host for feeding and dispersal. Although females acquire *Bartonella* (and other pathogens) via hematophagy, they return to the protected nest microclimate to oviposit. So, the host nest acts as a permanent physical and biological reservoir, buffered against the external environmental fluctuations that typically constrain flea populations. *Gigantolaelaps* ensures enzootic persistence to the host species and its offspring within the nest. This sex-biased division of roles functions as an ecological strategy that prevents *Bartonella* clearance from the rodent population, underscoring the critical and understudied epidemiological role of this mite genus [63–66].

Although *Rickettsia* DNA was not amplified in this study, its presence has been documented for the study area in *C. felis* collected from a white-eared opossum (*Didelphis albiventris*) [16]. *D. albiventris* is known to interact with rodents primarily through predation, sharing habitats, and serving as a host for common parasites. *R. felis* is an etiological agent within the Spotted Fever Group (SFG). Although it is a cosmopolitan zoonosis, in countries like Argentina it remains a neglected disease [67]. It is prevalent in both domestic animals and humans, yet frequently underdiagnosed in its early stages due to clinical symptoms that overlap with more common illnesses such as influenza and dengue [68,69].

Sampling point C of this work is located very close to the *Rickettsia* record of Acosta et al. (2025) [16]. The geographical coverage is an interface area between natural, rural and urban ecosystems with abundant domestic canids and felids roaming about. The absence of this bacterium in this rodent-focused study reinforces the need and importance of conducting comprehensive studies, evaluating the role of rodents as reservoirs.

Local studies are foundational for mapping the epidemiological networks of pathogenic microorganisms. Although these findings are site-specific and based on a relatively small sample, the data collected between 2017 and 2018 constitute an essential historical baseline for retrospectively assessing the impact of recent environmental changes. Consequently, replicating and expanding this line of research is critical to validating these trends over broader spatial and temporal scales. These results also serve as crucial indicators for neighboring regions or countries with similar bioclimatic conditions. Furthermore, fleas are well-known vectors; our positive molecular results in mites provide valuable information about other ectoparasites that could be involved in the maintenance and transmission cycles of *Bartonella*. These findings suggest an active wild cycle for this bacterium. Within the One Health framework, information regarding the links between wildlife, ectoparasites, and pathogens should ideally be prioritized when planning new urban developments.

5. Conclusions

This study confirms for the first time the presence of *Bartonella* sp., closely related to *B. quintana*, in fleas and mites from wild rodents in northeastern Argentine Patagonia. These results represent the first record for this region, as well as the first detection in South America of *Bartonella* in the flea species *Craneopsylla minerva wolffhuegeli*, *Ectinorus* sp., and *Polygenis rimatus*, and in mites of the genus *Gigantolaelaps*. These findings constitute an essential baseline for the surveillance of environmental impacts on the epidemiology of regional vector-borne diseases. The absence of *Rickettsia* in this study, despite previous reports in the area, highlights the need for continued, comprehensive research. In future research, it will be necessary to expand the sample size of ectoparasites and include the hosts in the studies, in order to define their role as reservoirs of both *Bartonella* and *Rickettsia*.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/zoonoticdis6030029/s1>, Supplementary Material Table S1. Molecular characterization of *Bartonella*-positive ectoparasite specimens analyzed in this study. The table shows the ectoparasite species, GenBank accession numbers for the *gltA* and *rpoB* sequences, and the polymorphic nucleotide sites identified among the sequences generated in this study. Nucleotide positions correspond to the aligned sequences for each marker. Dots (.) indicate nucleotide identity with the reference sequence used for the alignment, whereas letters indicate nucleotide substitutions; Supplementary Material Figure S1. Phylogenetic tree inferred using the Maximum Likelihood method based on partial *rpoB* sequences of *Bartonella* spp. detected in fleas and mites from Argentine Patagonia. Bootstrap support values > 50% are shown at the nodes. *Bartonella* genotypes identified in the present study are highlighted in bold; Supplementary Material Figure S2. Phylogenetic tree inferred using the Maximum Likelihood method based on partial *gltA* sequences of *Bartonella* spp. detected in fleas and mites from Argentine Patagonia. Bootstrap support values > 50% are shown at the nodes. *Bartonella* genotypes identified in the present study are highlighted in bold.

Author Contributions: Conceptualization, W.M., A.D.B., A.S.D. and S.J.P.; methodology, W.M., A.D.B., A.S.D. and S.J.P.; investigation, W.M., A.D.B., A.S.D. and S.J.P.; data curation, W.M., A.D.B., A.S.D. and S.J.P.; writing—original draft, W.M., A.D.B. and S.J.P.; writing—review and editing, W.M., A.D.B., A.S.D. and S.J.P.; visualization, W.M. and A.D.B.; supervision, A.S.D. and S.J.P.; project administration, W.M., A.D.B. and S.J.P.; funding acquisition, W.M., A.D.B., A.S.D. and S.J.P. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by Universidad Nacional de Río Negro projects number 40-C-665 and 40-C-983.

Institutional Review Board Statement: The rodent capture and removal protocol was approved by the Institutional Committee for the Care and Use of Laboratory Animals (CICUAL) of the Faculty of Veterinary Sciences of the University of Buenos Aires (2016/4, dated 16 June 2016). The study was approved by the Secretary of Environment and Sustainable Development of Río Negro (085206SAYDS/218/2015) and the Office of Flora and Fauna of Buenos Aires (22500-2952).

Informed Consent Statement: Not applicable.

Data Availability Statement: The original contributions presented in this study are included in the article/Supplementary Material. Further inquiries can be directed to the authors.

Acknowledgments: The authors thank the Secretary of Environment of the province of Río Negro, the Office of Flora and Fauna of the province of Buenos Aires, and the owners of fields where the rodent sampling was carried out.

Conflicts of Interest: The authors declare no conflicts of interest.

References

- Whiting, M.F.; Whiting, A.S.; Haslter, M.W.; Dittmar, K. A molecular phylogeny of fleas (Insecta: Siphonaptera): Origins and host associations. *Cladistics* **2008**, *24*, 677–707. [\[CrossRef\]](#)
- Krasnov, B.R. *Functional and Evolutionary Ecology of Fleas: A Model for Ecological Parasitology*; Cambridge University Press: New York, NY, USA, 2008; p. 610.
- Cutillas, C.; Trujillo, I.; Zurita, A.; García-Sánchez, A.M. Highlighting zoonotic importance of synanthropic fleas through microbiome analysis. *Sci. Rep.* **2025**, *15*, 37651. [\[CrossRef\]](#) [\[PubMed\]](#)
- Herrera-Mares, A.; Guzmán-Cornejo, C.; Ulloa-García, A.; Córdoba-Aguilar, A.; Silva-de la Fuente, M.C.; Suzán, G. Mites, rodents, and pathogens: A global review for a multi-species interaction in disease ecology. *Acta Trop.* **2022**, *232*, 106509. [\[CrossRef\]](#) [\[PubMed\]](#)
- Breitschwerdt, E.B.; Maggi, R.G.; Chomel, B.B.; Lappin, M.R. Bartonellosis: An emerging infectious disease of zoonotic importance to animals and human beings. *J. Vet. Emerg. Crit. Care* **2010**, *20*, 8–30. [\[CrossRef\]](#) [\[PubMed\]](#)
- García-Alvarez, L.; García-García, C.; Muñoz, P.; Fariñas-Alvarez, M.D.C.; Cuadra, M.G.; Fernández-Hidalgo, N.; García-Vázquez, E.; Moral-Escudero, E.; Alonso-Socas, M.d.M.; On behalf of Grupo de Apoyo al Manejo de la Endocarditis infecciosa en España (GAMES); et al. *Bartonella endocarditis* in Spain: Case reports of 21 cases. *Pathogens* **2022**, *11*, 561. [\[CrossRef\]](#) [\[PubMed\]](#)
- Deregibus, M.I.; Bagnara, E.I.; Buchovsky, A. Enfermedad por arañazo de gato: Experiencia en un hospital pediátrico de tercer nivel. *Arch. Argent. Pediatr.* **2023**, *121*, e202202592. [\[CrossRef\]](#)
- Lorenzatti, J.; De Salvo, M.N.; Díaz Pérez, P.; Cicuttin, G.L.; Samartino, L.E. Enfermedad por arañazo de gato en la interfaz humano-animal. Reporte de caso en la Ciudad de San Luis, Argentina. *Rev. Med. Vet.* **2022**, *103*, 97–99.
- Garré, L.; Guaraglia, W.; Cuatz, D.; Kaufman, S.; Gil, H.; De Rosa, A.F. Infective endocarditis due to *Bartonella quintana*. *Medicina* **2008**, *68*, 144–146. [\[PubMed\]](#)
- Cicuttin, G.L.; Brambati, D.F.; De Gennaro, M.F.; Carmona, F.; Isturiz, M.L.; Pujol, L.E.; Belerenian, G.C.; Gil, H. *Bartonella* spp. in cats from Buenos Aires, Argentina. *Vet. Microbiol.* **2014**, *168*, 225–228. [\[CrossRef\]](#) [\[PubMed\]](#)
- Cicuttin, G.; De Salvo, M.N.; Sanchez, J.; Cañón, C.; Lareschi, M. Molecular detection of *Bartonella* in fleas (Hexapoda, Siphonaptera) collected from wild rodents (Cricetidae, Sigmodontinae) from Argentina. *Med. Vet. Entomol.* **2019**, *33*, 541–545. [\[CrossRef\]](#) [\[PubMed\]](#)
- De Salvo, M.N.; Hercolini, C.; Arístegui, E.; Bruno, A.; Brambati, D.F.; Cicuttin, G.L. *Bartonella* spp. associated with rodents in an urban protected area, Buenos Aires (Argentina). *Comp. Immunol. Microbiol. Infect. Dis.* **2020**, *72*, 101515. [\[CrossRef\]](#) [\[PubMed\]](#)
- Urdapilleta, M.; Cicuttin, G.L.; De Salvo, M.N.; Pech-May, A.; Salomon, O.D.; Lareschi, M. Molecular detection and identification of *Bartonella* in the cat flea *Ctenocephalides felis felis* collected from companion animals in a border area in northeastern Argentina. *Vet. Parasitol. Reg. Stud. Rep.* **2020**, *19*, 100361. [\[CrossRef\]](#) [\[PubMed\]](#)
- López Berrizbeitia, M.F.; Acosta, D.B.; Sanchez, J.P. Wild rodent fleas carrying *Bartonella* and *Rickettsia* in an area endemic for vectorborne diseases from Argentina. *Sci. Rep.* **2024**, *14*, 23269. [\[CrossRef\]](#) [\[PubMed\]](#)
- Acosta, D.B.; Zanoeco, F.A.; Ruiz, M.; Sánchez, J.P. Domestic dogs as host of ectoparasites carrying *Rickettsia*, *Bartonella* and *Mycoplasma* in urban, peri-urban and rural areas from center Argentina. *Mastozool. Neotrop.* **2023**, *30*, e0991. [\[CrossRef\]](#)
- Acosta, D.B.; Winter, M.; Abate, S.D.; Sanchez, J.P. Fleas of wild mammals carrying pathogenic bacteria in Argentinian Patagonia: A study based on wildlife roadkill. *Med. Vet. Entomol.* **2025**, *39*, 653–663. [\[CrossRef\]](#) [\[PubMed\]](#)

17. Armitano, R.I.; Guillemi, E.; Escalada, V.; Govedic, F.; Lopez, J.L.; Farber, M.; Borras, P.; Prieto, M. Fiebre manchada en Argentina. Descripción de dos casos clínicos. *Rev. Argent. Microbiol.* **2019**, *51*, 339–344. [[CrossRef](#)] [[PubMed](#)]
18. Walker, D.H.; Myers, C.T.E.; Blanton, L.S.; Bloch, K.C.; Fowler, V.G., Jr.; Gaines, D.N.; Paddock, C.D.; Yaglom, H.D. Rickettsiosis subcommittee report to the tick-borne disease working group. *Ticks Tick Borne Dis.* **2022**, *13*, 101855. [[CrossRef](#)] [[PubMed](#)]
19. Rymaszewska, A.; Piotrowski, M. *Rickettsia* Species: Genetic Variability, Vectors, and Rickettsiosis—A Review. *Pathogens* **2024**, *13*, 661. [[CrossRef](#)] [[PubMed](#)]
20. Romer, Y.; Seijo, A.C.; Crudo, F.; Nicholson, W.L.; Varela-Stokes, A.; Lash, R.R.; Paddock, C.D. *Rickettsia parkeri* Rickettsiosis, Argentina. *Emerg. Infect. Dis.* **2011**, *17*, 1169–1173. [[CrossRef](#)] [[PubMed](#)]
21. Nava, S.; Perez-Martinez, L.; Venzal, J.; Portillo, A.M.; Santibanez, S.; Oteo, J.A. *Rickettsia felis* in *Ctenocephalides felis* from Argentina. *Vector-Borne Zoonotic Dis.* **2008**, *8*, 465–466. [[CrossRef](#)] [[PubMed](#)]
22. Ruiz, M.; Acosta, D.B.; Baricalla, A.; Sánchez, J.P. Molecular detection of *Rickettsia* in ectoparasites (Siphonaptera and Phthiraptera) of domestic and feral pigs from Argentina. *Parasitol. Res.* **2021**, *120*, 3611–3618. [[CrossRef](#)] [[PubMed](#)]
23. Maas, L.M.I.; Winter, M.; Herrmann, V.; Abate, S.D.; Obiegala, A.; Nava, S.; Sebastian, P.S. *Anaplasma platys* and *Rickettsia massiliae* in *Rhipicephalus sanguineus* sensu stricto ticks collected on dogs in the Patagonian region of Argentina. *Parasitology* **2024**, *151*, 848–852. [[CrossRef](#)] [[PubMed](#)]
24. Sebastian, P.S.; Winter, M.; Abate, S.D.; Tarragona, E.L.; Nava, S. Molecular Detection of *Candidatus Rickettsia andeanae* and *Ehrlichia* sp. in *Amblyomma pseudoconcolor* Aragão, 1908 (Acari: Ixodidae) from the Argentinian Patagonia. *Animals* **2022**, *12*, 3307. [[CrossRef](#)] [[PubMed](#)]
25. Oscherov, E.B.; Milano, A.M.F.; Lobo, B.; Anda, P.; Escudero, R. Detection of *Anaplasma platys* and other pathogens in ectoparasites from urban hosts in Northeast Argentine. *Rev. Ibero-Latinoam. Parasitol.* **2011**, *70*, 42–48.
26. Lamattina, D.; Tarragona, E.L.; Nava, S. Molecular detection of the human pathogen *Rickettsia parkeri* strain Atlantic rainforest in *Amblyomma ovale* ticks in Argentina. *Ticks Tick-Borne Dis.* **2018**, *9*, 1261–1263. [[CrossRef](#)] [[PubMed](#)]
27. Ruiz, M.; Alonso, R.J.; Rospide, M.; Acosta, D.B.; Cavia, R.; Sanchez, J.P. Diversity and eco-epidemiology of ectoparasites and *Rickettsia* spp. associated with the opossums *Didelphis albiventris* Lund in livestock farms from Argentinian Pampas region. *Med. Vet. Entomol.* **2025**, *39*, 431–444. [[CrossRef](#)] [[PubMed](#)]
28. Bitam, I.; Dittmar, K.; Parola, P.; Whiting, M.F.; Raoult, D. Fleas and flea-borne diseases. *Int. J. Infect. Dis.* **2010**, *14*, e667–e676. [[CrossRef](#)] [[PubMed](#)]
29. Hassell, J.M.; Begon, M.; Ward, M.J.; Fèvre, E.M. Urbanization and Disease Emergence: Dynamics at the Wildlife–Livestock–Human Interface. *Trends Ecol. Evol.* **2017**, *32*, 55–67. [[CrossRef](#)] [[PubMed](#)]
30. Rodriguez-Morales, A.J.; Shehata, A.A.; Parvin, R.; Tasnim, S.; Duarte, P.M.; Basiouni, S. Rodent-Borne Parasites and Human Disease: A Growing Public Health Concern. *Animals* **2025**, *15*, 2681. [[CrossRef](#)] [[PubMed](#)]
31. Abraham, E.; del Valle, H.F.; Roig, F.; Torres, L.; Ares, J.O.; Coronato, F.; Godagnone, R. Overview of the geography of the Monte Desert biome (Argentina). *J. Arid. Environ.* **2009**, *73*, 144–153. [[CrossRef](#)]
32. Oyarzabal, M.; Clavijo, J.; Oakley, L.; Biganzoli, F.; Tognetti, P.; Barberis, I.; Maturo, H.M.; Aragón, R.; Campanello, P.I.; Prado, D.; et al. Unidades de vegetación de la Argentina. *Ecol. Austral* **2018**, *28*, 40–63. [[CrossRef](#)]
33. Gómez Villafañe, I.E.; Miño, M.; Cavia, G.; Hodara, K.; Courtalón, P.; Suárez, O.; Busch, M. *Roedores: Guía de la Provincia de Buenos Aires*; Colin Sharp: Buenos Aires, Argentina, 2005; 96p.
34. Sanchez, J.P. Sifonápteros Parásitos de los Roedores Sigmodontinos de la Patagonia Norte de la Argentina: Estudios Sistemáticos y Ecológicos. Ph.D. Thesis, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, Buenos Aires, Argentina, 2013.
35. Sanchez, J.P.; Lareschi, M. Diversity, distribution and parasitism rates fleas (Insecta: Siphonaptera) on sigmodontine rodents (Cricetidae) from Argentinian Patagonia. *Bull. Entomol. Res.* **2019**, *109*, 72–83. [[CrossRef](#)] [[PubMed](#)]
36. Furman, D.P. Mites of the Family Laelapidae in Venezuela (Acarina: Laelapidae). *Brigh. Young Univ. Sci. Bull. Biol. Ser.* **1972**, *17*, 1–58.
37. Hopkins, G.H.; Rothschild, M. *An Illustrated Catalogue of Rothschild Collection of Fleas (Siphonaptera) in the British Museum (Natural History)*, British Museum, NH; Tungidae and Pulicidae: London, UK, 1953; Volume 1.
38. Johnson, P.T. *A Classification of the Siphonaptera of South America with Descriptions of New Species*; Memoirs of the Entomological Society of Washington: Washington, DC, USA, 1957.
39. Smit, F.G.A.M. An illustrated catalogue of the Rothschild collection of fleas (Siphonaptera) in the British museum (natural history). VII. In *Malacopsylloidea (Malacopsyllidae and Rhopalopsyllidae)*; Oxford University: Oxford, UK, 1987.
40. Moreno Salas, L.; Espinoza-Carniglia, M.; Lizama-Schmeisser, N.; Torres, L.G.; Silva-De La Fuente, M.C.; Lareschi, M.; González-Acuña, D. Fleas of black rats (*Rattus rattus*) as reservoir host of *Bartonella* spp. in Chile. *PeerJ* **2019**, *7*, e7371. [[CrossRef](#)] [[PubMed](#)]

41. Labruna, M.B.; Whitworth, T.; Horta, M.C.; Bouyer, D.H.; McBride, J.W.; Pinter, A.; Popov, V.; Gennari, S.M.; Walker, D.H. *Rickettsia* species infecting *Amblyomma cooperi* ticks from an area in the state of São Paulo, Brazil, where Brazilian spotted fever is endemic. *J. Clin. Microbiol.* **2004**, *42*, 90–98. [CrossRef] [PubMed]
42. Roux, V.; Fournier, P.E.; Raoult, D. Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein *rOmpA*. *J. Clin. Microbiol.* **1996**, *34*, 2058–2065. [CrossRef] [PubMed]
43. Roux, V.; Raoult, D. Phylogenetic analysis of members of the genus *Rickettsia* using the gene encoding the outer-membrane protein *rOmpB* (*ompB*). *Int. J. Syst. Evol. Microbiol.* **2000**, *50*, 1449–1455. [CrossRef] [PubMed]
44. Hall, T. *BioEdit 6.0.7*; Department of Microbiology, North Carolina State University: Raleigh, NC, USA, 2004.
45. Tamura, K.; Stecher, G.; Kumar, S. MEGA11: Molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* **2021**, *38*, 3022–3027. [CrossRef] [PubMed]
46. Swofford, D.L.; Sullivan, J. Phylogeny inference based on parsimony and other methods using PAUP*. In *The phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny*, Cáp; Cambridge University Press: Cambridge, UK, 2003; Volume 7, pp. 160–206.
47. Farris, J.S.; Källersjö, M.; Kluge, A.G.; Bult, C. Testing significance of incongruence. *Cladistics* **1994**, *10*, 315–319. [CrossRef]
48. Maddison, W.P.; Maddison, D.R. Mesquite: A Modular System for Evolutionary Analysis, Version 3.70. 2021. Available online: <https://www.mesquiteproject.org> (accessed on 15 May 2026).
49. Birtles, R.J.; Raoult, D. Comparison of partial citrate synthase gene (*gltA*) sequences for phylogenetic analysis of *Bartonella* species. *Int. J. Syst. Evol. Microbiol.* **1996**, *46*, 891–897. [CrossRef]
50. La Scola, B.; Zeaiter, Z.; Khamis, A.; Raoult, D. Gene-sequence-based criteria for species definition in bacteriology: The *Bartonella* paradigm. *Trends Microbiol.* **2003**, *11*, 318–321. [CrossRef] [PubMed]
51. Gil-Fernández, M.; Vargas-Sandoval, M.; Delfín-Alfonso, C.A.; Mendoza, E.; Godínez-Gómez, O.; Jiménez-Lara, N.K.; MacSwiney, G.M.C.; Carthey, A.; Blanco-García, A.; Le Roux, J.J. Host sweet host: Rodent communities support similar ectoparasite diversity regardless of anthropogenic disturbance. *J. Appl. Entomol.* **2024**, *148*, 537–552. [CrossRef]
52. Mendoza, H.; Rubio, A.V.; García-Peña, G.E.; Suzán, G.; Simonetti, J.A. Does land-use change increase the abundance of zoonotic reservoirs? Rodents say yes. *Eur. J. Wildl. Res.* **2020**, *66*, 6. [CrossRef]
53. Perez, C.; Maggi, R.G.; Diniz, P.P.; Breitschwerdt, E.B. Molecular and serological diagnosis of *Bartonella* infection in 61 dogs from the United States. *J. Vet. Intern. Med.* **2011**, *25*, 805–810. [CrossRef] [PubMed]
54. Brenner, E.C.; Chomel, B.B.; Singhasivanon, O.U.; Namekata, D.Y.; Kasten, R.W.; Kass, P.H.; Cortes-Vecino, J.A.; Gennari, S.M.; Rajapakse, R.P.; Huong, L.T.; et al. *Bartonella* infection in urban and rural dogs from the tropics: Brazil, Colombia, Sri Lanka and Vietnam. *Epidemiol. Infect.* **2013**, *141*, 54–61. [CrossRef] [PubMed]
55. Müller, A.; Soto, F.; Sepúlveda, M.; Bittencourt, P.; Benevenuto, J.L.; Ikeda, P.; Machado, R.Z.; André, M.R. *Bartonella vinsonii* subsp. *berkhoffii* and *B. henselae* in dogs. *Epidemiol. Infect.* **2018**, *146*, 1202–1204. [CrossRef] [PubMed]
56. Álvarez-Fernández, A.; Breitschwerdt, E.B.; Solano-Gallego, L. *Bartonella* infections in cats and dogs including zoonotic aspects. *Parasites Vectors* **2018**, *11*, 624. [CrossRef] [PubMed]
57. Barbieri, R.; Drancourt, M.; Raoult, D. The role of louse-transmitted diseases in historical plague pandemics. *Lancet Infect. Dis.* **2021**, *21*, e17–e25. [CrossRef] [PubMed]
58. Raoult, D.; Angelakis, E.; Socolovschi, C. *Bartonella quintana* in *Cimex hemipterus*, Rwanda. *Am. J. Trop. Med. Hyg.* **2013**, *89*, 986–987. [CrossRef]
59. Boodman, C.; Gupta, N.; van Griensven, J.; Van Bortel, W. *Bartonella quintana* detection among arthropods and their hosts: A systematic review and meta-analysis. *Parasites Vectors* **2024**, *17*, 328. [CrossRef] [PubMed]
60. Schott, D.; Umeno, K.; Dall’Agnol, B.; Araújo Souza, U.; Webster, A.; Michel, T.; Peters, F.; Uarth Christoff, A.; Rogério André, M.; Ricardo Ott, R.; et al. Detection of *Bartonella* sp. and a novel spotted fever group *Rickettsia* sp. in neotropical fleas of wild rodents (Cricetidae) from southern Brazil. *Comp. Immunol. Microbiol. Infect. Dis.* **2020**, *73*, 101568. [CrossRef] [PubMed]
61. Araújo Souza, U.; Webster, A.; Dall’Agnol, B.; Bortolotto Peters, F.; Ochoa Favarini, M.; Diogo Schott, D.; Caló Zitelli, L.; Dias Mazim, F.; Benhur Kasper, C.; Ott, R.; et al. Ticks, mites, fleas, and vector-borne pathogens in free-ranging neotropical wild felids from southern Brazil. *Ticks Tick Borne Dis.* **2021**, *12*, 101706. [CrossRef] [PubMed]
62. Müller, A.; Gutiérrez, R.; Seguel, M.; Monti, G.; Otth, C.; Bittencourt, P.; Sepúlveda, P.; Alabí, A.; Nachum-Biala, Y.; Harrus, S. Molecular survey of *Bartonella* spp. in rodents and fleas from Chile. *Acta Trop.* **2020**, *212*, 105672. [CrossRef] [PubMed]
63. Lareschi, M.; Nieri-Bastos, F.; Barros-Battesti, D.M.; Nava, S.; Beldomenico, P.; Autino, A.; Gettinger, D. *Gigantolaelaps gilmorei* Fonseca, 1939 (Acari: Laelapidae): Taxonomic status, lectotype and paralectotype designation and new distributional records. *Syst. Parasitol.* **2004**, *59*, 235–236. [CrossRef] [PubMed]
64. Lareschi, M. Artrópodos ectoparásitos. In *Macroparásitos. Diversidad y Biología*; Drago, F.B., Ed.; Editorial de la Universidad Nacional de La Plata (EDULP): Buenos Aires, Argentina, 2017; pp. 167–185.

65. Gettinger, D.; Martins-Hatano, F.; Gardner, S.L. Some laelapine mites (Acari: Laelapidae) ectoparasitic on small mammals in the Galapagos Islands, including a new species of *Gigantolaelaps* from *Aegialomys galapagoensis*. *J. Parasitol.* **2011**, *97*, 574–576. [[CrossRef](#)] [[PubMed](#)]
66. Fuenzalida-Araya, K.; González-Aguayo, F.; Moreno, L.; Landaeta-Aqueveque, C.; Santodomingo, A.; Silva-de la Fuente, C.; González-Acuña, D. New records of *Gigantolaelaps wolffsohni* (Mesostigmata: Laelapidae) in Chile, an ectoparasite of *Oligoryzomys longicaudatus* (Rodentia: Cricetidae): Ecological aspects and relation to body size and sex of their host. *Acarologia* **2022**, *62*, 965–973. [[CrossRef](#)]
67. Venzal, J.M.; Nava, S. El género *Rickettsia* como agente de zoonosis en el Cono Sur de Sudamérica. *Rev. Méd. Urug.* **2011**, *27*, 98–106.
68. López, J.A.K.; Azócar, T. Evidencia clínica y serológica de rickettsiosis canina en Chile. *Rev. Chil. Infectol.* **2007**, *24*, 189–193. [[CrossRef](#)] [[PubMed](#)]
69. Piranda, E.M.; Faccini, J.L.; Pinter, A.; Saito, T.B.; Pacheco, R.C.; Hagiwara, M.; Labruna, M.B. Experimental infection of dogs with a Brazilian strain of *Rickettsia* fleas: Clinical and laboratory findings. *Mem. Inst. Oswaldo Cruz* **2008**, *103*, 696–701. [[CrossRef](#)] [[PubMed](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.