Title Prevalence of *Bartonella* Species in Shelter Cats and their Ectoparasites in Southeastern Brazil

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Abstract

Background: Feline Bartonella can be transmitted to humans through cat scratches or bites, and between cats by Ctenocephalides felis flea.

Methods: The occurrence of Bartonella DNA was assessed in ectoparasites and their cat hosts living in shelters based on the ITS region and gltA gene.

Results: Bartonella DNA was detected in 47.8% of cat blood samples, in 18.3% of C. felis fleas, 13.3% of flea eggs pools and 12.5% of lice pools. B. henselae and B. clarridgeiae DNA were detected in cat fleas, while B. henselae, B. clarridgeiae, and B. koehlerae in blood samples from bacteremic cats. Cats infested by positive ectoparasites showed approximately twice the chance of being infected.

Conclusions: Our results indicate shelter cats have a high prevalence of Bartonella species known to be human pathogens and highlight the importance of controlling their infestation by ectoparasites to avoid cat and human infection.

1. Introduction

Considering One Health concepts, studies approaching bartonellosis are important because this bacterial genus infects a broad variety of animals, are linked to an ever increasing number of human diseases, and are transmitted by arthropod vectors [1]. According to the List of Prokaryotic Names with Standing in Nomenclature (LPSN 2021), the genus Bartonella contains 37 species and 3 subspecies. Potential domesticated and wild animal reservoirs includes horse, cats, dogs, rodent, rabbits, ruminants, sea mammals, wild felines, coyotes, deer, elk, and foxes. The list of vectors and potential vectors associated with bacterial transmission includes flies, fleas, ticks, lice, and mites [2]. To date, natural infections in cats have been reported for six Bartonella species: B. henselae, B. clarridgeiae, B. koehlerae, B. bovis, B. quintana, B. vinsonii subsp. Berkhoffii, and more recently B. capreoli [3–5]. Most Bartonella species infecting humans are zoonotic, and cats appear to be the primary mammalian reservoir for B. henselae, B. clarridgeiae, and B. koehlerae [6]. Feline Bartonella can be transmitted to humans through scratches or bites. Transmission between cats most often occurs via the Ctenocephalides felis flea [7–9], which harbors B. henselae, B. clarridgeiae, B. quintana, and B. koehlerae DNA [10].

In Brazil, little information is available about Bartonella occurrence in animals and humans, and to date no study has verified the occurrence of Bartonella spp. in cat shelters in the Southeast region. Therefore, the objective of this study was to investigate the prevalence of Bartonella infection in shelter cats and ectoparasites collected from them, and the relationship between bacteremia in cats and their ectoparasites.

2. Materials And Methods

2.1. Cat sample
The study protocol was approved by the animal use ethics committee at Universidade Federal Rural do Rio de Janeiro under process number 027/2014.

The survey was carried out in six shelters in the Metropolitan Region of Rio de Janeiro State, Brazil, from September 2014 through September 2015. After obtaining shelter owner’s permission, approximately 2 mL of blood was aseptically obtained from cats by cephalic phlebotomy, transferred into sterile tubes containing the anticoagulant ethylenediamine tetraacetic acid, and maintained at −80°C until used for molecular analysis.

2.2. Ectoparasite collection and identification

Ectoparasites were retrieved manually from the cats, placed into dry sterile tubes, and stored at −20°C until used. All ectoparasites were morphologically identified to genus or species based on morphological criteria observed with a stereoscopic microscope, according to standard taxonomic keys [11–13].

2.3. Molecular detection

Fleas and ticks were individually packed in separate tubes. And lice were separated in pairs or trio per tube. Some fleas laid eggs inside the tubes, permitting their separation into a single pool per specimen for DNA extraction, as described in literature [14]. Briefly, each flea or tick and pool of flea eggs or lice was ground in 40 µl of TE buffer (10 mM Tris-HCl; 0.5 mM EDTA; pH 9.0) in sterile micro tubes. The final suspension was boiled at 100°C for 30 minutes and maintained at -20°C until tested by PCR. For cats, DNA was extracted from 200µL of whole blood sample using Kit Relia PrepTM Blood gDNA Miniprep System (Promega®), according to the manufacturer’s instructions. For quality assurance, a negative control was processed at the same time as the study samples.

All DNA samples were screened for the presence of Bartonella spp. 16S-23S rRNA intergenic spacer region (ITS) using primers 321s and 983as [15], and citrate synthase gene (gltA) using primers BhCS.781p and BhCS.1137n [16]. Following amplification, PCR products were subjected to horizontal electrophoresis on 1% agarose gel and stained with GelRed (Biothium, CA, USA). The positive control consisted of B. henselae (Houston strain) cultured in HEp-2 cells. All PCR runs were performed with nuclease-free water (Invitrogen, USA) as negative control. In order to prevent PCR contamination, DNA extraction, reaction setup, PCR amplification, and electrophoresis were performed in separated rooms.

Positives flea and cat samples were randomly selected and purified using the Illustra GFX PCR Purification Kit (GE Healthcare, Buckinghamshire England, UK). Purified DNA fragments were submitted to sequence confirmation in an automatic sequencer (ABI3730xl, Applied Biosystem, CA, USA). Sense and antisense sequences were analyzed using DNA Sequence Assembler version 4 software and compared with those deposited in the GenBank DNA database using the Basic Local Alignment Search Tool (BLAST, National Center for Biotechnology Information, available at https://blast.ncbi.nlm.nih.gov). The phylogenetic reconstruction was inferred using the Maximum Likelihood method. The nucleotide substitution models were selected based on Bayesian Information Criterion (BIC scores) and Tamura 3-parameter model was used to calculate the evolutionary distances. The combination of phylogenetic
clusters was assessed using a bootstrap test with 1000 replicates to test different phylogenetic reconstructions. The phylogenetic valuation was conducted using the Molecular Evolutionary Genetics Analysis (MEGA) software version 7.0.18.

2.4. Statistical analysis

The relationship between Bartonella infection status of cats and their fleas was evaluated by Chi-square test and association between them was expressed as Odds Ratio (OR) at 95% confidence interval. All analysis were implemented using the Bioestat 5.0 statistical software.

3. Results

A total of 115 fleas, 21 lice and one tick were collected from 46 cats. All flea and lice specimens were identified as Ctenocephalides felis and Felicola subrostratus adults, respectively. The tick specimen was identified as a Rhipicephalus sanguineus nymph. All sampled cats presented ectoparasites on their bodies. On average, approximately three fleas or lice were collected per cat (range 1–9 fleas and 2–4 lice).

Overall, 47.8% (22/46) of cats tested positive for Bartonella DNA according to both ITS and gltA gene (Table 1). Sequencing confirmed Bartonella henselae, Bartonella clarridgeiae, and Bartonella koehlerae infection among the blood samples. Cases in which ITS and gltA sequences from a single same cat corresponded to different feline Bartonella species were considered coinfections.
Table 1
Prevalence of *Bartonella* DNA in cats and their ectoparasites in shelters, Rio de Janeiro, Brazil

<table>
<thead>
<tr>
<th>Cats</th>
<th>Ectoparasites</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Flea</td>
</tr>
<tr>
<td>DNA samples</td>
<td>Blood</td>
<td>Adults</td>
</tr>
<tr>
<td>Total of samples</td>
<td>46</td>
<td>115</td>
</tr>
<tr>
<td>Total PCR positive no.(%)</td>
<td>22 (47.8)</td>
<td>21 (18.3)</td>
</tr>
<tr>
<td><em>gltA</em> positive no.(%)</td>
<td>21 (45.7)</td>
<td>18 (15.7)</td>
</tr>
<tr>
<td>ITS positive no.(%)</td>
<td>12 (26.1)</td>
<td>5 (4.3)</td>
</tr>
</tbody>
</table>

*Number of pools

*Bartonella* DNA was detected in 18.3% (21/115) of *C. felis* fleas, of which 15.7% (18/115) were by means of the *gltA* gene and 4.3% (5/115) by the ITS region. Bacterial DNA was amplified for both ITS and *gltA* fragments in three samples. Among 15 pools of eggs laid by fleas and 8 pools of lice, 13.3% and 12.5% showed amplification of the expected *Bartonella* spp. *gltA* gene, respectively. *Bartonella henselae* DNA was detected in cat fleas and their respective eggs, while *Bartonella clarridgeiae* DNA was only identified in fleas. No eggs or lice tested positive for the ITS region. No amplification of *Bartonella* DNA was obtained in the *Rhipicephalus sanguineus* nymph. *Bartonella henselae* was the predominant species in both fleas and cats (Table 2).
Table 2
*Bartonella* species in cats and their fleas (99 to 100% identities), Rio de Janeiro, Brazil

<table>
<thead>
<tr>
<th>Ectoparasites</th>
<th>Host cat</th>
<th>Adult</th>
<th>Eggs</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Flea</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Shelter 1</td>
<td>Host cat</td>
<td></td>
<td></td>
</tr>
<tr>
<td>211</td>
<td><em>B. henselae</em></td>
<td><em>B. henselae</em></td>
<td><em>B. henselae</em></td>
</tr>
<tr>
<td>208</td>
<td>Negative</td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>76</td>
<td>*</td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>Shelter 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>175</td>
<td><em>B. clarridgeiae</em></td>
<td><em>B. henselae</em></td>
<td><em>B. henselae</em></td>
</tr>
<tr>
<td>171</td>
<td><em>B. koehlerae</em></td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>168</td>
<td><em>B. henselae</em></td>
<td>Negative</td>
<td>Negative</td>
</tr>
<tr>
<td>172</td>
<td><em>B. henselae</em></td>
<td>Negative</td>
<td>Negative</td>
</tr>
<tr>
<td>178</td>
<td>*</td>
<td>Negative</td>
<td>Negative</td>
</tr>
<tr>
<td>180</td>
<td>Negative</td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>173</td>
<td>Negative</td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>Shelter 3</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>205</td>
<td><em>B. clarridgeiae</em></td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>207</td>
<td><em>B. clarridgeiae</em></td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>201</td>
<td><em>B. clarridgeiae + B.henselae</em></td>
<td>Negative</td>
<td>Negative</td>
</tr>
<tr>
<td>206</td>
<td>Negative</td>
<td><em>B. clarridgeiae</em></td>
<td>Negative</td>
</tr>
<tr>
<td>202</td>
<td><em>B. clarridgeiae</em></td>
<td>Negative</td>
<td>Negative</td>
</tr>
<tr>
<td>Shelter 4</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>117</td>
<td><em>B. henselae</em></td>
<td><em>B. henselae</em></td>
<td>Negative</td>
</tr>
<tr>
<td>116</td>
<td><em>B. henselae</em></td>
<td>*</td>
<td>Negative</td>
</tr>
<tr>
<td>Shelter 5</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>132</td>
<td>Negative</td>
<td><em>B. clarridgeiae</em></td>
<td>Negative</td>
</tr>
<tr>
<td>131</td>
<td><em>B. clarridgeiae</em></td>
<td>Negative</td>
<td>Negative</td>
</tr>
</tbody>
</table>

*Positive sample, but showing weak bands whose DNA concentration was too low to be sequenced.*
Ectoparasites

<p>| | | | |</p>
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</thead>
<tbody>
<tr>
<td>129</td>
<td>*</td>
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<tr>
<td>Shelter 6</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>193</td>
<td>*</td>
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<td>200</td>
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</tr>
<tr>
<td>198</td>
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</tbody>
</table>

*Positive sample, but showing weak bands whose DNA concentration was too low to be sequenced.

At least one *Bartonella* species was detected in fleas in each shelter. Additionally, all bacteria species detected in each shelter’s fleas were also identified in at least one of its cats. *Bartonella* spp. was also amplified from fleas belonging to apparently uninfected cats and from bacteremic cats infested by negative fleas. Not all fleas had the same *Bartonella* species as their hosts. Two of three fleas collected from infected cats carried the same *Bartonella* species as their cat hosts (Table 2). Whereas 60% (9/15) of cats infested by positive ectoparasites was bacteremic, the prevalence was only 40% (10/25) in those infested by negative ectoparasites. Although cats infested by positive ectoparasites, especially fleas, had more than twice the chance of being infected, there was no statistical correlation between cats’ bacteremia status and parasitism by positive fleas (Table 3).

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
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<tbody>
<tr>
<td>Cat blood</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fleas</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>aSame letters in the same column did not differ by Chi-square test at 5% significance.</td>
<td></td>
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</tr>
</tbody>
</table>

All sequences showed 99 to 100% homology with *B. henselae, B. clarridgeiae* and *B. koehlerae* reference sequences. Sequences were deposited into Genbank under accession no.: MT112180 - MT112197 and MT095045 - MT095055 for *gltA* gene and ITS region, respectively (Fig. 1; 2).
4. Discussion

One Health is an initiative aiming to bring together human, animal, and environmental health and plays a significant role in zoonosis prevention and control [17]. The increasingly close health relationship between humans and their domestic animals, especially cats, is conspicuous. According to the Brazilian Association of Pet Products Industry, the cat population has shown an accelerated annual growth in Brazil. Based on these facts, zoonosis studies have become ever more important. From a public health perspective, cats are a major reservoir host for at least three zoonotic *Bartonella* species (*B. henselae*, *B. clarridgeiae*, and *B. koehlerae*) and they are commonly infested by *C. felis* fleas, which also represent the great majority of fleas observed in peoples’ homes [18]. To the best of our knowledge, this is the first study in Brazil to investigate *Bartonella* DNA in shelter cats and their ectoparasites.

The overall prevalence of *Bartonella* DNA was 47.5% in cat blood, 18.3% in fleas, 13.3% in flea egg pools, and 12.5% in lice pools. The occurrence of *Bartonella* DNA was higher than previously reported, especially in shelter cats [19–25]. However, a previous study reported 97.3% positivity in one shelter in Rio de Janeiro, Brazil [26]. Risk factors which appear to influence the occurrence of bacteremia in cats includes age, flea infestation status, neutering status, historic of fghts, outdoor access and multiple cat households [25, 27–29]. Flea infestation status is particularly important as all cats in this study had ectoparasites on their body surface. *Bartonella* DNA detected in *C. felis* varies worldwide, with prevalence ranging from 7.3–75.6% [10, 20, 30–32]. *Bartonella* DNA was not detected in *R. sanguineus* ticks or *F. subrostratus* lice collected from shelter cats in Taiwan [30].

This study confirmed *Bartonella henselae*, *Bartonella clarridgeiae*, and *Bartonella koehlerae* single infection as well as coinfection by *B. henselae* and *B. clarridgeiae* in feline blood samples. Occurrence of concurrent infection by two or more *Bartonella* species are uncommon in the literature, being documented in low percentages of cats or being absent [5, 31, 33]. The *Bartonella* species encountered in the present study in cat fleas (*B. henselae* and *B. clarridgeiae*) have also been detected in cat fleas in previous studies [20, 34–36].

In all shelters, *Bartonella* spp. were detected in fleas and their hosts. In one shelter, the *Bartonella* species detected in fleas and their eggs were different from those in their respective hosts. However, the discrepant bacteria species was detected in other cats sharing the same environment. For such non coincident cases, it is possible that fleas previously fed on different bacteremic cats from the one on which they were collected.

Interestingly, bacteria DNA was detected in fleas collected from non-bacteremic hosts and detected in cats harboring negative fleas. It is noteworthy that in this study, fleas collected from cats represent a sample of the real flea population present on cats and in the local environment. Thus, newly emerged or not yet infected fleas may have been collected. Examples of different bacterial species in fleas and cat hosts has been documented previously [31, 36–39].
The presence of Bartonella DNA in C. felis fleas collected in bacteremic cats also suggests that these ectoparasites play an essential role in the transmission of Bartonella species to cats. A study has shown C. felis to be a potential vector for Bartonella species including those for which cats serve as natural reservoir, such as B. henselae and B. claridgeiae [40]. In fact, there is a positive correlation between previous or current flea infestation and Bartonella bacteremia in shelter cats [25]. Although there was no statistical association, cats infested by fleas have at least twice the chance of becoming infected by Bartonella species. Similarly, previous studies found no apparent correlation [37, 39].

To the best of the authors’ knowledge, Bartonella DNA was detected for the first time in lice collected from bacteremic cat. This cat was infested with lice at the time of collection, had historic of flea infestation and lived at shelter 6, where Bartonella species DNA was also detected in fleas and contactant cats. Considering the flea importance on Bartonella transmission between cats [9, 25] and the absent link of lice infestation to Bartonella infection in cats in this and previous studies [25, 30], it is necessary to be cautious to infer that the louse was responsible for the transmission of bacteria to the cat in the present study. In order to analyse the importance of the lice as a vector of Bartonella spp. to cats, one must invest on further studies.

The possibility of vertical Bartonella spp. transmission among fleas remains as a hypothesis. In our study, B. henselae DNA was detected in naturally infected fleas and their respective eggs. Consistent with our findings, Bartonella DNA was detected in reproductive tissues (ovary) of flea species collected from several mammals, suggesting that transovarian transmission of this organism among fleas may be is possible [41]. However, no Bartonella DNA was amplified in eggs laid by infected fleas, but the authors concluded that their results cannot be extended to natural conditions [40]. Knowledge of Bartonella behavior and dispersal in fleas is limited and the question of whether fleas can acquire Bartonella by mechanisms other than ingestion of infected blood remains. Additional studies are needed to validate the vertical transmission hypothesis. According to a study evaluating ticks as a possible bacterial vector, transovarian transmission was not supported because no bacterial amplification was obtained in larvae even though B. henselae DNA was detected in the respective egg pools laid by female ticks that had fed on infected blood [42].

This study shows that three distinct Bartonella species occur in shelter cats in metropolitan region of Rio de Janeiro and that B. henselae and B. claridgeiae circulate among fleas collected from them, reinforcing the importance of this ectoparasite in bacterial transmission between cats. For public health purposes, it is important to note that Bartonella species identified in ectoparasites and their host cats are agents associated with human disease. Thus, ectoparasites control measures should be implemented to prevent flea infestation and, consequently, Bartonella infection in cats and the humans with whom they have close contact.

**Declarations**

5. Consent for publication
Not applicable.

6. Competing interests

The authors declare that they have no competing interests.

7. Availability of data and materials

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

8. Funding

This research was financially supported by Carlos Chagas Filho Foundation for Research Support in the State of Rio de Janeiro (FAPERJ; grant number: E-26/110.386/2014).

9. Author’s contributions

JMR is the first author, conducted the experiments, analyzed all data and wrote the manuscript. AG performed data collection and helped in phylogenetical analysis. GMA, ATS and CJCR contributed in blood sample collection. HAS and ERSL provided access to biology molecular equipment. ARMF is the co-advisor, provided access to biology molecular equipment and helped to draft the paper. CBD is the advisor, conceived of the study, participated in its design and coordination and helped to draft the paper. All authors read, revised and approved the final manuscript.

10. Acknowledgements

We acknowledge the researchers Maria L. Corrêa, and Raisa B. Rodrigues for helping in the blood sample collection, Adriana Ribeiro da Silva for assisting in molecular analysis and James R. Welch for revising English language of this

References


**Figures**
Figure 1

Phylogenetic relationship of Bartonella species detected in shelter cats and ectoparasites based on gltA gene. Phylogenetic position of Bartonella species isolates from shelter cats (●), cat fleas (▲) and cat flea eggs (Δ), Rio de Janeiro, Brazil. The phylogenetic tree was constructed using the Maximum (T92+G) and the numbers on the tree nodes indicate bootstrap values with 1000 replicates. Accession numbers are indicated. Bartonella bacilliformis was used as outgroup. Scale bar indicates nucleotide substitutions per site.
Figure 2

Phylogenetic relationship of Bartonella species detected in shelter cats and fleas based on ITS region
Phylogenetic position of Bartonella sp. isolates from shelter cats (●) and their fleas (▲), Rio de Janeiro, Brazil. The phylogenetic tree was constructed using the Maximum Likelihood (T92+I) and the numbers on the tree nodes indicate bootstrap values with 1000 replicates. Accession numbers are indicated. Bartonella bacilliformis was used as outgroup. Scale bar indicates nucleotide substitutions per site.

Supplementary Files

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- GraphicalAbstractParasitesandvectors.png