

Evidence and molecular characterization of *Bartonella* spp. and hemoplasmas in neotropical bats in Brazil

P. IKEDA¹, M. C. SEKI², A. O. T. CARRASCO², L. V. RUDIAK²,
J. M. D. MIRANDA², S. M. M. GONÇALVES², E. G. L. HOPPE¹,
A. C. A. ALBUQUERQUE³, M. M. G. TEIXEIRA⁴, C. E. PASSOS¹,
K. WERTHER¹, R. Z. MACHADO¹ AND M. R. ANDRÉ^{1*}

¹ Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista (Unesp), Jaboticabal, SP, Brazil

² Universidade Estadual do Centro-Oeste, Campus CEDETEG, Guarapuava, Paraná, Brazil

³ Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista (Unesp), Botucatu, SP, Brazil

⁴ Instituto de Ciências Biomédicas, Universidade de São Paulo (USP), São Paulo, Brazil

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SUMMARY

The order Chiroptera is considered the second largest group of mammals in the world, hosting important zoonotic virus and bacteria. *Bartonella* and hemotropic mycoplasmas are bacteria that parasite different mammals' species, including humans, causing different clinical manifestations. The present work aimed investigating the occurrence and assessing the phylogenetic positioning of *Bartonella* spp. and *Mycoplasma* spp. in neotropical bats sampled from Brazil. Between December 2015 and April 2016, 325 blood and/or tissues samples were collected from 162 bats comprising 19 different species sampled in five states of Brazil. Out of 322 bat samples collected, while 17 (5.28%) were positive to quantitative PCR for *Bartonella* spp. based on *nuoG* gene, 45 samples (13.97%) were positive to cPCR assays for hemoplasmas based on 16S rRNA gene. While seven sequences were obtained for *Bartonella* (*nuoG*) ($n = 3$), *gltA* ($n = 2$), *rpoB* ($n = 1$), *ftsZ* ($n = 1$), five 16S rRNA sequences were obtained for hemoplasmas. In the phylogenetic analysis, the *Bartonella* sequences clustered with *Bartonella* genotypes detected in bats sampled in Latin America countries. All five hemoplasmas sequences clustered together as a monophyletic group by Maximum Likelihood and Bayesian Inference analyses. The present work showed the first evidence of circulation of *Bartonella* spp. and hemoplasmas among bats in Brazil.

Key words: Bartonellaceae, Chiroptera, hemotropic mycoplasmas, phylogenetic analyses, South America.

INTRODUCTION

The order Chiroptera is considered the second largest group of mammals in the world, composed by ~20% of mammals with more than 1200 species that are

present in all continents, except Antarctica [1]. These animals are known to be hosts of important zoonotic virus (e.g. lyssavirus and hantavirus) and bacteria (e.g. *Leptospira* spp. and *Pasteurella* spp.) [2].

* Author for correspondence: M. R. André, Laboratório de Imunoparasitologia, Departamento de Patologia Veterinária, Faculdade de Ciências Agrárias e Veterinárias Júlio de Mesquita Filho (UNESP), Campus de Jaboticabal, Via de Acesso Prof. Paulo Donato Castellane, s/n, Zona Rural, CEP: 14884-900, Jaboticabal, São Paulo, Brazil.
(Email: marcos_andre@fcav.unesp.br)

The genus *Bartonella* spp., belonging to the order Rhizobiales, comprises Gram-negative facultative intracellular α -proteobacteria that parasite mammals' erythrocytes and endothelial cells [3]. These re-emerging agents have been identified in a wide variety of mammals and incriminated as important cause of diseases in humans and animals, causing different clinical manifestations ranging from self-limiting to potentially fatal syndromes [4–6].

Hemotropic mycoplasmas (hemoplasmas) are Gram-negative bacteria belonging to the order Mycoplasmatales, family Mycoplasmataceae, genus *Mycoplasma* [7]. These pathogens are known to cause manifestations ranging from asymptomatic and chronic disease to severe hemolytic anemia due to the capacity of adhesion to the erythrocyte surface, causing indentation or deformation of the target-cell membrane. Acute infected animals can also present anorexia, fever, icterus, and hypoglycemia, depending on the species involved [8–10]. These agents have also been detected in different mammals' species, including humans [11–13].

Bartonella species can be transmitted by arthropod vectors, scratch, or by direct contact with blood or bodily fluids from animals [14]. Similarly, hemoplasmas are supposed to be transmitted mainly by blood-sucking arthropod transmission or aggressive interactions between animals [8, 9].

Bartonella spp. and *Mycoplasma* spp. have been detected in a variety of wild animals all over the world. In Brazil, these agents have been reported in several wild mammals, such as wild carnivores [15–17], deer [18], peccary [19], non-human primates [20, 21], and rodents [22–26].

The presence of *Bartonella* spp. in Chiroptera has been reported in bats sampled in the UK [27], Kenya [4], Taiwan [28], Peru [29], Nigeria [30], Puerto Rico [31], Finland [32], Madagascar [33], Costa Rica [34], Guatemala [35, 36], French Guiana [37], Gana [38], Algeria [39], and South Africa [40]. On the other hand, *Mycoplasma* spp. have already been molecularly detected in bats in the USA [13] and Spain [14].

The present work aimed to investigate the occurrence and assessing the phylogenetic positioning of *Bartonella* spp. and *Mycoplasma* spp. in bats sampled from Brazil.

MATERIAL AND METHODS

Between December 2015 and April 2016, tissue and/or blood samples were collected from 162 bats, comprising 19 species belonging to four different families,

namely Vespertilionidae, Phyllostomidae, Molossidae, and Natalidae, sampled in five states in Brazil (Mato Grosso, Pará, Paraná, São Paulo, and Tocantins) (Fig. 1).

The bat captures were performed in accordance with the licenses obtained from the Brazilian Government Institute for Wildlife and Natural Resources Care (IBAMA) (license numbers 48306–1 and 10080–2), and were endorsed by the Ethics Committee of FCAV/UNESP University (Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista 'Júlio de Mesquita Filho', Câmpus Jaboticabal) n° 8189/15. The captures were performed as previously described [41, 42] using mist net (Zootech™, Curitiba, Paraná, Brazil) with variable sizes (3 m × 6 m, 3 m × 9 m, 3 m × 12 m). The nets were placed before sunset and kept closed until nightfall. Once opened, they were checked every 30 min until reaching sample effort of eight animals or until midnight. The animals were carefully removed from the mist nets with leather gloves, taken to the field laboratory to weight, determine species and gender, and then taken to the university's laboratory for euthanasia, necropsy procedures, and tissue samples collections.

DNA was extracted from 10 mg of spleen tissue and 25 mg of liver and heart tissues using the DNeasy™ Blood & Tissue Kit (Qiagen™, Valencia, California, USA), according to the manufacturer's instructions. The DNA quality was evaluated by concentration and 260/280 and 260/230 nm absorbance ratios using a spectrophotometer (Nanodrop, Thermo Scientific, Wilmington, Delaware, USA), in which the purity for DNA samples is considered when ratios are ~1.8 and ~2.0, respectively. Also, a conventional PCR (cPCR) assay, based on a 400 pb fragment of GAPDH gene [43], was performed in order to evaluate the absence of inhibitors in DNA-extracted samples. Positive samples in the above-mentioned cPCR assay were submitted to additional *Bartonella* spp. and hemoplasmas PCR assays. All the cPCR assays were performed in a T100™ Thermal Cycler (BioRad™, Hercules, California, USA).

A previously described quantitative PCR (qPCR) protocol based on *nuoG* gene [45] was used aiming to detect and quantify *Bartonella* spp. DNA copies (number of copies/μl) in bats' biological samples. The qPCR assays were performed in 10 μl final volume reaction mixtures, containing 1 μl of DNA sample, 1.2 μM of each primer F-Bart (5' – CAATCTTCTTTTGCTTC ACC – 3'), R-Bart (5' – TCAGGGCTTTATGTGAAT AC – 3'), and hydrolysis probe TexasRed-5' – TT YGTCATTTGAACACG-3'(BHQ2a-Q) – 3', Master

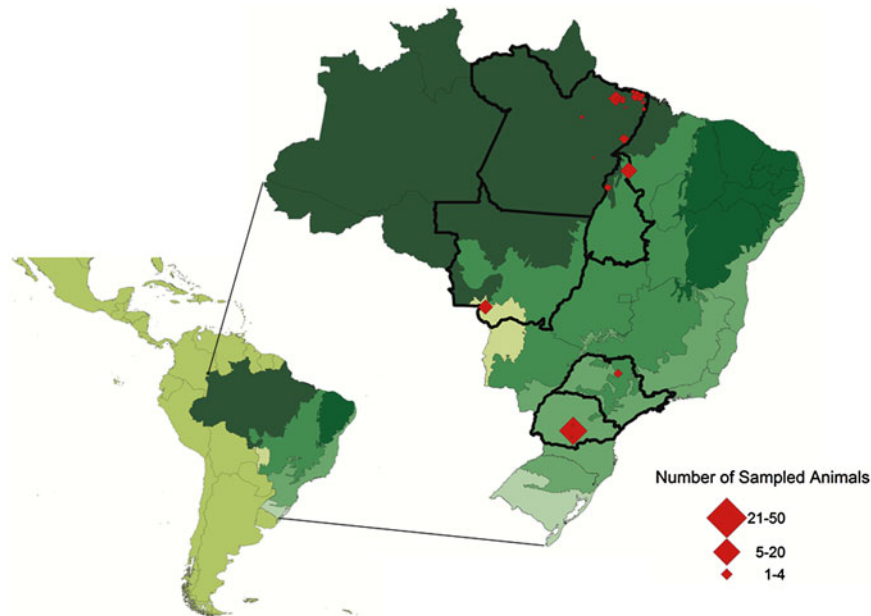


Fig. 1. Locations where bats were sampled in the present study. Each state is outlined in the map and the number of sampled animals is represented by a diamond symbol.

Mix 2× buffer (GoTaq™ Probe qPCR Master Mix, Promega Corporation, Madison, Wisconsin, USA) and ultra-pure sterilized water (Nuclease-Free Water, Promega Corporation, Madison, Wisconsin, USA) q. s.p. 10 µl. The amplification conditions were 95 °C for 3 min followed by 40 cycles at 95 °C for 10 s and 52.8 °C for 30 s [44]. PCR amplifications were conducted in low-profile multiplate unskirted PCR plates (BioRad™, Hercules, California, USA), using a CFX96 Thermal Cycler (BioRad™, Hercules, California, USA). Standard curves were constructed with serial dilutions of plasmid DNA (pIDTSMART – Integrated DNA Technologies, Coralville, Iowa, USA) (2.0×10^7 – 2.0×10^0 copies/µl), which encoded an 83 bp *Bartonella henselae*-*nuoG* gene fragment. The number of plasmid copies was determined in accordance following the formula:

$$\left(\frac{x \text{ g/}\mu\text{l DNA}}{\text{plasmid length in bp} \times 660 \text{ g/mol}} \right) \times 6.022 \times 10^{23} \text{ copies/mol} = Y \text{ copies/}\mu\text{l}.$$

Each qPCR assay was performed including duplicates of each bat DNA sample and plasmids. All duplicates showing *Cq* values difference higher than 0.5 were retested in triplicates. Amplification efficiency (*E*) was calculated from the slope of the standard curve in each run using the following formula ($E = 10^{-1/\text{slope}}$). The standard curves generated by 10-fold dilutions

were used to determine the amount of DNA that could be detected with 95% of sensitivity [45].

In order to perform the molecular characterization of *Bartonella* spp., DNA samples from positive bats in qPCR reactions were submitted to previously described cPCR assays targeting eight different genes, namely *nuoG* (400 bp) [46], *ribC* (420 bp) [47], *gltA* (750 bp) [48], *rpoB* (800 bp) [49], the intergenic region 16S–23SrRNA ITS (453–717 bp) [50], *groEL* (752 bp) [49, 51], *fstZ* (600 bp) [49], 16SrRNA (400 bp) [49], and *pap-31* (564 bp) [52]. *B. henselae* DNA obtained from a naturally infected cat [45] and sterilized ultrapure water (Nuclease-Free Water, Promega™, Madison, Wisconsin, USA) were used as positive and negative controls, respectively.

In order to amplify *Mycoplasma* spp. DNA, two cPCR assays based on 16SrRNA gene were performed, using two sets of primers, namely HemMycop16S-41s (5'-GYATGCMATAAYACATGCAAGTCGARCG-3') and HemMycop16S-938as (5'-CTCCACCACTTGTT CAGGTCCCCGTC-3') (fragment of ~800 bp), and HemMycop16S-322s (5'-GCCCATATTCCTACGG GAAGCAGCAGT-3') and HemMycop16S-1420 as (5'-GTTTGACGGGCGGTGTGTACAAGACC-3') (fragment of ~800 bp) [53]. Five microliters of DNA were used as a template in 25 µl reaction mixtures containing 10× PCR buffer, 1.0 mM MgCl₂, 0.8 mM deoxynucleotide triphosphate mixture, 1.5 U Taq Platinum DNA Polymerase (Life Technologies™, Carlsbad,

California, USA), and 0.3 µM of each primer. *Mycoplasma haemofelis* DNA obtained from a naturally infected cat [54] and ultra-pure sterile water (Nuclease-Free Water, Promega™, Madison, Wisconsin, USA) were used as positive and negative controls, respectively. PCR amplifications were performed at 94 °C for 2 min followed by 55 repetitive cycles of 94 °C for 15 s, 68 °C for 15 s, and 72 °C for 18 s, followed by a final extension at 72 °C for 1 min. The 16S rRNA-*Mycoplasma* spp. positive samples were additionally submitted to an RNaseP gene-*Mycoplasma* sp. (165 bp) cPCR assay using the oligonucleotides HemoMycoRNaseP30s (5'-GATKGT GYGAGYATATAAAAAATAAARCTCRAC - 3') and HemoMyco RNaseP200as (5' - GMGGRGTTT ACCGCGTTTCAC - 3'). The conditions of amplification were the same as described above, except for the annealing temperature (59 °C) [53].

The products obtained in all the cPCR assays were separated by electrophoresis on a 1% agarose gel stained with ethidium bromide (Life Technologies™, Carlsbad, California, USA) under 100 V/150 mA for 50 min. The gels were imaged under ultraviolet light (ChemiDoc MP Imaging System, Bio Rad™, Hercules, California, USA) using the Image Lab Software version 4.1.

Amplified products were purified using the Silica Bead DNA gel extraction kit (Thermo Fisher Scientific™, Waltham, Massachusetts, USA) and submitted to sequencing, which was performed using the BigDye™ Terminator v3.1 Cycle Sequencing Kit (Thermo Fisher Scientific™) and ABI PRISM 310DNA Analyzer (Applied Biosystems™, Foster City, California, USA) [55].

The sequences obtained from positive samples were first submitted to a screening test using Phred-Phrap software version 23 [56, 57] to evaluate the electropherogram quality and to obtain consensus sequences from the alignment of the sense and antisense sequences. The BLAST program [58] was used to analyze the sequences of nucleotides (BLASTn), aiming to browse and compare with sequences from an international database (GenBank) [59]. The consensus sequences obtained in the present study and those retrieved from GenBank were aligned using the Clustal/W software [60] via Bioedit version 7.0.5.3 [61]. Phylogenetic inference was based on Bayesian Inference (BI) and Maximum Likelihood (ML) methods. The BI analysis was performed with MrBayes 3.1.2 [62] via CIPRES Science Gateway [63]. Markov Chain Monte Carlo (MCMC) simulations

were run for 10⁶ generations with a sampling frequency of every 100 generations and a burn-in of 25%. The ML analysis was inferred with the W-IQ-Tree tool available online (<http://iqtree.cibiv.univie.ac.at/>) [64, 65] using 1000 bootstrapping replicates. The best model of evolution was selected by the program jModelTest2 (version 2.1.6) on XSEDE [66], under the Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) [67]. All the trees were examined in Treegraph 2.0.56–381 β [68].

RESULTS

A total of 122 liver tissue samples, 107 spleen tissue samples, 56 heart tissue samples, and 40 blood samples collected from 162 bats in different states of Brazil were used in this study. So, out of 325 bats' biological samples, 322 samples were positive in cPCR for GAPDH gene (Table 1). The mean and standard deviation of the values of concentration and absorbance ratios (260/280 and 260/230 nm) are shown in Table 2.

Seventeen (5.28%) out of 322 samples were positive for *Bartonella* spp. in qPCR assays based on the *nuoG* gene, including four samples collected from three bats from the state of Paraná (*Sturnira lilium* ($n = 3$)); six from the state of Pará (*Phyllostomus hastatus* ($n = 1$), *Carollia perspicillata* ($n = 4$), and *Natalus espirosantensis* ($n = 1$)); and seven from the state of Tocantins (*C. perspicillata* ($n = 2$) and *Glossophaga soricina* ($n = 5$)). The efficiency, R^2 , slope, and Y -intercept of reactions ranged from 90.8% to 98.6% (mean = 95.09%), 0.987 to 1 (mean = 0.995), -3.355 to -3.566 (mean = -3.447), and 37.284 to 38.871 (mean = 38.067), respectively. The quantification positive *nuoG* *Bartonella* spp. ranged from 4.4×10^3 to 6.95×10^3 copies/µl (Table 3).

Thirteen (76.47%) out of 17 positive samples in the qPCR were also positive for at least one target gene in cPCR assays for *Bartonella* spp. Four (30.77%) of them were positive for the *ftsZ* gene, three (23.07%) for the *nuoG* gene, three (23.07%) for the *ribC* gene, two (15.38%) for the *groEL* gene, and one (7.69%) was positive for the *rpoB* gene. None of them were positive for *pap-31* and *16SrRNA* genes and for the intergenic region 16S–23S rRNA (ITS). Due to the low intensity of some amplified products, which precluded high-quality sequencing, only seven *Bartonella* spp. sequences were obtained (*nuoG* ($n = 3$), *gltA* ($n = 2$), *rpoB* ($n = 1$), *ftsZ* ($n = 1$)). The sequences obtained were deposited to the GenBank under accession numbers KY356752–KY356758.

Table 1. Number of bat species positive for *Bartonella* spp. and hemoplasmas in Brazil, according to locality and tissue sampled

State	Species	Number of sampled animals	Tissue sample	Total number of samples	Number of positive samples for <i>Bartonella</i> spp.	Number of positive samples for hemoplasmas			
Paraná	<i>Sturnira lilium</i>	24	Liver, spleen and heart	150	04	13			
	<i>Molossus molossus</i>	20			—	18			
	<i>Eptesicus</i> sp.	05			—	02			
	<i>Sturnira tildae</i>	01			—	—			
Pará	<i>Carollia perspicillata</i>	26	Liver and spleen	117	04	—			
	<i>Artibeus planirostris</i>	08			—	03			
	<i>M. molossus</i>	07			—	02			
	<i>Glossophaga soricina</i>	06			—	—			
	<i>Artibeus lituratus</i>	03			—	—			
	<i>Molossus rufus</i>	03			—	—			
	<i>Eumops glaucinus</i>	02			—	—			
	<i>S. lilium</i>	02			—	—			
	<i>Artibeus cinereus</i>	01			—	—			
	<i>Phyllostomus discolor</i>	01			01	—			
	<i>Phyllostomus hastatus</i>	01			—	—			
	<i>Myotis nigricans</i>	01			—	01			
	<i>Natalus espiritosantensis</i>	01			01	—			
	<i>Uroderma bilobatum</i>	01			—	—			
	<i>Micronycteris minuta</i>	01			—	—			
	<i>Eumops auripendulos</i>	01			—	01			
	<i>Mimon crenulatum</i>	01			—	—			
	Tocantins	<i>G. soricina</i>			19	Whole blood	24	05	04
		<i>C. perspicillata</i>			5			02	—
São Paulo	<i>M. molossus</i>	03	Liver, spleen and heart	18	—	—			
	<i>Artibeus</i> sp.	02			—	—			
	<i>Myotis</i> sp.	01			—	—			
Mato Grosso	<i>M. rufus</i>	15	Whole blood	16	—	01			
	<i>G. soricina</i>	01			—	—			
TOTAL				325	17	45			

Table 2. Mean and standard deviation values of concentration and absorbance ratios (260/280; 260/230 nm) of DNA samples extracted from each type of bats' biological sample

	Whole blood	Liver tissue	Spleen tissue	Heart tissue
Concentration (ng/μl)	5.03 ± 5.40	211.91 ± 140.35	139.06 ± 168.89	55.09 ± 24.02
260/280	2.49 ± 2.32	1.91 ± 0.27	1.86 ± 1.10	1.99 ± 0.07
260/230	0.52 ± 0.25	1.69 ± 0.44	2.30 ± 2.91	1.67 ± 0.39

Regarding the occurrence of hemoplasmas among bats, while 45 samples (13.97%) were positive for the first 16S rRNA protocol (using HemMycop16S-41s and HemMycop16S-938 as primers), 14 samples (4.34%) were positive for the second 16S rRNA protocol (using HemMycop16S-322s and HemMycop16S-1420 as primers). Among positive animals, 33 samples were collected from 18 bats in the state of Paraná (*Molossus molossus* ($n=10$), *S. lilium* ($n=8$), *Eptesicus* spp. ($n=1$)); seven samples were collected from bats in the state of Pará (*Artibeus planirostris* ($n=3$), *M. molossus* ($n=2$), *Eumops auripendulos* ($n=1$), *Myotis nigricans* ($n=1$)); four from bats in the state of Tocantins (*G. soricina* ($n=4$)); and one from a bat in the state of Mato Grosso (*Molossus rufus*). Twelve (26.66%) out of 45 samples positive for hemoplasmas based on 16S rRNA gene were also positive at RNAaseP gene-cPCR assay. A total of five (1.55%) samples were positive for the three performed protocols. Unfortunately, only five 16S rRNA hemoplasmas sequences (Paraná ($n=4$), Pará ($n=1$)), detected in specimens of *M. molossus*, were obtained due to the low intensity of some amplified products, which precluded high-quality sequencing. The sequences were deposited to the GenBank data under the accession numbers KY356747–KY356751. Only one bat sampled in Tocantins state belonging to *G. soricina* species was positive for both *Bartonella* sp. and *Mycoplasma* sp.

Based on BLAST analysis, the found *Bartonella* *nuoG* sequences ($n=3$) showed 89–90% identity to *B. taylorii* (GenBank accession number EF659943) and 92% to *B. koehlerae* (GenBank accession number EF659942). Two *Bartonella* *gltA* sequences showed 98–100% identity to *Bartonella* sp. from bats sampled in Costa Rica (GenBank accession numbers KJ816674 and KJ816690). One *Bartonella* *rpoB* sequence showed 89% identity to *Bartonella* sp. Khabarovsk from Asian mammals (GenBank accession number AB779537). Finally, one *Bartonella* *ftsZ* sequence showed 98% identity to *Bartonella* sp. Honshu from deer sampled in Japan (GenBank accession number AB703117). The query coverage ranged from 96% to 100% in all

BLAST analyses run for *Bartonella* sequences. In the phylogenetic inferences based on ML and BI methods (Figs 2–5), the *Bartonella* sequences obtained in the present study were mainly closely related to other *Bartonella* sequences obtained from New World bats. When present, *Bartonella* sequences obtained from Old World bats clustered separately with high branch support.

The concatenated phylogenetic assessment of positive sequences for both *nuoG* (400 pb) and *gltA* (750 pb) genes showed a very similar topology in BI and ML methods, forming two different clusters. The sequences from bats detected in a specimen of *S. lilium* sampled in the state of Paraná was closely related to *Bartonella* sequences detected in a Hippoboscidae bat fly (*Aspidoptera delatorrei*) from Costa Rica and in a specimen of *C. perspicillata* from Guatemala with 100/100% of branch support. A *Bartonella* genotype detected in a specimen of *C. perspicillata* sampled in Tocantins was positioned in the same cluster (with 59% and 71% of support in BI and ML analyses, respectively) than genotypes detected in bats from Peru and Guatemala, rodents from Brazil and the USA, and from an ectoparasite (*Polygenis gwyni*) collected from rodents also in the USA. Moreover, a *Bartonella* sequence obtained in a specimen of *G. soricina* sampled in Tocantins state was positioned in a more basal clade and closely related to *Bartonella* genotypes detected in specimens of *Carollia sowelli* and its Streblidae dipteran *Strebla guajiro* from Costa Rica (with branch support of 100%) and genotypes detected in bats from Peru and Guatemala with 66% in both analyses (ML and BI) (Fig. 2).

The *Bartonella* *rpoB* sequence obtained in a specimen of *S. lilium* sampled in the state of Paraná was positioned alone in a branch, but closely related to two *Bartonella* genotypes detected in wild rodents from Asia (AB779537; AB290276) and *B. taylorii* (AF165995), with a branch support of 85% in ML and 94% of probability in BI analyses (Fig. 3).

The *Bartonella* *ftsZ* sequence obtained in a specimen of *C. perspicillata* sampled in the state of Pará was positioned alone in a branch, but closely related

Table 3. Positive samples for *Bartonella* sp. in qPCR assays based on *nuoG* gene with the reactions parameters

Sample	Species	Biological sample	Locality	Cq (mean)	Number of copies/ μ l	Efficiency (%)	R ²	Slope	Y-int
38019 B	<i>Phyllostomus hastatus</i>	Spleen	Viseu, Pará	34.23	8.208×10^0	98.1	0.998	-3.368	37.252
38197 B	<i>Carollia perspicillata</i>	Spleen	Castanhal, Pará	33.05	1.8035×10^1	98.1	0.998	-3.368	37.252
38295 B	<i>C. perspicillata</i>	Spleen	Belém-Mosqueiro, Pará	33.9	9.33×10^0	98.1	0.998	-3.368	37.252
38296 F	<i>C. perspicillata</i>	Liver	Belém-Mosqueiro, Pará	28.97	4.3945×10^2	93.7	1.000	-3.482	38.482
38706 F	<i>C. perspicillata</i>	Liver	Cachoeira do Piriá, Pará	32.69	2.2575×10^1	98.1	0.998	-3.368	37.252
37987 F	<i>Natalus espirosantensis</i>	Liver	Belém-Outeiro, Pará	33.51	1.292×10^1	98.1	0.998	-3.368	37.252
45 B	<i>Sturnira lilium</i>	Spleen	Parque das Araucárias, Guarapuava, Paraná	32.69	2.22615×10^1	98.1	0.998	-3.368	37.252
48 B	<i>S. lilium</i>	Spleen	Parque das Araucárias, Guarapuava, Paraná	34.02	1.876×10^2	93.6	0.997	-3.486	38.444
49 B	<i>S. lilium</i>	Spleen	Parque das Araucárias, Guarapuava, Paraná	31.21	1.1875×10^2	93.6	0.997	-3.486	38.444
49 F		Liver		34.30	7.623×10^0	98.1	0.998	-3.368	37.252
#30	<i>C. perspicillata</i>	Blood	Arapoema, Tocantins	24.31	6.9575×10^3	98.1	0.998	-3.368	37.252
# 42	<i>C. perspicillata</i>	Blood	Arapoema, Tocantins	30.67	2.1435×10^2	92.5	0.997	-3.515	38.871
M5	<i>Glossophaga soricina</i>	Blood	Aguiarnópolis, Tocantins	36.65	4.4065×10^0	92.5	0.997	-3.515	38.871
M16	<i>G. soricina</i>	Blood	Aguiarnópolis, Tocantins	33.07	1.9385×10^1	98.6	0.988	-3.555	37.389
M21	<i>G. soricina</i>	Blood	Aguiarnópolis, Tocantins	32.66	2.6425×10^1	98.6	0.988	-3.555	37.389
M23	<i>G. soricina</i>	Blood	Aguiarnópolis, Tocantins	33.40	1.3905×10^1	98.1	0.998	-3.368	37.252
M41	<i>G. soricina</i>	Blood	Aguiarnópolis, Tocantins	35.12	4.7855×10^0	98.6	0.988	-3.555	37.389

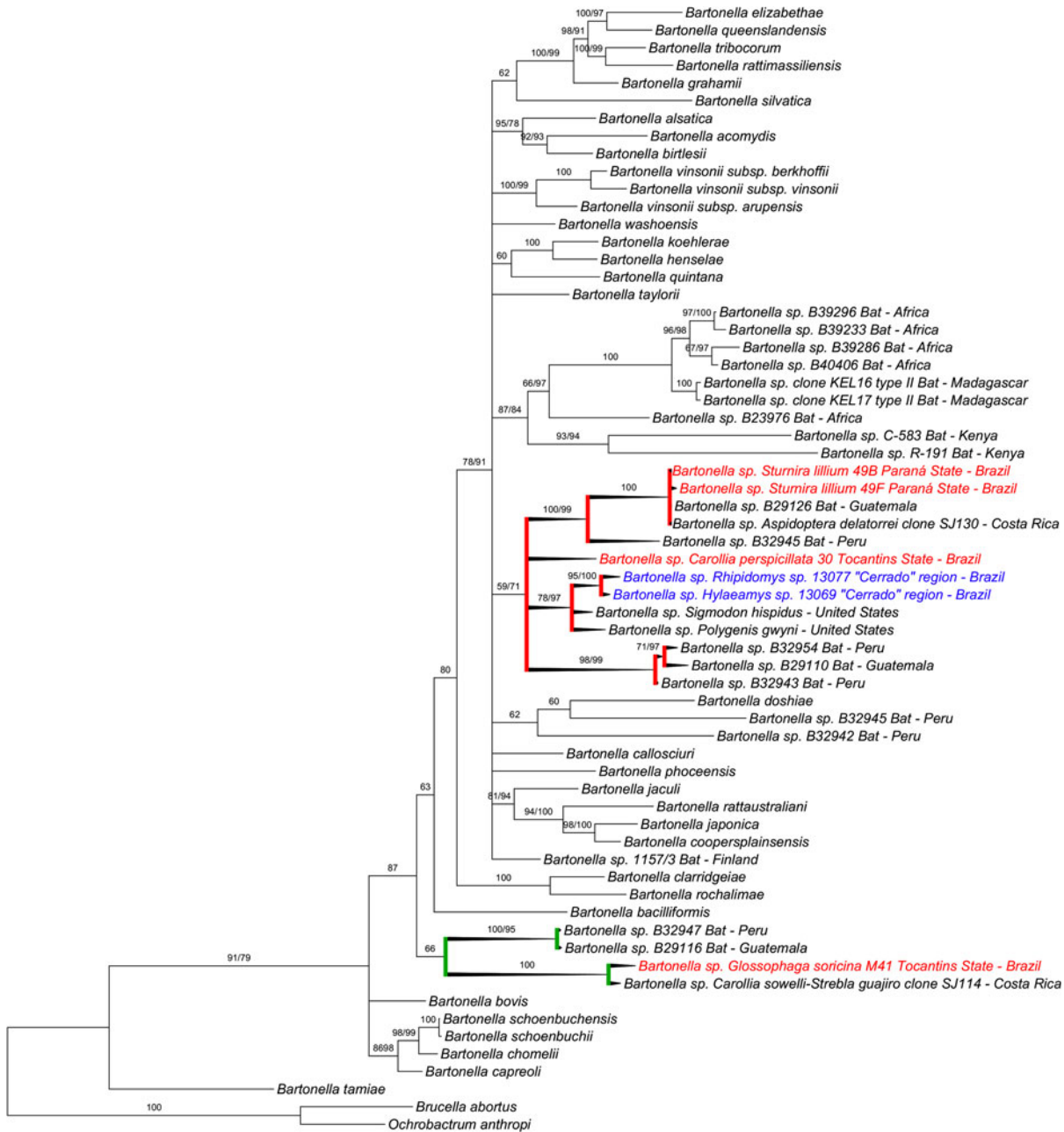


Fig. 2. Concatenated phylogenetic analysis of *Bartonella nuoG* and *gltA* sequences (3370 bp after alignment) based on the topology generated on the BI method. The values of support of posterior probability/bootstrap higher than 50% are shown in each branch. The sequences of the present work were highlighted in red composing two different clusters. One comprising three sequences of the present study (red branches) clustering with sequences obtained from bats from Guatemala and Peru and from rodents sampled in Brazil (sequences highlighted in blue) and in the USA with a 59/71% of probability. The other cluster (green branches) comprises one sequence obtained in the present study with sequences obtained from bats sampled in Costa Rica, Peru, and Guatemala, with 66% of probability. *Brucella abortus* and *Ochrobactrum anthropi* were used as outgroups.

(100% of branch support) to a *Bartonella* genotype detected in a deer in Japan (AB703117), *Bartonella chomelii* (KM215689/AB290193) and *Bartonella schoenbuchensis* (AF467765) (Fig. 4).

All five 16S rRNA hemoplasmas sequences detected in specimens of *M. molossus* sampled in the states of Paraná and Pará shared identity (93–96%) with *Mycoplasma coccoides* (AY171918), with query

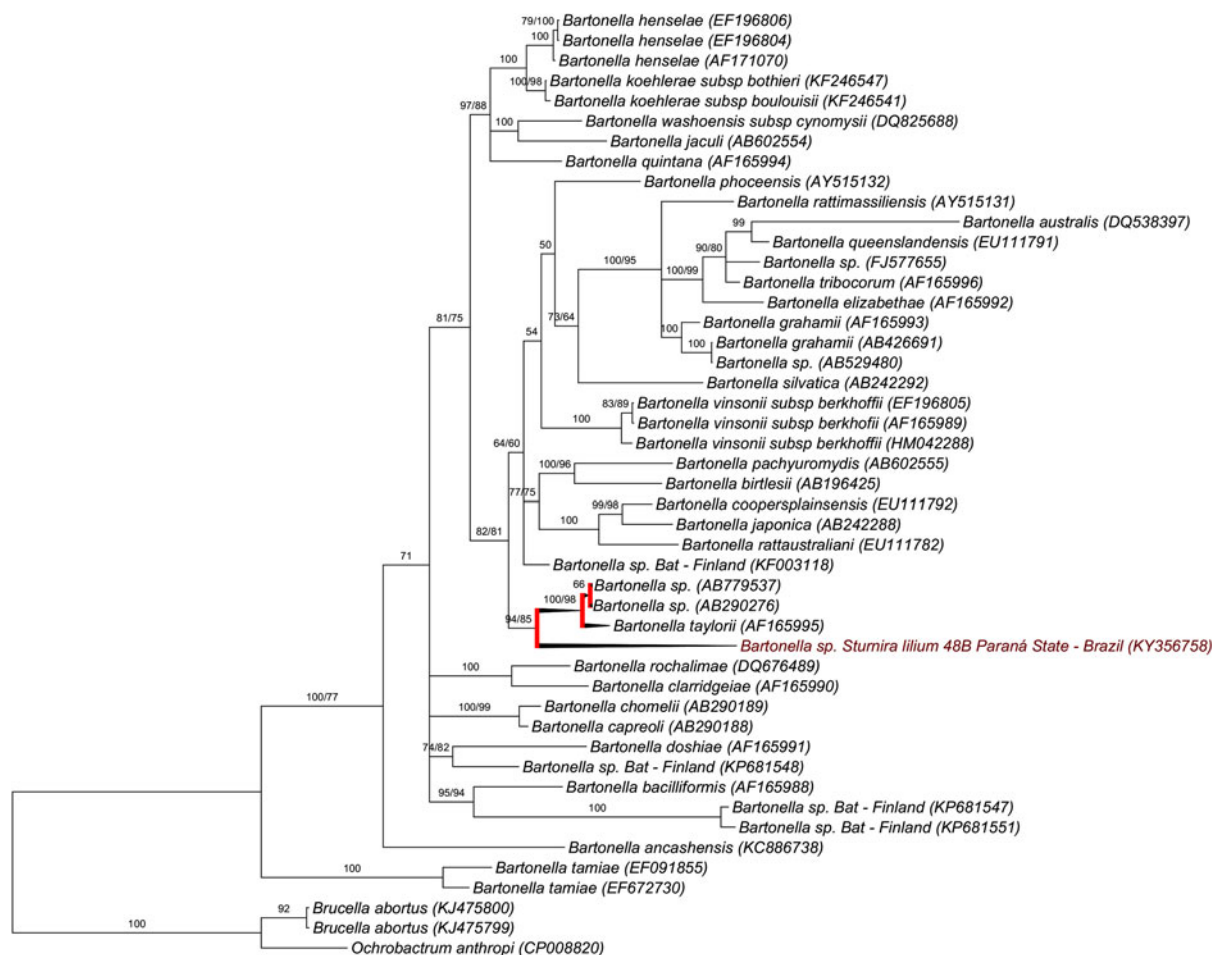


Fig. 3. Phylogenetic analysis of *Bartonella rpoB* sequences (1500 bp after alignment) based on the topology generated on the BI method. The values of support of posterior probability/bootstrap higher than 50% are shown in each branch. The sequence of the present work is highlighted in red. The sequence was positioned alone in one branch and clustered with *Bartonella* sp. from wild mammals from Asia with 94/85% of probability (red branches). *Brucella abortus* and *Ochrobactrum anthropi* were used as outgroups.

coverage ranging from 87% to 100%. Additionally, the found hemoplasma sequences showed 92–96% identity with an uncultured *Mycoplasma* sp. detected in an *Akodon* rodent from Brazil (KT215636), with query coverage ranging from 87% to 99%. All the hemoplasmas sequences obtained in the present study clustered together as a monophyletic group with branch support of 95/100% by ML and BI analyses. This group of sequences was positioned between *M. coccoides* (AY171918) and hemoplasma genotypes detected in rodents from Brazil (KM203857; KT215636). The hemoplasmas sequences detected in bats in the present study were positioned in the *Haemofelis* group (Figure 5).

DISCUSSION

The present work reported the occurrence and molecular characterization of *Bartonella* spp. and

Mycoplasma spp. among bat's population sampled in five different states of Brazil. This group of mammals has been incriminated as potential reservoirs for several pathogens due to their high mobility, worldwide distribution, and social behavior [35].

The *Bartonella* occurrence found in the present study (5.28%) was similar to that found in bats (3.38% (13/384)) sampled in Swaziland and South Africa, Africa [40]. Overall there is a relatively higher occurrence of *Bartonella* in bats sampled in the Old World, such as in Algeria (60% (6/10) by qPCR) [39], Nigeria (51.35% (76/148) by qPCR and 15.54% (23/148) by culture) [30], Kenya (32.02% (106/331) by culture) [4], and Madagascar (44.68% (21/47) by PCR) [33]. In neotropical species, *Bartonella* species have been already detected by solid culture followed by cPCR or only by PCR in bats sampled from Guatemala, Peru, and Costa Rica, whose

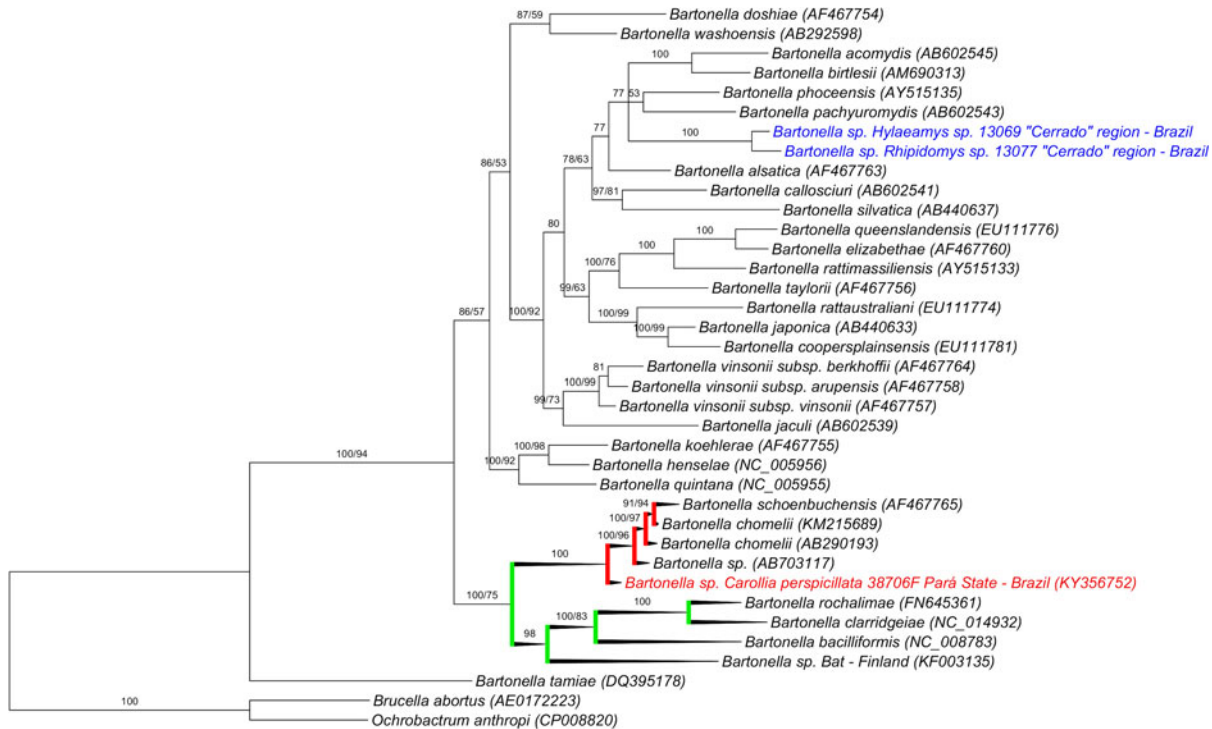


Fig. 4. Phylogenetic analysis of *Bartonella ftsZ* sequences (790 bp after alignment) based on the topology generated on the BI method. The values of support of posterior probability/bootstrap higher than 50% are shown in each branch. The *Bartonella* sequence of the present work was highlighted in red. The *Bartonella* sequences highlighted in blue were previously detected in rodents from the same research group. The *Bartonella* sequence detected in a specimen of *Carollia perspicillata* was positioned alone in one branch and clustered with *Bartonella* sp. detected in a deer from Asia and other *Bartonella* spp. with 100% of probability (red branches). A *Bartonella* genotype detected in a bat sampled in Finland was closely positioned with the sequence of the present study, with 100/75% of probability (green branches). *Brucella abortus* and *Ochrobactrum anthropi* were used as outgroups.

overall prevalence ranged from 24.1% to 33.3% [29, 34, 35].

Although a low occurrence of *Bartonella* in *S. lilium* and *G. soricina* bat specimens is reported [35], these animals together with *C. perspicillata* were the main Chiroptera species that showed positivity for *Bartonella* in the present study. Despite the high number of *Molossus* spp. individuals (29.01% (47/162)) sampled in the present study, none of them was positive for *Bartonella* sp., as previously reported [29] as well. *Bartonella* genotypes have already been described previously in the bat species sampled in the present work [29, 35], except for *N. espiritosantensis*.

Even though it is suggested that the spleen is the sample of choice to detect *Bartonella* spp. [69], no difference was observed among the tissues collected in the present study, since seven were from blood, six from splenic tissue, and four from liver tissue.

Bartonella host transitions are supposed to occur with bats within the same family, but transitions between bats belonging to different families,

superfamilies and suborders seem to occur infrequently [70]. It had already been hypothesized that a different pressure on the coevolutionary relationships between Old and New World bats host species, since Old World species seem to be more rustic and show a longer evolutionary time for the establishment of this sort of relationship [71]. This hypothesis could explain the different positioning of *Bartonella* genotypes detected in neotropical bats, including those sampled in the present study, when compared with those from Africa (Megachiroptera/Yangpteroptera). However, it is noteworthy to observe that *Bartonella* genotypes detected in bats from the present study were closely related to those detected in wild mammals, such as rodents and deer from Asia, based on *ftsZ* and *rpoB* phylogenetic analyses. Regarding to these findings, intra- and inter-specific *Bartonella* transmission has been already suggested, since different *Bartonella* species/genotypes can be found in only one individual [35].

Interestingly, *Bartonella* genotypes detected in Brazilian rodents were positioned in the same clade

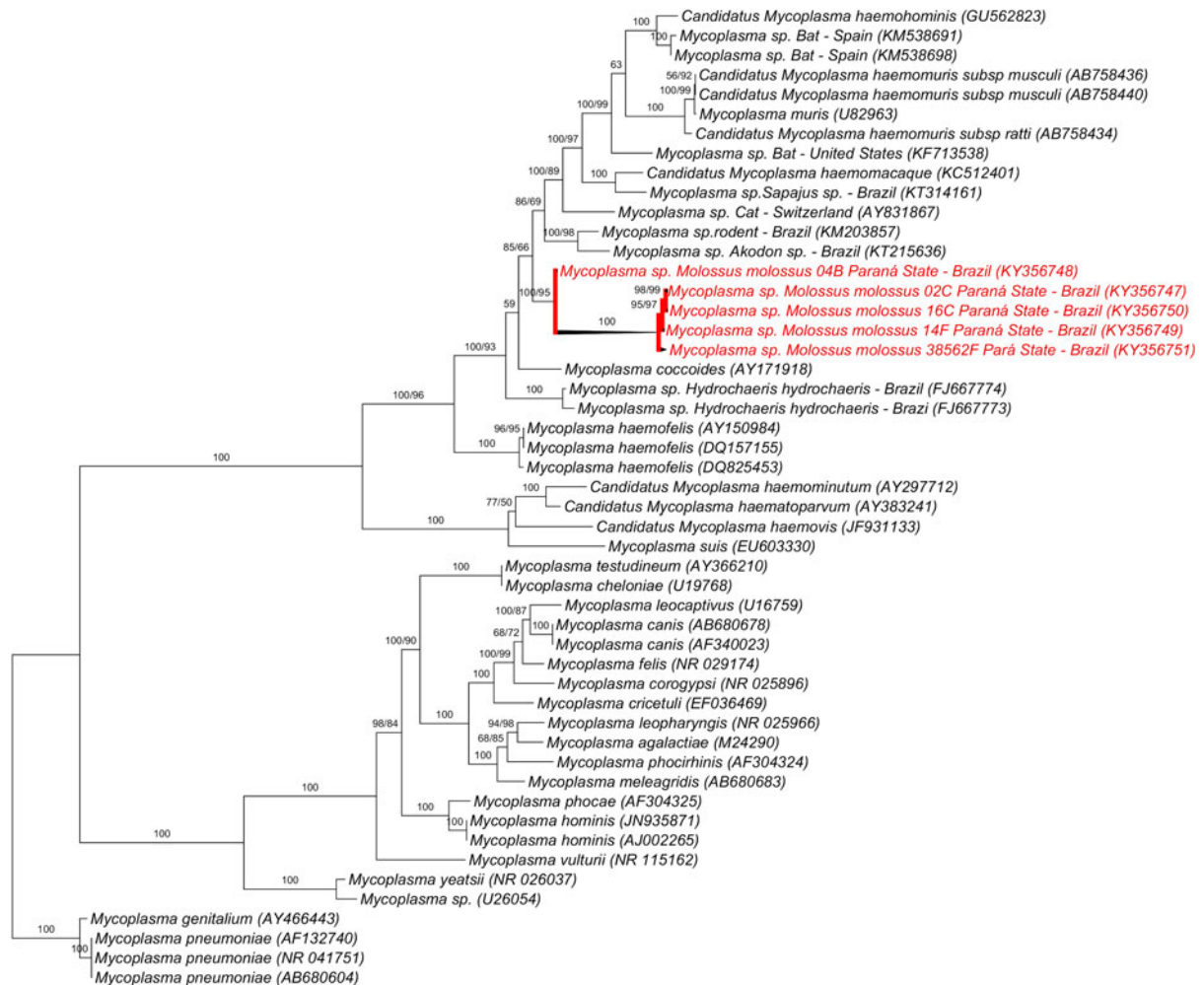


Fig. 5. Phylogenetic analysis of hemoplasmas 16S rRNA sequences (1770 bp after alignment) based on the topology generated on the BI method. The values of support of posterior probability/bootstrap higher than 50% are shown in each branch. The sequences of the present work were highlighted in red and placed together in a same branch with 100/95% of probability (red branches). *Mycoplasma pneumoniae* was used as outgroup.

with the sequences obtained from bats sampled in the present study with a 59/71% of node support based on the concatenated *nuoG* and *gltA* analysis. However, a *Bartonella* genotype detected in a specimen of *G. soricina* sampled in the state of Tocantins was positioned distant from the other *Bartonella* genotype detected in the state of Paraná, clustering with a *Bartonella* genotype detected in specimens of *C. soweri* and its Streblidae dipteran, namely *S. guajiro* from Costa Rica, based in *gltA/nuoG* concatenated analysis. These findings suggest the occurrence of different *Bartonella* genotypes among bats in Brazil. On the other hand, *Bartonella* genotypes amplified from different tissue samples (spleen and liver) belonging to a specimen of *S. lilium* sampled in Paraná state clustered together, probably representing the same *Bartonella* genotype.

Regarding the occurrence of hemoplasmas among bats, *Mycoplasma* spp. has been poorly reported in this group of mammals. Despite the *Molossus* spp. was the main group of bats positive for hemoplasmas in the present study, to the best authors' knowledge, this is the first molecular detection of hemoplasmas in eight bat species, namely *A. planirostris*, *Eptesicus* sp., *Eumops auripendulus*, *G. soricina*, *M. molossus*, *M. rufus*, *M. nigricans* and *S. lilium*.

High prevalence rates for hemoplasmas have been found in small populations of bats sampled in the USA (47% (32/68)) [12] and Spain (41–93% (13/31)) [13]. Interestingly, hemoplasmas genotypes detected in bats from both studies were similar to each other, but different for *Mycoplasma* genotypes detected in bats sampled in Brazil. The hemoplasmas sequences

detected in bats sampled in the USA and Spain clustered with ‘*Candidatus Mycoplasma haemohominis*’ that was detected in a human patient in England [72], and with *Mycoplasma haemomuris*, which has been detected in domestic, laboratory, and wild rodents [8]. Based on the phylogenetic positioning, hemoplasmas genotypes detected in bats in the present study seem to be different from those previously detected in bats sampled in the USA and Spain, since comprised a monophyletic group with high node support and closely related to *M. coccoides*.

Despite the higher positivity to hemoplasmas than to *Bartonella* spp., only one animal was co-positive for both studied pathogens. The pathogenic potential of both group of pathogens in bats have not been investigated.

Finally, it is important to highlight that *Bartonella* and *Mycoplasma* genotypes detected in bats from the present study were closely related to previously reported genotypes detected in rodents. From an evolutionary point of view, bats and rodents are large groups belonging to ancient orders of mammals [71], which have shown a high adaptation as hosts for different groups of pathogens.

To the best of authors’ knowledge, the present work presented the first molecular evidence of circulation of *Bartonella* and hemoplasmas among bats in Brazil. Future studies aiming at assessing the role of bats as reservoirs for *Bartonella* and *Mycoplasma* species showing zoonotic potential are much needed.

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DECLARATION OF INTEREST

None.

ETHICAL STANDARDS

The authors assert that all procedures contributing to this work comply with the ethical standards according

to the Ethical Principles in Animal Research adopted by the Brazilian College of Animal Experimentation, and to the 2000 Report of the AVMA Panel on Euthanasia (American Veterinary Medical Association, 2001).

REFERENCES

1. Schipper J, *et al.* The status of the world’s land and marine mammals: diversity, threat, and knowledge. *Science* 2008; **322**: 255–230. doi: 10.1126/science.1165115.
2. Mühldorfer K. Bats and bacterial pathogens: a review. *Zoonoses and Public Health* 2013; **60**: 93–103. doi: 10.1111/j.1863-2378.2012.01536.x.
3. Morse SF, *et al.* Global distribution and genetic diversity of *Bartonella* in bat flies (Hippoboscoidea, Streblidae, Nycteribiidae). *Infection, Genetics and Evolution* 2012; **12**: 1717–1723. doi: 10.1016/j.meegid.2012.06.009.
4. Kosoy M, *et al.* *Bartonella* spp. in bats, Kenya. *Emerging Infectious Diseases* 2010; **16**: 1875–1881. doi: 10.3201/eid1612.100601.
5. Pitassi LH, *et al.* *Bartonella* spp. Bacteremia in Blood Donors from Campinas, Brazil. *PLoS Neglected Tropical Diseases* 2015; **9**(1).
6. Vieira-Damiani G, *et al.* *Bartonella clarridgeiae* bacteremia detected in an asymptomatic blood donor. *Journal of Clinical Microbiology* 2015; **53**: 352–356. doi: 10.1128/JCM.00934-14.
7. Euzéby JP. List of bacterial names with standing in nomenclature: a folder available on the Internet (list of prokaryotic names with standing in nomenclature. <http://www.bacterio.net>). *International Journal of Systematic Bacteriology* 1997; **47**: 590–592. doi: 10.1099/00207713-47-2-590.
8. Neimark H, *et al.* Proposal to transfer some members of the genera *Haemobartonella* and *Eperythozoon* to the genus *Mycoplasma* with descriptions of ‘*Candidatus Mycoplasma haemofelis*’, ‘*Candidatus Mycoplasma haemomuris*’, ‘*Candidatus Mycoplasma haemosuis*’ and ‘*Candidatus Mycoplasma wenyonii*’. *International Journal of Systematic and Evolutionary Microbiology* 2001; **51**: 891–899. doi: 10.1099/00207713-51-3-891.
9. Biondo AW, *et al.* A review of the occurrence of hemoplasmas (hemotropic mycoplasmas) in Brazil. *Revista Brasileira de Parasitologia Veterinária (Online)* [Online] 2009; **18**: 1–7 doi: 10.4322/rbpv.01803001.
10. Tasker S. Clinical review: haemotropic mycoplasmas what’s their real significance in cats? *Journal of Feline Medicine and Surgery* 2010; **12**: 369–381. doi: 10.1016/j.jfms.2010.03.011.
11. dos Santos AP, *et al.* Hemoplasma infection in HIV-positive patient, Brazil. *Emerging Infectious Diseases* 2008; **14**: 1922–1924. doi: 10.3201/eid1412.080964.
12. Mascarelli P, *et al.* Hemotropic mycoplasmas in little brown bats (*Myotis lucifugus*). *Parasites & Vectors* 2014; **7**: 117. doi: 10.1186/1756-3305-7-117.
13. Millán J, *et al.* Widespread infection with hemotropic mycoplasmas in bats in Spain, including a hemoplasma

- closely related to “*Candidatus Mycoplasma hemohominis*”. *Comparative Immunology, Microbiology and Infectious Diseases* 2015; **39**: 9–12. doi: 10.1016/j.cimid.2015.01.002.
14. Breitschwerdt EB, *et al.* Bartonellosis: an emerging infectious disease of zoonotic importance to animals and human beings. *Journal of Veterinary Emergency and Critical Care* 2010; **20**: 8–30. doi: 10.1111/j.1476-4431.2009.00496.x.
 15. Guimarães AM, *et al.* Detection of *Bartonella* spp. in neotropical felids and evaluation of risk factors and hematological abnormalities associated with infection. *Veterinary Microbiology* 2010; **142**: 346–351. doi: 10.1016/j.vetmic.2009.10.002.
 16. André MR, *et al.* Hemoplasmas in wild canids and felids in Brazil. *Journal of Zoo and Wildlife Medicine* 2011; **42**: 342–347. doi:10.1638/2010-0198.1.
 17. Fleischman DA, *et al.* *Bartonella clarridgeiae* and *Bartonella vinsonii* subsp. *berkhoffii* exposure in captive wild canids in Brazil. *Epidemiology & Infection* 2014; **143**: 573–577. doi: 10.1017/S0950268814001277.
 18. Graziotin AL, *et al.* Prevalence and molecular characterization of *Mycoplasma ovis* in selected free-ranging Brazilian deer populations. *Journal of Wildlife Diseases* 2011; **47**: 1005–1011. doi: 10.7589/0090-3558-47.4.1005.
 19. Castro AMMG, *et al.* Swine infectious agents in *Tayassu pecari* and *Pecari tajacu* tissue samples from Brazil. *Journal of Wildlife Diseases* 2014; **50**: 205–209. doi: 10.7589/2013-01-021.
 20. Santos LC, *et al.* Hemotropic mycoplasma in a free-ranging black howler monkey (*Alouatta caraya*) in Brazil. *Journal of Wildlife Diseases* 2013; **49**: 728–731. doi: 10.7589/2012-06-159.
 21. Bonato L, *et al.* Occurrence and molecular characterization of *Bartonella* spp. and hemoplasmas in neotropical primates from Brazilian Amazon. *Comparative Immunology, Microbiology and Infectious Diseases* 2015; **42**: 15–20. doi: 10.1016/j.cimid.2015.09.001.
 22. Vieira RF, *et al.* Detection of a novel hemoplasma based on 16S rRNA gene DNA in captive and free-ranging capybaras (*Hydrochaeris hydrochaeris*). *Veterinary Microbiology* 2009; **139**: 410–413. doi: 10.1016/j.vetmic.2009.06.018.
 23. Conrado FO, *et al.* Occurrence and identification of hemotropic mycoplasmas (Hemoplasmas) in free ranging and laboratory rats (*Rattus norvegicus*) from two Brazilian zoos. *BMC Veterinary Research* 2015; **11**:286. doi: 10.1186/s12917-015-0601-8.
 24. Favacho AR, *et al.* Zoonotic *Bartonella* species in wild rodents in the state of Mato Grosso do Sul, Brazil. *Microbes and Infection* 2015; **17**: 889–892. doi: 10.1016/j.micinf.2015.08.014.
 25. Gonçalves LR, *et al.* Diversity and molecular characterization of novel hemoplasmas infecting wild rodents from different Brazilian biomes. *Comparative Immunology, Microbiology and Infectious Diseases* 2015; **43**: 50–56. doi: 10.1016/j.cimid.2015.10.006.
 26. Gonçalves LR, *et al.* Association of *Bartonella* species with wild and synanthropic rodents in different Brazilian biomes. *Applied and Environmental Microbiology* 2016; **82**: 7154–7164. doi: 10.1128/AEM.02447-16.
 27. Concannon R, *et al.* Molecular characterization of haemoparasites infecting bats (Microchiroptera) in Cornwall, UK. *Parasitology* 2005; **131**: 489–496. doi: 10.1017/S0031182005008097.
 28. Lin JW, *et al.* Identification of novel *Bartonella* spp. in bats and evidence of Asian gray shrew as a new potential reservoir of *Bartonella*. *Veterinary Microbiology* 2012; **156**: 119–126. doi: 10.1016/j.vetmic.2011.09.031.
 29. Bai Y, *et al.* Prevalence and diversity of *Bartonella* spp. in bats in Peru. *American Journal of Tropical Medicine and Hygiene* 2012; **87**: 518–523. doi: 10.4269/ajtmh.2012.12-0097.
 30. Kamani J, *et al.* *Bartonella* species in bats (Chiroptera) and bat flies (Nycteribiidae) from Nigeria, West Africa. *Vector-Borne and Zoonotic Diseases* 2014; **14**: 625–32. doi: 10.1089/vbz.2013.1541.
 31. Olival KJ, *et al.* *Bartonella* spp. in a Puerto Rican bat community. *Journal of Wildlife Diseases* 2015; **51**: 274–278. doi: 10.7589/2014-04-113.
 32. Lilley TM, Veikkolainen V, Pulliainen AT. Molecular detection of ‘*Candidatus Bartonella hemsundetiensis*’ in bats. *Vector-Borne and Zoonotic Disease* 2015; **15**: 706–708. doi: 10.1089/vbz.2015.1783.
 33. Brook CE, *et al.* *Bartonella* spp. in Fruit Bats and Blood-Feeding Ectoparasites in Madagascar. *PLOS Neglected Tropical Diseases* 2015; **10**(2). doi: 10.1371/journal.pntd.0003532.
 34. Judson SD, Frank HK, Hadly EA. Bartonellae are prevalent and diverse in Costa Rican bats and bat flies. *Zoonoses Public Health* 2015; **62**: 609–617. doi: 10.1111/zph.12188.
 35. Bai Y, *et al.* *Bartonella* spp. in bats, Guatemala. *Emerging Infectious Diseases* 2011; **17**: 1269–1272. doi: 10.3201/eid1707.101867.
 36. Wray AK, *et al.* Viral Diversity, Prey Preference, and *Bartonella* Prevalence in *Desmodus rotundus* in Guatemala. *EcoHealth* 2016; **13**:761–774. doi: 10.1007/s10393-016-1183-z.
 37. Davoust B, *et al.* Evidence of *Bartonella* spp. in blood and ticks (*Ornithodoros hasei*) of Bats, in French Guiana. *Vector-Borne and Zoonotic Diseases* 2016; **16**: 516–519. doi: 10.1089/vbz.2015.
 38. Mannerings AO, *et al.* Exposure to bat-associated *Bartonella* spp. among humans and other animals, Ghana. *Emerging Infectious Diseases* 2016; **22**: 922–924. doi: 10.3201/eid2205.151908.
 39. Leulmi H, *et al.* Detection of *Bartonella tamiae*, *Coxiella burnetii* and rickettsiae in arthropods and tissues from wild and domestic animals in northeastern Algeria. *Parasites & Vectors* 2016; **9**:27. doi: 10.1186/s13071-016-1316-9.
 40. Dietrich M, *et al.* Diversity of *Bartonella* and *Rickettsia* spp. in bats and their blood-feeding ectoparasites from South Africa and Swaziland. *PLoS ONE* 2016; **11**(3). doi: 10.1371/journal.pone.0152077.
 41. Kunz TH, Kurta A. Capture methods and holding devices. In: Kunz TH, ed. *Ecological and Behavioural Methods for the Study of Bats*. Washington/London: Smithsonian Institution Press, 1988, pp. 1–29.

42. **Peracchi AL, Nogueira MR.** Lista anotada dos morcegos do Estado do Rio de Janeiro, sudeste do Brasil. *Chiroptera Neotropical* 2010; **16**: 508–519.
43. **Birkenheuer AJ, Levy MG, Breitschwerdt EB.** Development and evaluation of a seminested PCR for detection and differentiation of *Babesia gibsoni* (Asian genotype) and *B. canis* DNA in canine blood samples. *Journal of Clinical Microbiology* 2003; **41**: 4172–4177. doi: 10.1128/JCM.41.9.4172-4177.2003.
44. **André MR, et al.** Assessment of a quantitative 5' nuclease real-time polymerase chain reaction using the nicotinamide adenine dinucleotide dehydrogenase gamma subunit (*nuoG*) for *Bartonella* species in domiciled and stray cats in Brazil. *Journal of Feline Medicine and Surgery* 2015; **18**: 783–790. doi: 10.1177/1098612X15593787.
45. **Bustin SA, et al.** The MIQE guidelines: minimum information for publication of quantitative real-time PCR experiments. *American Association of Clinical Chemists* 2009; **55**: 611–622. doi: 10.1373/clinchem.2008.112797.
46. **Colborn JM, et al.** Improved detection of *Bartonella* DNA in mammalian hosts and arthropod vectors by real-time PCR using the NADH dehydrogenase gamma subunit (*nuoG*). *American Society for Microbiology* 2010; **48**: 4630–4633. doi: 10.1128/JCM.00470-10.
47. **Johnson G, et al.** Detection and identification of *Bartonella* species pathogenic for humans by PCR amplification targeting the riboflavin synthase gene (*ribC*). *Journal of Clinical Microbiology* 2003; **41**: 1069–1072. doi: 10.1128/JCM.41.3.1069-1072.2003.
48. **Norman AF, et al.** Differentiation of *Bartonella*-like isolates at the species level by PCR restriction fragment length polymorphism in the citrate synthase gene. *Journal of Clinical Microbiology* 1995; **33**: 1797–1803.
49. **Paziewska A, et al.** Recombination within and between species of the alpha proteobacterium *Bartonella* infecting rodents. *International Society for Microbial Ecology* 2011; **61**: 134–145. doi: 10.1007/s00248-010-9735-1.
50. **Maggi RG, Breitschwerdt EB.** Potential limitations of the 16S-23S rRNA intergenic region for molecular detection of *Bartonella* species. *Journal of Clinical Microbiology* 2005; **43**: 1171–1176. doi: 10.1128/JCM.43.3.1171-1176.2005.
51. **Zeaiter Z, et al.** Phylogenetic classification of *Bartonella* species by comparing *groEL* sequences. *International Journal of Systematic and Evolutionary Microbiology* 2002; **52**: 165–171. doi: 10.1099/00207713-52-1-165.
52. **Maggi RG, Breitschwerdt EB.** Isolation of bacteriophages from *Bartonella vinsonii* subsp. *berkhoffii* and the characterization of pap-31 gene sequences from bacterial and phage DNA. *Journal of Molecular Microbiology and Biotechnology* 2005; **9**: 44–51. doi: 10.1159/000088145.
53. **Maggi RG, et al.** Novel hemotropic *Mycoplasma* species in white-tailed deer (*Odocoileus virginianus*). *Comparative Immunology, Microbiology and Infectious Diseases* 2013; **36**: 607–611. doi: 10.1016/j.cimid.2013.08.001.
54. **Miceli NG, et al.** Molecular detection of feline arthropod-borne pathogens in cats in Cuiabá, state of Mato Grosso, central-western region of Brazil. *Revista Brasileira de Parasitologia Veterinária* 2013; **23**: 385–390. doi: 10.1590/S1984-29612013000300011.
55. **Sanger F, Nicklen S, Coulson AR.** DNA sequencing with chain terminating inhibitors. *Proceedings of the National Academy of Sciences of the United States of America* 1977; **74**(12): 5463–5467.
56. **Ewing GB, Green P.** Base calling of automated sequencer traces using phred. II. Error probabilities. *Genome Research* 1998; **8**: 186–194. doi: 10.1101/gr.8.3.186.
57. **Ewing B, et al.** Base calling of automated sequencer traces using phred. I. Accuracy assessment. *Genome Research* 1998; **8**: 175–185. doi: 10.1101/gr.8.3.175.
58. **Altschul SF, et al.** Basic local alignment search tool. *Journal of Molecular Biology* 1990; **215**: 403–410. doi: 10.1016/S0022-2836(05)80360-2.
59. **Benson DA, et al.** GenBank. *Nucleic Acids Research* 2013; **41**: D37–D42. doi: 10.1093/nar/gks1070.
60. **Thompson JD, Higgins DG, Gibson TJ.** Clustal W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position specific gap penalties and weight matrix choice. *Nucleic Acids Research* 1994; **22**: 1673–4680.
61. **Hall TA.** BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 1999; **41**: 95–98.
62. **Ronquist F, Huelsenbeck JP.** MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 2003; **19**: 1572–1574. doi: 10.1093/bioinformatics/btg180.
63. **Miller MA, Pfeiffer W, Schwartz T.** Creating the CIPRES Science Gateway for inference of large phylogenetic trees In *Proceedings of the Gateway Computing Environments Workshop (GCE)*, 2010, pp. 01–08.
64. **Trifinopoulos J, et al.** W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research* 2016; **44**: W232–W235. doi: 10.1093/nar/gkw256.
65. **Nguyen LT, et al.** IQ-TREE: a fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. *Molecular Biology and Evolution*, 2015; **32**: 268–274. doi: 10.1093/molbev/msu300.
66. **Darriba D, et al.** ModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* 2012; **9**: 772. doi: 10.1038/nmeth.2109.
67. **Posada D, Buckley TR.** Model selection and model averaging in phylogenetics: advantages of Akaike information criterion and Bayesian approaches over likelihood ratio tests. *Systematic Biology* 2004; **53**: 793–808. doi: 10.1080/10635150490522304.
68. **Stover BC, Muller KF.** TreeGraph 2: combining and visualizing evidence from different phylogenetic analyses. *BMC Bioinformatics* 2010; **11**: 01–09. doi: 10.1186/1471-2105-11-7.
69. **Gutiérrez R, et al.** Guidelines for the isolation, molecular detection, and characterization of *Bartonella* species. *Vector Borne Zoonotic Diseases* 2017; **17**: 42–50. doi: 10.1089/vbz.2016.1956.

70. **Mckee CD, *et al.*** Phylogenetic and geographic patterns of *Bartonella* host shifts among bat species. *Infection, Genetics and Evolution* 2016; **44**: 382–394. doi: 10.1016/j.meegid.2016.07.033.
71. **Lei BR, Olival KJ.** Contrasting Patterns in Mammal–Bacteria Coevolution: *Bartonella* and *Leptospira* in Bats and Rodents. *PLoS Neglected Tropical Diseases* 2014; **8**(3). doi: 10.1371/journal.pntd.0002738.
72. **Steer JA, *et al.*** A novel hemotropic *Mycoplasma* (hemoplasma) in a patient with hemolytic anemia and pyrexia. *Clinical Infectious Diseases* 2011; **53**: 147–151. doi: 10.1093/cid/cir666.