AMANDA CARVALHO ROSADO FERREIRA

Bats and zoonotic bacterial pathogens

Lavras - MG

2021

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Dissertação apresentada à Universidade Federal de Lavras, como parte das exigências do Programa de Pós-graduação em Ciências Veterinárias, área de concentração em Sanidade Animal e Saúde Coletiva, para obtenção do título de Mestre.

Profa. Dra. Elaine Maria Seles Dorneles

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Ficha catalográfica elaborada pelo Sistema de Geração de Ficha Catalográfica da Biblioteca Universitária da UFLA, com dados informados pelo(a) próprio(a) autor(a).

Ferreira, Amanda Carvalho Rosado.
Bats and zoonotic bacterial pathogens / Amanda Carvalho Rosado Ferreira. - 2019.
119 p. : il.

Orientador(a): Elaine Maria Seles Dorneles.

Dissertação (mestrado acadêmico) - Universidade Federal de Lavras, 2019.
Bibliografia.

1. Chiroptera. 2. Wildlife. 3. Zoonoses. I. Dorneles, Elaine Maria Seles. II. Título.

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APROVADA em 29 de Outubro de 2021

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Orientadora

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It is dedicated to God, without whom nothing would be possible.

ACKNOWLEDGMENT

There are no words that worthily express the gratitude in my heart for the completion of this completed step in my life.

I first thank God, my creator and redeemer for the daily support, for each blessing, each miracle, each sprout and each dawn in his presence. Thank you for always listening to my prayers and instructing me and leading me on the path we choose to follow, advising me and caring for me every day of my life.

I thank my family, my parents Heloísa and Maurício, my siblings Sara, Guilherme, and Sofia and my in-laws Adriana and Walter for all their support. I especially thank my beloved husband Walter, for facilitating my days throughout this journey with so much affection, care, help and understanding, who I am sure will be an excellent daddy.

I thank my dear advisor Elaine, for so much teaching and knowledge transmitted and for always encouraging me and making me see every time I could go beyond what I imagined. I would also like to thank Professor Thallyta and Professor Andrey, for the partnership and trust which made it possible to carry out much of this work.

I thank all LEM friends for sharing so much knowledge. I especially thank my “amiga de PCR” Dirceia for all her help each day in the labs, and together with my friends Raisa and Isaac for making the walk lighter and more fun. I also thank Blenda for all her patience and commitment.

I would like to thank the entire DMV team, professors and technicians, from the Federal University of Lavras and Capes, CNPq and Fapemig, for the opportunity of knowledge and financial support for the realization of this master's degree. “This study was financed in part by the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Brasil (CAPES) – Finance Code 001”.

ABSTRACT

Zoonotic diseases cause great impacts on public and animal health, leading to huge economic losses. In this context, bats have gained prominence as potential transmitters of various diseases, with known importance in viral zoonoses and emergence in bacterial zoonoses. Thus, the aim of this dissertation was to contribute to the knowledge of the role of these animals in the cycle of zoonotic diseases, focusing on their importance as a carrier of bacterial pathogens. For this, a systematic review of zoonotic bacterial pathogens found in bats was carried out, and a cross-sectional study investigating the presence of *Brucella* spp., *Leptospira* spp. and *Salmonella* spp. in bats from Montes Claros, Minas Gerais, Brazil. The systematic review followed the guidelines of PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-analyses) and retrieved 146 studies. One hundred and one bacterial genera were detected in 66.7% (14/21) families of bats surveyed around the world, in a variety of clinical samples (blood, heart, lung, kidney, liver, spleen, feces, saliva, skin, among others). In the cross-sectional study, the investigation of the DNA of pathogens was carried out using molecular biology techniques in blood, liver and spleen samples of bats from the urban and wild areas of Montes Claros. The presence of DNA from *Salmonella* spp. was identified in a blood sample of an insectivorous female bat of the species *Lasiurus blossevilli,* showing the capacity of this animal to host this pathogen. Overall, our results showed that bats harbor several bacterial pathogens, having potential to act as transmitters or reservoirs of important bacterial agents from the public and animal health point of view. These results can drive the design of preventive and surveillance measures considering the One Health context.

Keywords: Bacterial Pathogens, One Health, Chiroptera, Zoonoses**.**

RESUMO

As doenças zoonóticas causam grandes impactos na saúde pública e animal, gerando enormes perdas econômicas. Nesse contexto, os morcegos, vêm ganhando destaque como potenciais transmissores de diversas doenças, com conhecida importância em zoonoses virais e emergência em zoonoses bacterianas. Assim, o objetivo desta dissertação foi contribuir para o conhecimento do papel desses animais no ciclo das doenças zoonóticas, focando em sua importância como carreadores de patógenos bacterianos. Para isso, foi realizada uma revisão sistemática de patógenos bacterianos zoonóticos encontrados em morcegos e um estudo transversal investigando a presença de *Brucella* spp., *Leptospira* spp. e *Salmonella* spp. em morcegos de Montes Claros, Minas Gerais, Brasil. A revisão sistemática seguiu as diretrizes do PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-analyses) e recuperou 146 estudos. Cento e um gêneros bacterianos foram detectados em 66,7%(14/21) das famílias de morcegos pesquisadas ao redor do mundo, em uma variedade de amostras clínicas (sangue, coração, pulmão, rim, fígado, baço, fezes, saliva, pele, entre outros). No estudo transversal, a investigação do DNA de patógenos foi realizada por meio de técnicas de biologia molecular em amostras de sangue, fígado e baço de morcegos da área urbana e silvestre de Montes Claros. A presença de DNA de *Salmonella* spp. foi identificada em uma amostra de sangue de morcego fêmea insetívora da espécie *Lasiurus blossevilli*, demonstrando a capacidade dessa espécie animal em hospedar esse patógeno. No geral, nossos resultados mostraram que os morcegos abrigam vários patógenos bacterianos, com potencial para atuar como transmissores ou reservatórios de importantes agentes bacterianos do ponto de vista da saúde pública e animal. Esses resultados podem orientar o desenho de medidas preventivas e de vigilância considerando o contexto da Saúde Única.

Palavras-chave: Patógenos bacterianos, Saúde Única, Quiroptéros, Zoonoses

SUMMARY

1. GENERAL INTRODUCTION

Bats are part of one of the groups of mammals that have the greatest richness and diversity of species. Among the numerous characteristics that contribute to these animals being able to harbor zoonotic pathogens, the ability to fly (bats are the only mammals that have true flight) and to adapt to different ecological niches that are linked to the fragmentation of habitats stand out. However, the greater contact of bats with humans and domestic animals due to their synanthropism raise serious concerns about zoonoses transmission.

Bacterial zoonotic diseases are of great importance among infectious diseases for humans, domestic animals and also for bat conservation, being responsible for significant disease burden and economic losses worldwide. In this context, the formulation of surveillance measures is essential to prevent transmission of bacterial agents from bats to other species, since the great mobility of these winged animals can contribute to the dispersion of zoonotic agents. Nevertheless, for the surveillance actions to be effective, they must be based on evidence from studies that seek to understand the epidemiology of these diseases under the One health perspective.

Therefore, the aim of this dissertation was to generate qualified information about the identification of bacterial pathogens in different bat species and locations, seeking to contribute to the understanding of the role of bats in the epidemiology of bacterial zoonoses. For this, we performed a systematic review on zoonotic bacterial pathogens found in different clinical samples of different species of bats over the years, and a cross-sectional study to determine the prevalence of *Brucella* spp., *Leptospira* spp., and *Salmonella* spp. in bats from Montes Claros, Minas Gerais, Brazil.

CHAPTER 1: Formatted according to the submission guidelines of Emerging Infectious Diseases

Systematic review of zoonotic bacterial pathogens from bats: a One Health approach

Running Title: Zoonotic bacterial pathogens in bats

Abstract

Studies on the association of bats with zoonotic pathogens are important to shed some light on their potential as carriers of priority agents in public and animal health. Therefore, the aim of this systematic review was to describe the zoonotic bacterial pathogens already reported and their frequency in different bat species. Six databases were searched, without restriction on year or location where the studies were carried out. According to inclusion and exclusion criteria, 146 studies were selected, which were published between 1964 and 2020 (most after 2005). In these studies, 101 zoonotic bacterial genera were described in different clinical samples of fifteen bat families, in 58 countries, suggesting a possible role of bats as hosts for these pathogens. In conclusion, the information provided by this systematic review expanded the knowledge about zoonotic bacterial pathogens already identified in bats, which can guide epidemiological surveillance policies for these pathogens in different countries.

Introduction

The order Chiroptera represented by bats is one of the richest mammal orders (> 1000 species), comprising about 25% of living mammal species (1). These animals are found across the globe, being absent only in the polar regions (2). Bats explore many environmental niches, performing in cold regions such as the poles, and have a versatile feeding behavior, feeding on insects, flowers, leaves, fruits, pollen, nectar, small animals and blood, acting as pollinators and playing an important role in ecosystems (3). Nevertheless, the diversity of species and eating habits, the wide geographic distribution, the longevity, the synanthropic behavior of some species, and the ability to fly, to adapt to different ecological niches, and to harbor viral pathogens without manifesting obvious pathologies, favor the possibility of bats being reservoir hosts or vectors of some zoonotic agents(2, 4,5).

The association of bats with zoonotic pathogens has been known since the first identification of *Lyssavirus*, the virus that causes rabies, in 1911, in these animals (6). Over the years, several studies have sought to understand the role of bats in emerging infectious diseases and their relevance to public and animal health (7-10). This has gained more strength in recent years with the emergence of the One Health strategy, which is a multidisciplinary approach that treats human, animal, and environmental health as inseparable, allowing the achievement of sustainable health at all levels. Epidemics and pandemics of the last 20 years, such as Severe Acute Respiratory Syndrome (SARS-CoV), Nipah virus (NiV), Ebola virus (EBOV), Hendra virus (HeV), Rabies virus (RABV), Middle East Respiratory Syndrome (MERS) (CoVs) and, more recently, Coronavirus Disease 2019 (COVID-19 / SARS-CoV-2), highlight a recurrent trend in the emergence of zoonotic viral pathogens that have bat as probable reservoirs (4, 11, 12). In addition to the importance in the transmission and emergence of viral pathogens, recent studies also feature bats as a potential source of fungal (13), protozoa (14) and bacterial agents (15, 16).

Regarding to bacterial pathogens, several genera with zoonotic potential have been described in bats around the world, such as *Bartonella, Brucella, Campylobacter, Clostridium*, *Escherichia, , Leptospira, Listeria, Pasteurella, Salmonella*, *Staphylococcus* and *Yersinia,* from different clinical samples (feces, intestine, gastrointestinal tract, heart, spleen, liver, kidney, blood, etc) (9, 15-20). Studies investigating the presence and frequency of zoonotic bacterial pathogens in bats have increased substantially in recent years. A review on the subject has already been published, but so far there has not been a systematic review on the subject. The knowledge about the public health risks associated with different bat species, considering their importance as potential reservoirs and disseminators of pathogens, is essential for the design of health surveillance actions, and consequently for risk mitigation and disease prevention in the human and animal population. In addition, this comprehension is also important for the conservation of these species and for the maintenance of environmental balance. Therefore, this systematic review aimed to describe the zoonotic bacterial pathogens already reported in different bat species and compile the wide range of information on this subject, discussing the implications of these findings under the One health perspective.

Methods

Search strategy

The guidelines of the PRISMA statement (Preferred Reported Items for Systematic Reviews and MetaAnalyses) were formally adopted in this review and details can be seen in Appendix S1. The search was conducted on August 25th, 2020. Original papers on bacterial pathogens common among humans and bats were searched in six databases (Web of Science, PubMed, Scielo, Cochrane, Scopus and Cabi), without restriction on year or location where the studies were carried out. The search was performed based on population (bat OR bats OR flittermouse OR Chiroptera), intervention (reservoirs OR carriers OR transmitters OR preval* OR incidenc* OR occur* OR detection), and outcomes [disease* AND (communicable OR animal OR emerging) OR (bacterial AND (pathogen* OR infect* OR diseas*)) OR bacter* OR Leptospira OR Salmonella OR Brucella OR Bartonella OR Campylobacter OR Clostridium OR Listeria OR Shigella OR Yersinia OR Borrelia OR Neorickettsia*)]. The outcome terms for the search were selected based on those already described in the literature. Detailed information about the terms used in the search is shown in the Appendix S2. The selected words were investigated within all the sections of papers (title, abstract, keywords and full text) in all the databases, except for Scopus, in which the search was limited to title, abstract and keywords.

After searching the databases, the articles were imported to EndNote X7.8 (Thomson Reuters, USA) and the duplicates were removed. The screening for articles was also conducted in the reference list of the reviews recovered in the primary search.

Selection of the studies

All papers identified in the initial search were first selected by two independent reviewers (ACRF and RABC) according to the selection criteria. In the second stage, abstract from those studies selected based on their titles were independently evaluated (ACRF and RABC). Subsequently, full texts were evaluated (ACRF and RABC) in terms of its relevance and considering the inclusion/exclusion criteria. Disagreements over the inclusion or exclusion of a paper were solved by a third reviewer (EMSD), responsible for the final decision.

Inclusion and exclusion criteria

Articles (i) centered on bats and (ii) bacterial zoonoses were included in the review. The following characteristics were considered for the exclusion of articles: focusing on (i) non-bacterial zoonoses, (ii) bacterial zoonoses in other species than bats, (iii) commensal microbiota or (iv) ecology of bats; (v) written in languages other than English, Spanish or Portuguese; files that were not original research articles (thesis, conference proceedings, abstract, reviews and book chapters). Full inclusion and exclusion criteria are shown in Appendix S3.

Data extraction

Data were extracted from papers by one of the reviewers (ACRF) and then checked for accuracy by another reviewer (EMSD). Desagreements regarding data extraction among the reviewers were solved by consensus. Extracted data included the the following: first author, publication year, environment in which bats were captured (urban or wild), year in which sampling was performed, place where the study was carried out (country), clinical samples collected, diagnostic technique employed, number of animals or samples tested, number of positive animals or samples, genus or species of bacteria found and family or species of bat in which the bacteria was found (Appendix S4). The identification of bacterial genera and families from the species informed in the selected papers was performed according to National Center for Biotechnology Information Taxonomy Database. The same database was used for the identification of bat families.

Results

Selected articles

The search for terms in the databases retrieved 12,987 articles, including 3,057 duplicates, which were removed resulting in 9,930 studies. In the selection by title, 9,342 studies were removed, whereas in the selection by abstract 337 were excluded, remaing 251 papers. For these, full texts were not retrieved for 16, being 235 screened by full text. In this step, 89 were excluded with reason, resulting in 146 articles included in the systematic review (Figure 1). The main characteristics of the selected studies are shown in Appendix S4.

The selected studies were published between 1964 and 2020, most of them after 2005 [95.2% (139/146)]. The highest number of articles were published in 2017 [11.6% (17/146)], 2018 [15% (22/146)], 2019 [14.4% (21/146)] and 2020 [10.5% (16/146)] (Figure 2A).

The 146 selected articles were conducted in 58 different countries. In 4 studies, two countries were assessed. The country with the highest number of studies was Brazil [8.9% (13/146)], followed by China [6.8% (10/146)], Australia [4.8% (7/146)], Germany, India, United States and Malasya [4.1% (6/146)], and Nigeria and Peru [3.4% (5/146)]. Detailed information on distribuition of countries searched in the selected papers are shown in Figure 2B.

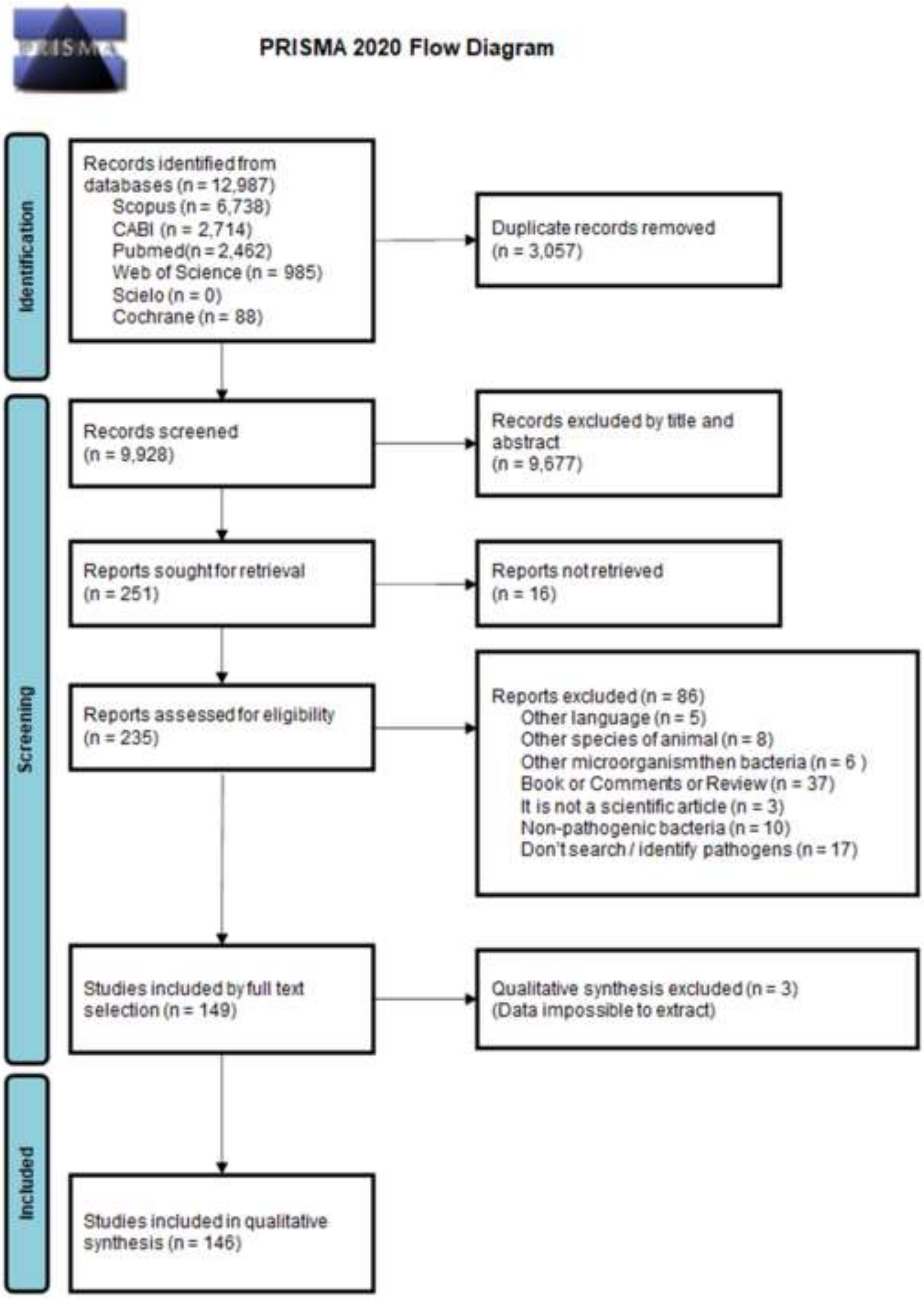


Figure 1: Flow Diagram of the articles recovered from the databases searched.

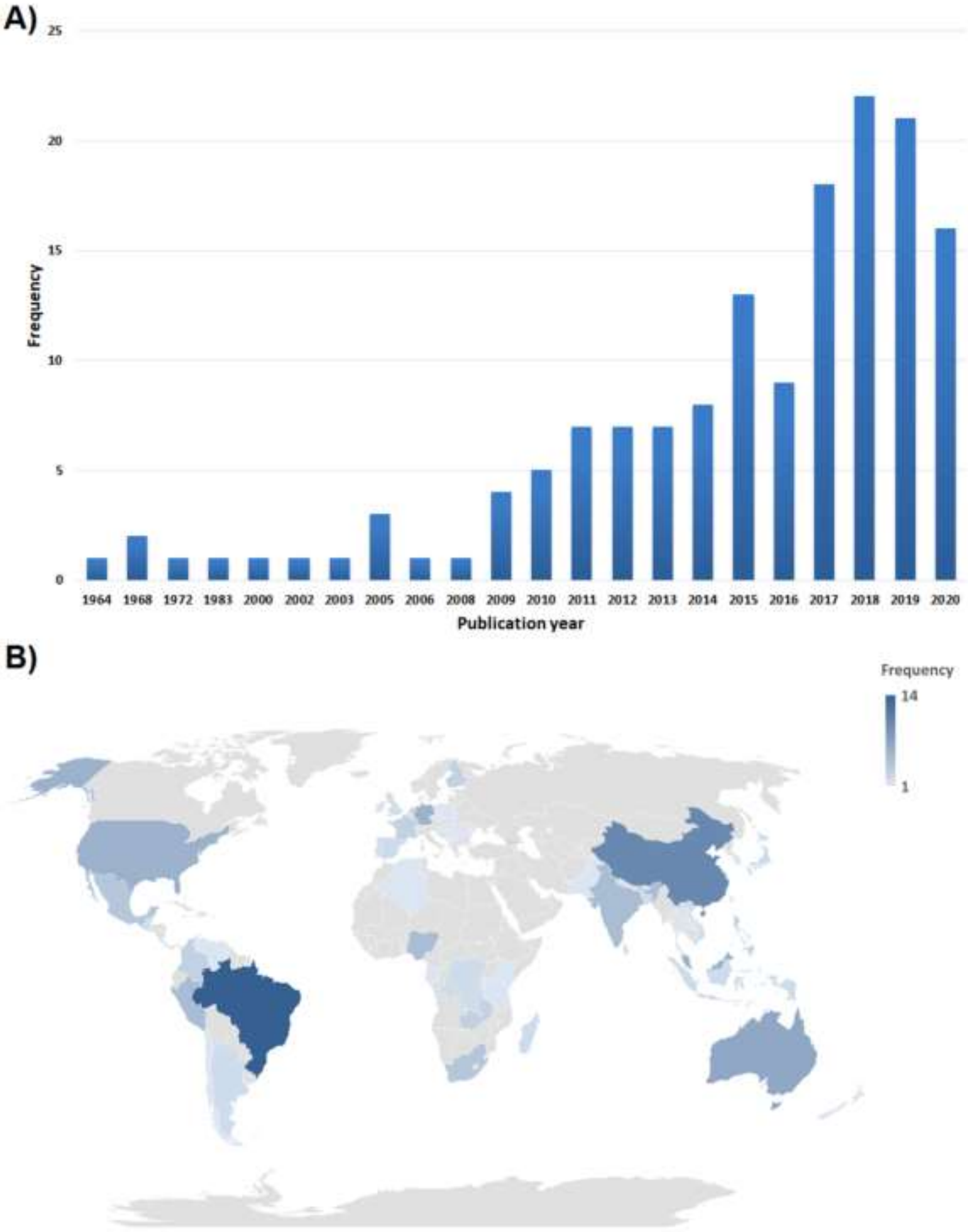


Figure 2: Temporal and geographical distribution of the selected articles. A) Distribution of the selected articles according to the year of publication. B) Distribution of the selected articles according to the country where the study was performed.

Pathogens researched and found in bat samples

One hundred and one different bacteria genera, described as pathogenic and with zoonotic potential, were researched and found in bats in the selected articles (Figure 3). The bacterial pathogens most researched were: *Bartonella* spp. [28.1% (41/146)], *Leptospira* spp. [21.2% (31/146)] and *Staphylococcu*s spp. [14.4% (21/146)]. *Bartonella* spp. and *Staphylococcu*s spp. were found in 100% of the studies that investigated these genera, while *Leptospira* spp. was detected in 96.7% (30/31) of the studies that researched them. Enteric pathogens were also researched with considerable frequency, such as *Salmonella* spp. [9.6% (17/146)], *Yersinia* spp. [9.6% (14/146)], *Escherichia* spp. [8.4% (12/146)], *Clostridium* spp. [5.5% (8/146)] and *Campylobacter* spp. [3.4% (5/146)]. Regarding respiratory tract pathogens, the most assessed were *Serratia* spp. [10.3% (15/146)], *Klebsiella* spp. [3.4% (10/146)], *Streptococcus* spp. [5.5% (8/146)], *Burkholderia* spp. [4.1% (6/146)], *Corynebacterium* spp. and *Mycobacterium* spp. [3.4% (5/146)]. The relationship between bacterial genera surveyed and found are described in Figure 3.

Genera of great importance in public health that cause systemic diseases with different clinical signs, such as mycoplasmosis, brucellosis and rickettsiosis (or spotted fever) were also researched and found in bats samples (Figure 3). Fifteen [15/146 (10.3%)] studies searched for *Mycoplasma* spp. and all found; *Brucella* spp. was searched in 4 [4/146 (2.7%)] and found in 3 of them [75% (3/4)]; *Rickettsia* spp. was surveyed in 9.6% (14/146) of the studies and found in 78.6% (11/14). The relationship between the others researched and found bacterial genera are described in Figure 3.

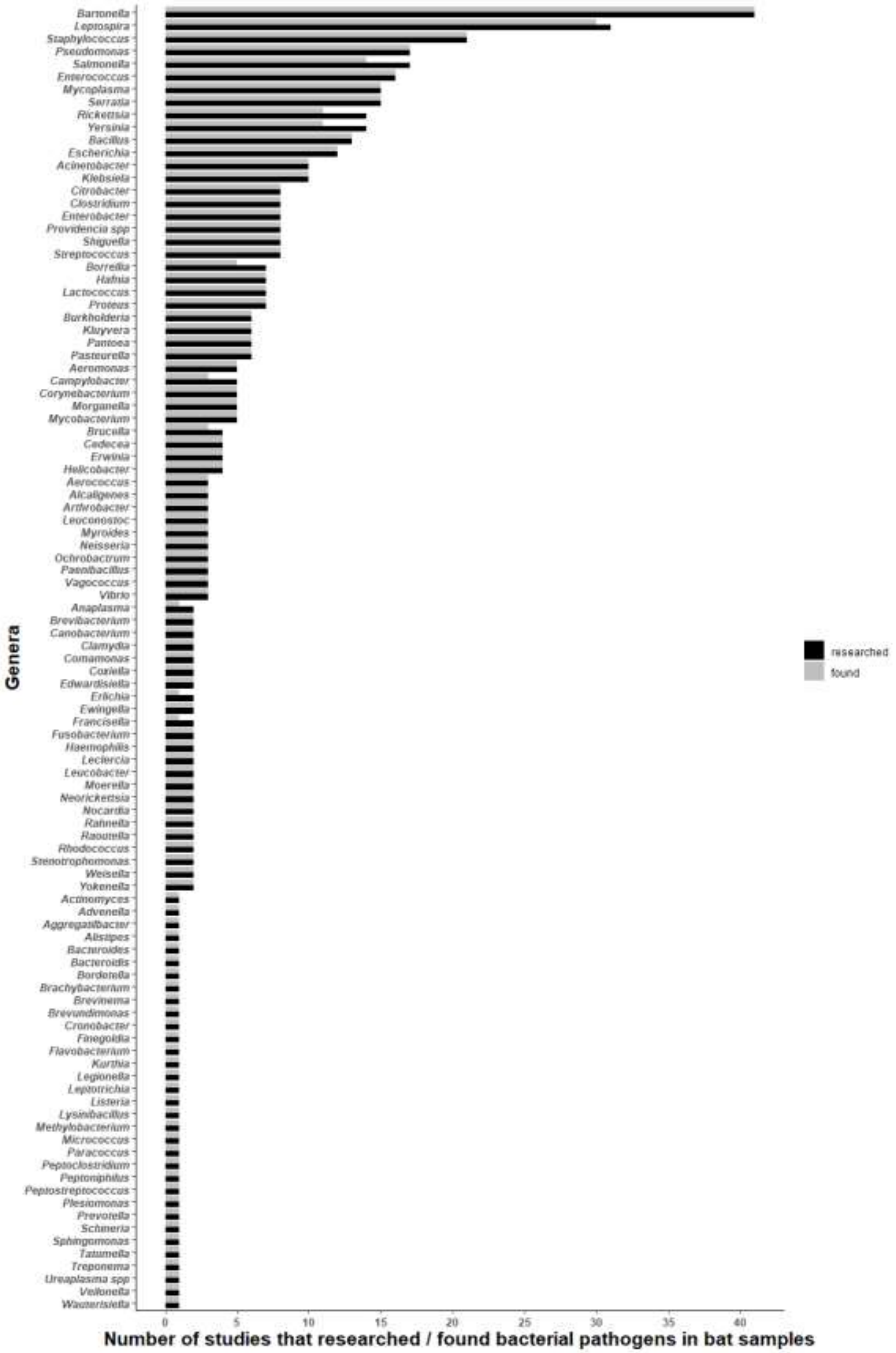


Figure 3: Number of studies that researched/found pathogens in bat samples among those selected by this systematic review.

Bat species and families surveyed

Fourteen families of bats were researched and in all them at least one zoonotic bacterial pathogen was observed: Emballonuridae, Hipposideridae, Megadermatidae, Molossidae, Mormoopidae, Natalidae, Noctilionidae, Nycteridae, Phyllostomidae, Pteropodidae Rhinolophidae, and Rhinopomatidae (Figure 3). Three hundred and eighty-two different bat species were searched for some bacterial pathogen, generating 914 combinations of bat species that were searched for different pathogens. The most researched bat families were Phyllostomidae [31.2% (286/914)] and Vespertilionidae [30.1% (276/914)]. In 57.8% (221/382) of the bat species surveyed at least one bacterial agent was detected, generating 455 combinations of bat species that were positive or seropositive for some pathogen. The bat families in which pathogens were most reported were Vespertilionidae [30.5% (139/455)] and Phyllostomidae [25.9% (118/455)] (Figure 4).

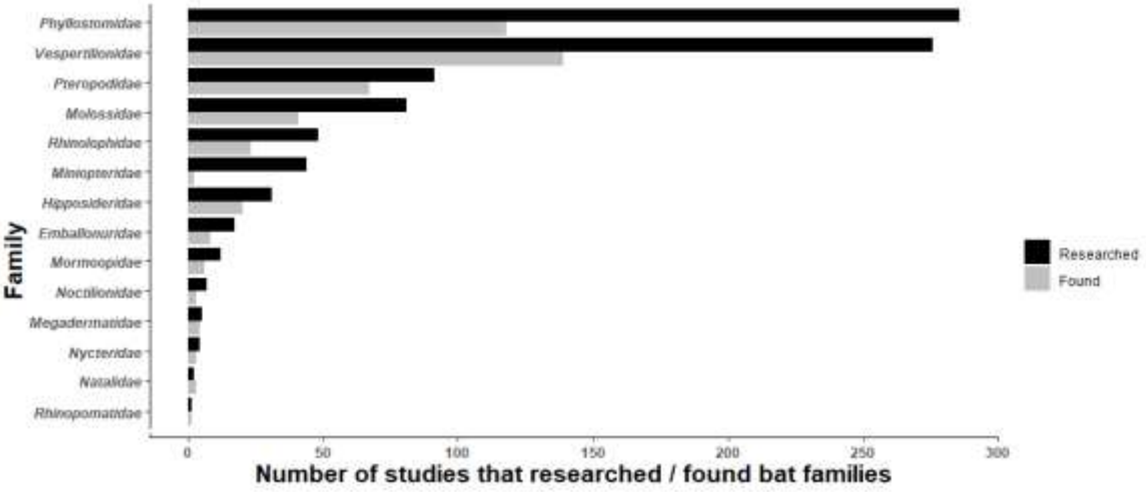
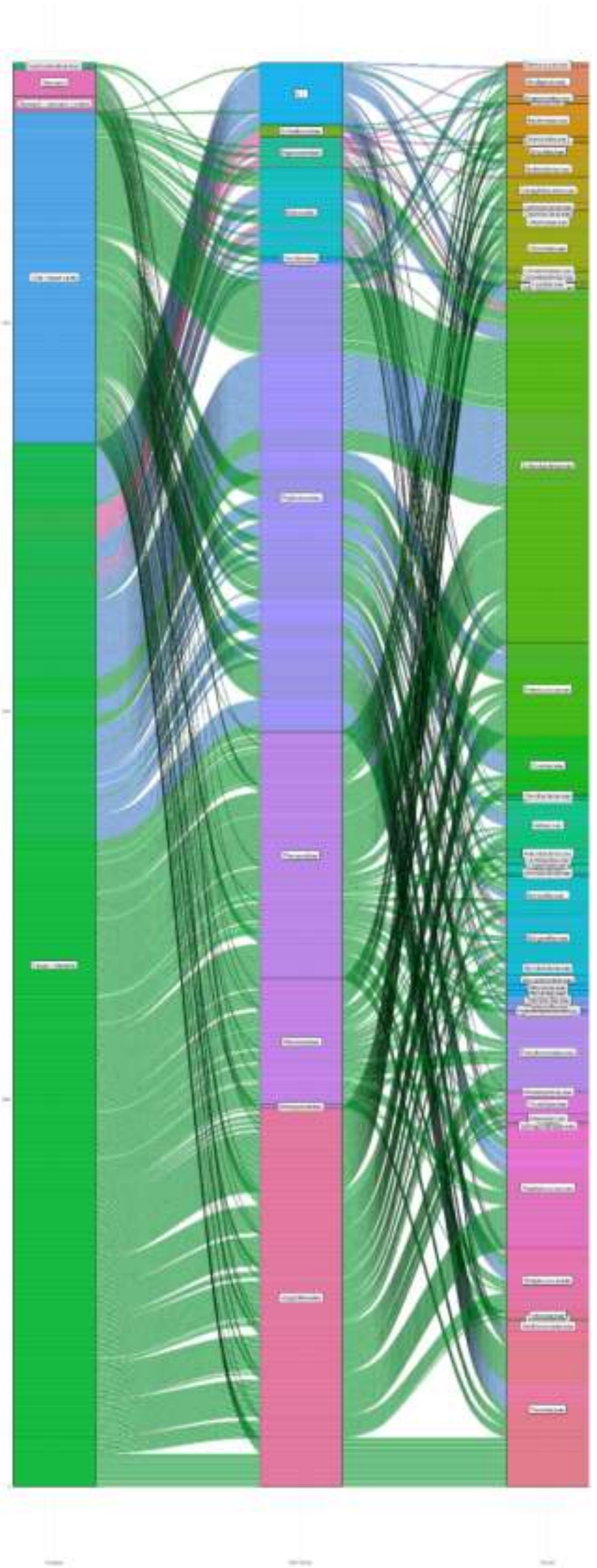


Figure 4: Number of studies that researched/found in bat families for some pathogens among those selected by this systematic review.

Pathogens found according to bat family and clinical sample assessed

Regarding the clinical samples in which the pathogens were found or evidence of their presence (seropositive animals), they were grouped into six large groups: gastrointestinal tract (TGI) (feces/intestine, oral/nasal cavity, stomach and stomach/stomach content); kidney-urine; blood serum (serological tests); whole blood; organs (brain, heart, liver, lung, mammary gland, spleen, tongue and chest); skin (body smear, dorsal interscapular patch, shoulders, skin lesions, skin swab).

Ten different bat families [10/14 (71.4%)] exhibited TGI samples positives for at least one bacterial pathogen searched. In this group of samples, 734 combinations of positive bat species for some bacterial genus were identified. Most species of positive bats belonged to the Phyllostomidae 32.9% (242/734), followed by Vespertilionidae 26.7% (196/734), Pteropodidae 20.0% (147/734), Rhinolophidae 8.8% (65/734), Molossidae 6.3% (46/734), Hipposideridae 2.1% (16/734), Emballonuridae 0.8% (6/734), Nycteridae and Rhinopomatidae 0.2% (2/734), and Noctilionidae 0.1% (1/734) (Figure 4). In some cases, the bat species or family in which the bacteria were found was not identified [4.3% (32/734)]. Regarding the bacterial genera, 91.2% (94/103) of all those detected in this review were found in TGI group. The genera most observed were *Serratia* [9.2% (67/734)], *Staphylococcus* [8.4% (62/734)], *Enterococcus* [6.2% (46/734)], *Enterobacter* [5.8%(43/734)], *Pseudomonas* [5.4%(40/734)], *Klebsiella* [4.4%(33/734)], *Salmonella* [3.2%(24/734)], *Hafnia* [3.2% (24/734)], *Clostridium* [2.8% (21/734)], *Pantoea* [2.8% (21/734)], and *Acinetobacter* [2.7%(20/734)] (Appendix S5). Feces was the clinical sample most researched and with most positive results in the TGI group (Figure 4).



192

193 Figure 5: Family of bacterial pathogens found according to bat family and clinical sample assessed

194 among those grouped in gastrointestinal tract samples.

Seven bat families [7/14 (50.0%)] were positive for at least one bacterial pathogen searched in the kidney-urine group. In this group, 115 combinations of positive bat species for some bacterial genus were observed. Vespertilionidae [37.4% (43/115)] was the most frequent family with positive results, followed by Phyllostomidae [28.7% (33/115)], Pteropodidae [17.4% (20/115)], Molossidae [7.8% (9/115)], Nycteridae [3.5% (4/115)], and Hipposideridae and Mormoopidae [0.8% (1/115) each]. It was not possible to identify the bat species or family in which the bacteria or antibodies were found in some cases [3.5% (4/115)]. The genus *Leptospira* was the most found in this group [83.5% (96/115)]. *Rickettsia* spp. [3.5% (4/115%)], *Pasteurella* spp. [6.0% (7/115%)], *Yersinia* spp. [0.8% (1/115)], *Bartonella* spp. [0.8% (1/115)], *Burkholderia* spp. [0.8% (1/115)], *Carnobacterium* spp. [0.8% (1/115)] and *Micrococcus* spp. [0.8% (1/115)] were also detected. The genera *Leptospira* and *Rickettsia* were found in both kidney and urine samples, whereas *Pasteurella* and *Yersinia* in kidney, and the other genera in urine samples (Figure 5).

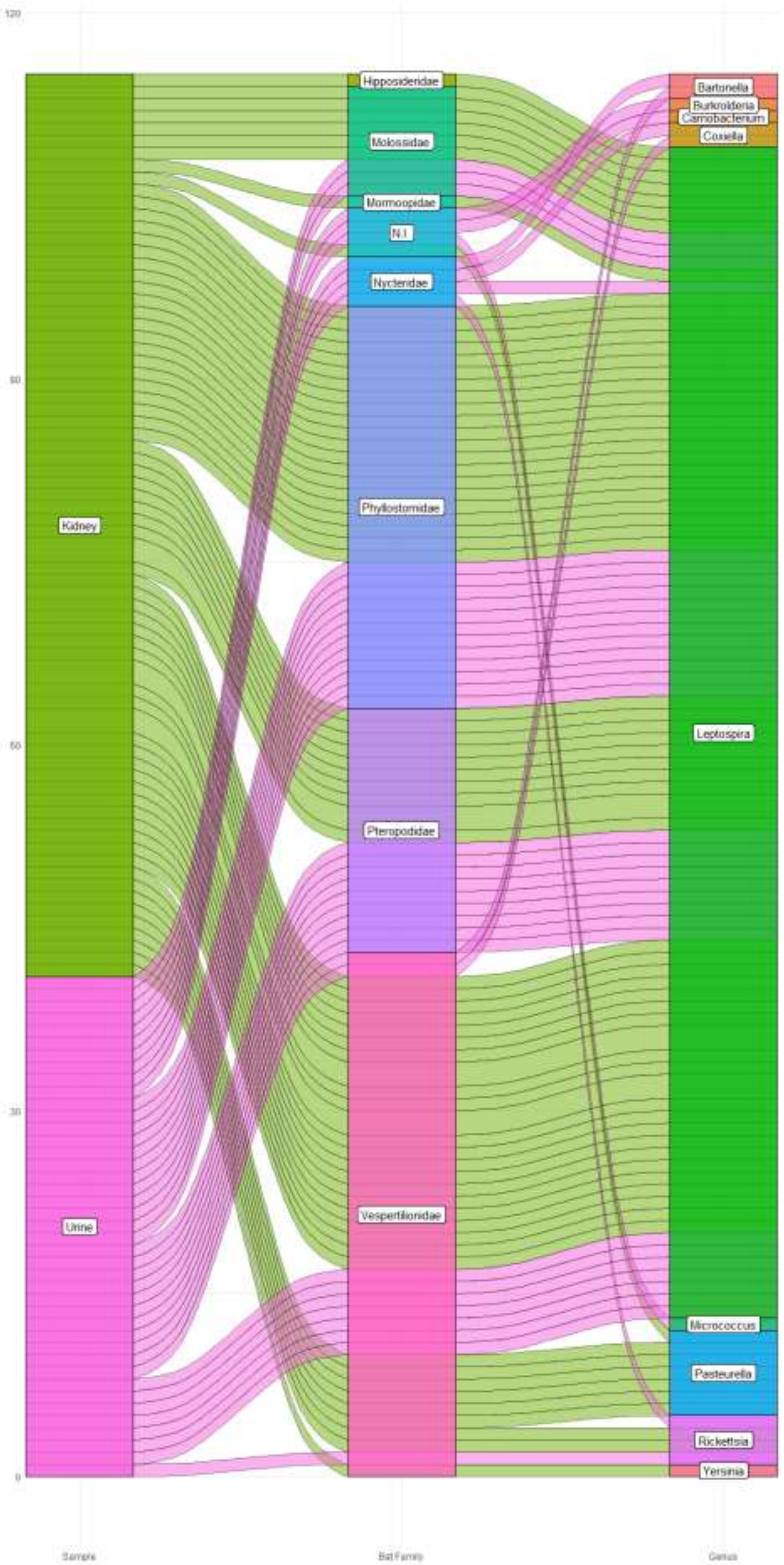

120
90
60
30
0
Kidney
Urine
Hipposideridae
Molossidae
Mormoopidae
N.I
Nycteridae
Phyllostomidae
Pteropodidae
Vespertilionidae
Bartonella
Burkrolderia
Carnobacterium
Coxiella
Leptospira
Micrococcus
Pasteurella
Rickettsia
Yersinia
Sample
Bat Family
Genus

Figure 6: Genera of bacterial pathogens found according to bat family assessed in kidney and urine samples.

In the blood serum group, also seven of the fourteen families of bats (50.0%) were found seropositive for at least one bacterial pathogen searched. Eighty-eight combinations of positive bat species for some bacterial genus were observed in this group, which belonged to the following families: Phyllostomidae [31.8% (28/88)], Molossidae [22.7% (20/88)], Pteropodidae [12.5% (11/88)], Vespertilionidae [11.4% (10/88)], Hipposideridae and Nycteridae [2.3% (2/88) each], and Mormoopidae [1.1% (1/88)]. In this group, there were also unidentified bat families [4.5% (4/88)]. Anti-*Leptospira* spp. antibodies were the most frequently observed [60.2% (53/88)], followed by anti-*Rickettsia* spp. [36.4% (32/88)], anti-*Borrelia* spp. [2.3% (2/88)] and anti-*Bartonella* spp. [1.1% (1/88)] (Figure 6).

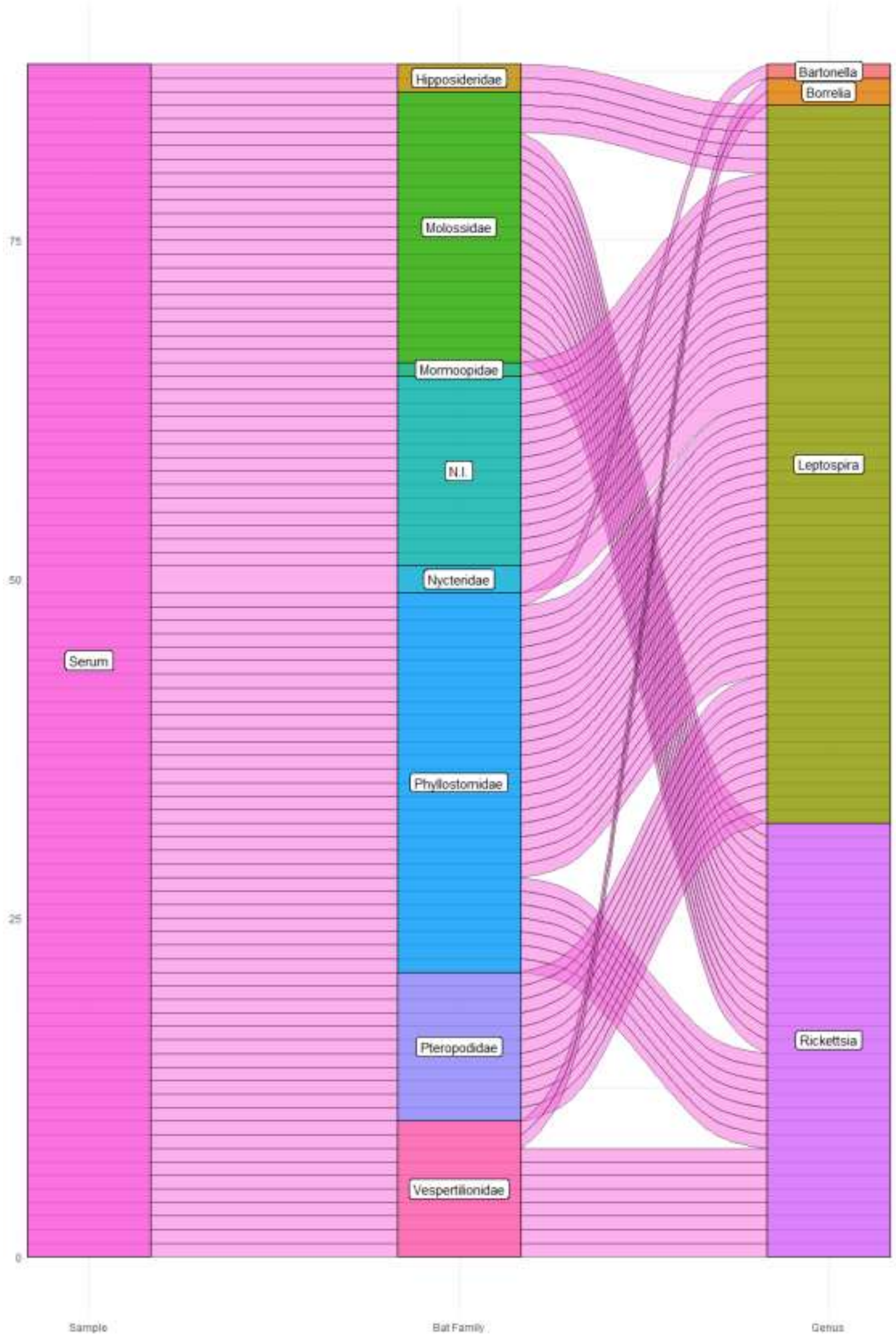


Figure 7: Genera of bacterial pathogens found according to bat family assessed in serological tests.

In whole blood samples, 85.7% (12/14) of bat families were positive for at least one bacterial pathogen searched. In this group, 155 combinations of positive bat species for some bacterial genus were observed, which belonged to the following families: Phyllostomidae [38.7% (60/155)], Vespertilionidae [17.4% (27/155)], Pteropodidae [12.5% (19/155)], Rhinolophidae [7% (11/155)], Hipposideridae [6.5% (10/155)], Molossidae [5.1% (8/269)], Megadermatidae [3.2%(5/155)], Emballonuridae [3.2% (5/155)], Mormoopidae [2.6% (4/155)], Noctilionidae[1.3% (2/155)], Nycteridae [1.3%(2/155)], and Natalidae [0.6%(1/155)]. In some cases, the bat species or family in which the bacteria were found was not identified [0.6% (1/155)]. The genus *Bartonella* was the most observed in this group [69% (107/155)], followed by *Mycoplasma* [23.8% (37/155)], *Rickettsia* [4.5% (7/155)] and *Erlichia, Borrelia, Leptospira*, and *Kluyvera* [0.6% (1/155) each] (Figure 7).

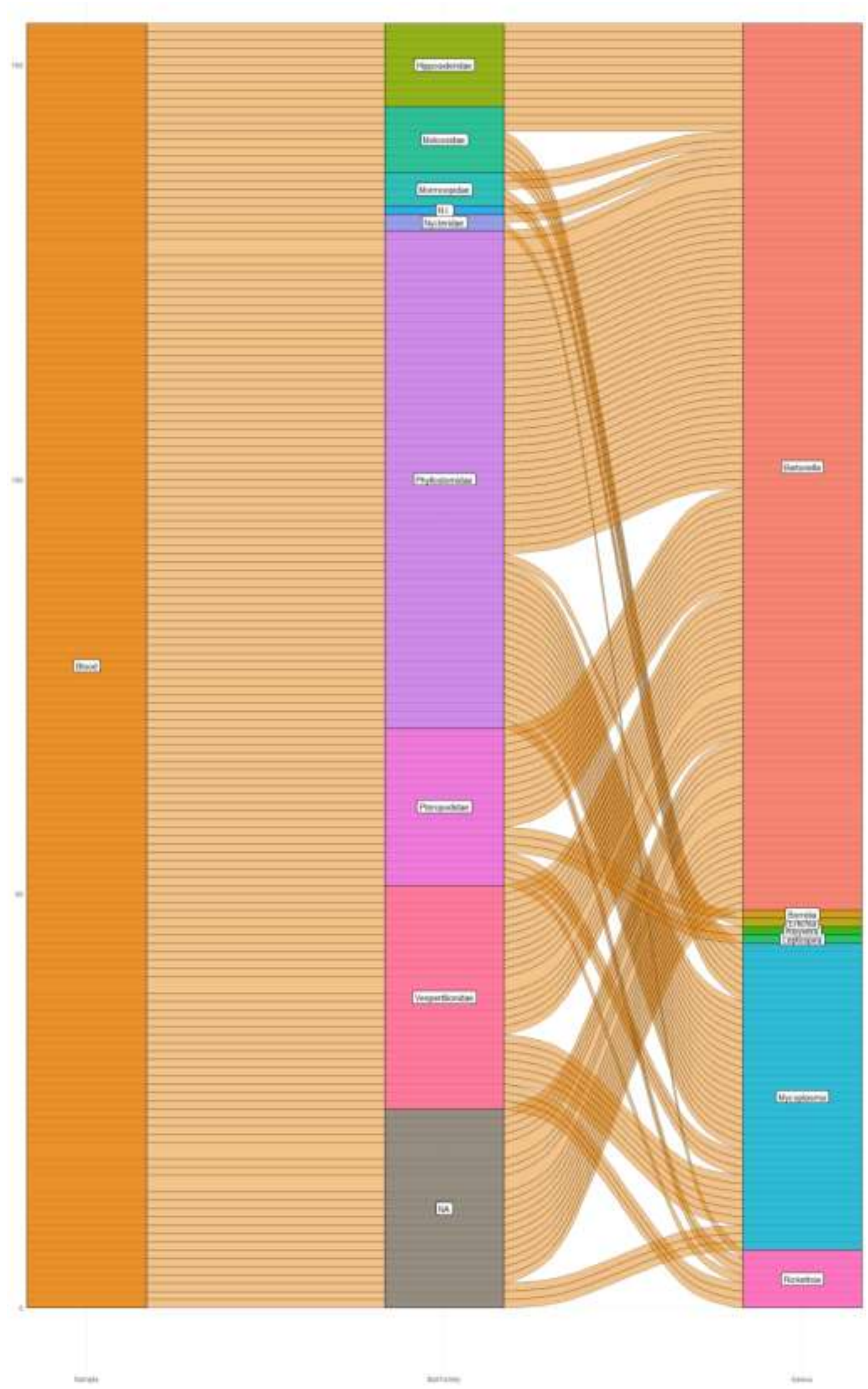


Figure 8: Genera of bacterial pathogens found according to bat family assessed in whole blood samples

Six bat families among fourteen (42.9%) were positive for at least one bacterial pathogen searched organ samples. In this group, 114 combinations of positive bat species for some bacterial genus were found. Most species of positive bats belonged to the Vespertilionidae [56.2% (64/114)], Phyllostomidae [30.8% (35/114), Molossidae [4.4% (5/114)], Natalidae [1.8% (2/114)], and Mormoopidae and Emballonuridae [0.9% (1/114) each] families. Bat species or family in which the bacteria were found was not identified in 5.3% (6/114) of cases. The main bacterial genera found were *Bartonella* [33.4% (38/114)], *Pasteurella* [28.9% (33/114)], *Mycoplasma* [16.7% (19/114)], *Rickettsia* [5.3% (6/114)], *Yersinia* [4.4% (5/114)], *Streptococcus* and *Borrelia* [2.6% (3/114) each], *Chlamydia* [1.8% (2/114)], *Salmonella, Bacillus, Brucella, Hafnia,* and *Klebsiella* [0.8% (1/114) each] (Figure 8).

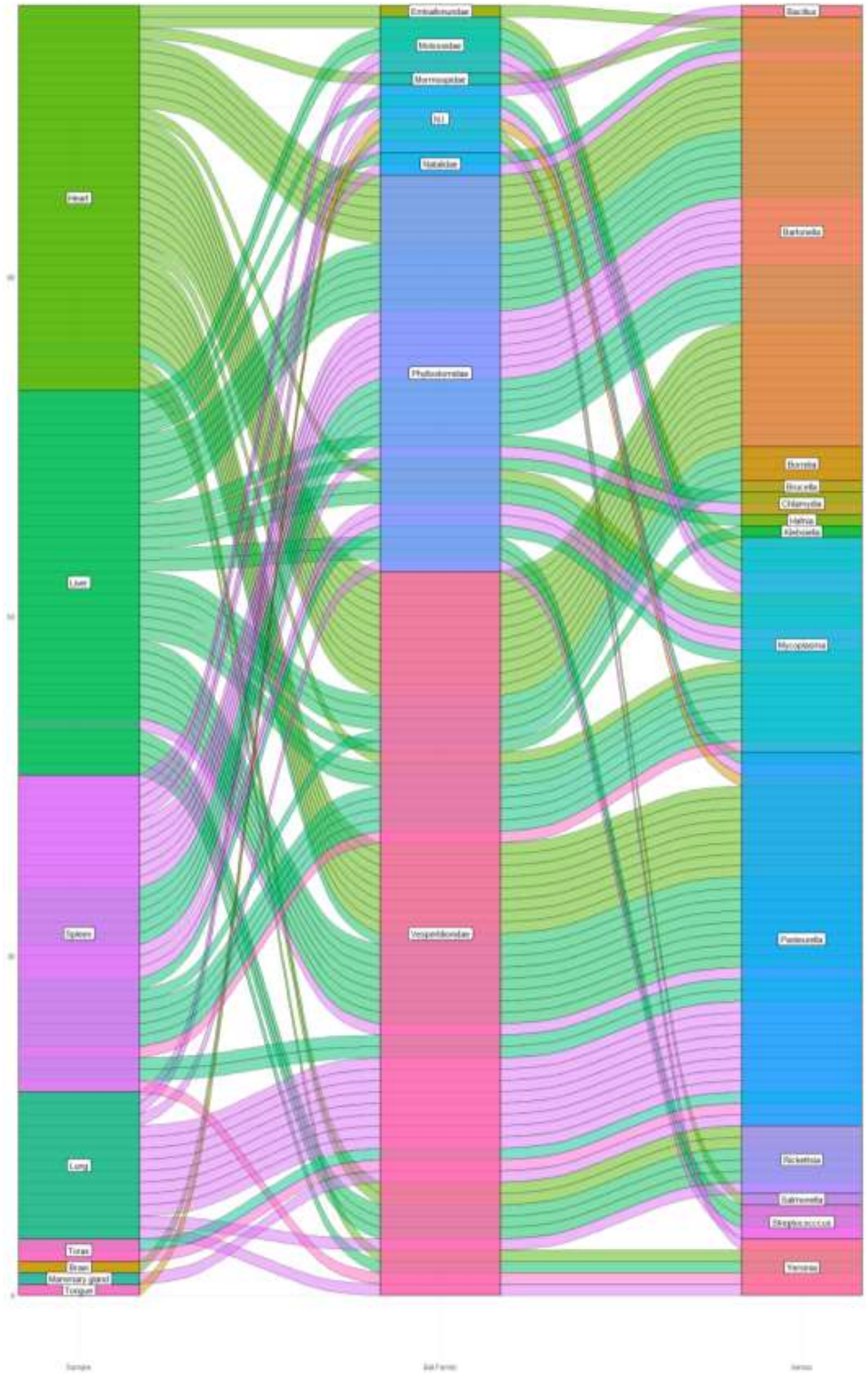


Figure 9: Genera of bacterial pathogens found according to bat family assessed in different organ samples

The skin group of clinical samples was the least diverse both in number of bat families [3/14 (21.4%)] and species (n=4) in which some pathogen (n=46) was observed. However, this group was the second considering the diversity bacterial genera [35.0% (36/103)] found. Bacterial genera found in skin samples according to bat families are depicted in Figure 9.

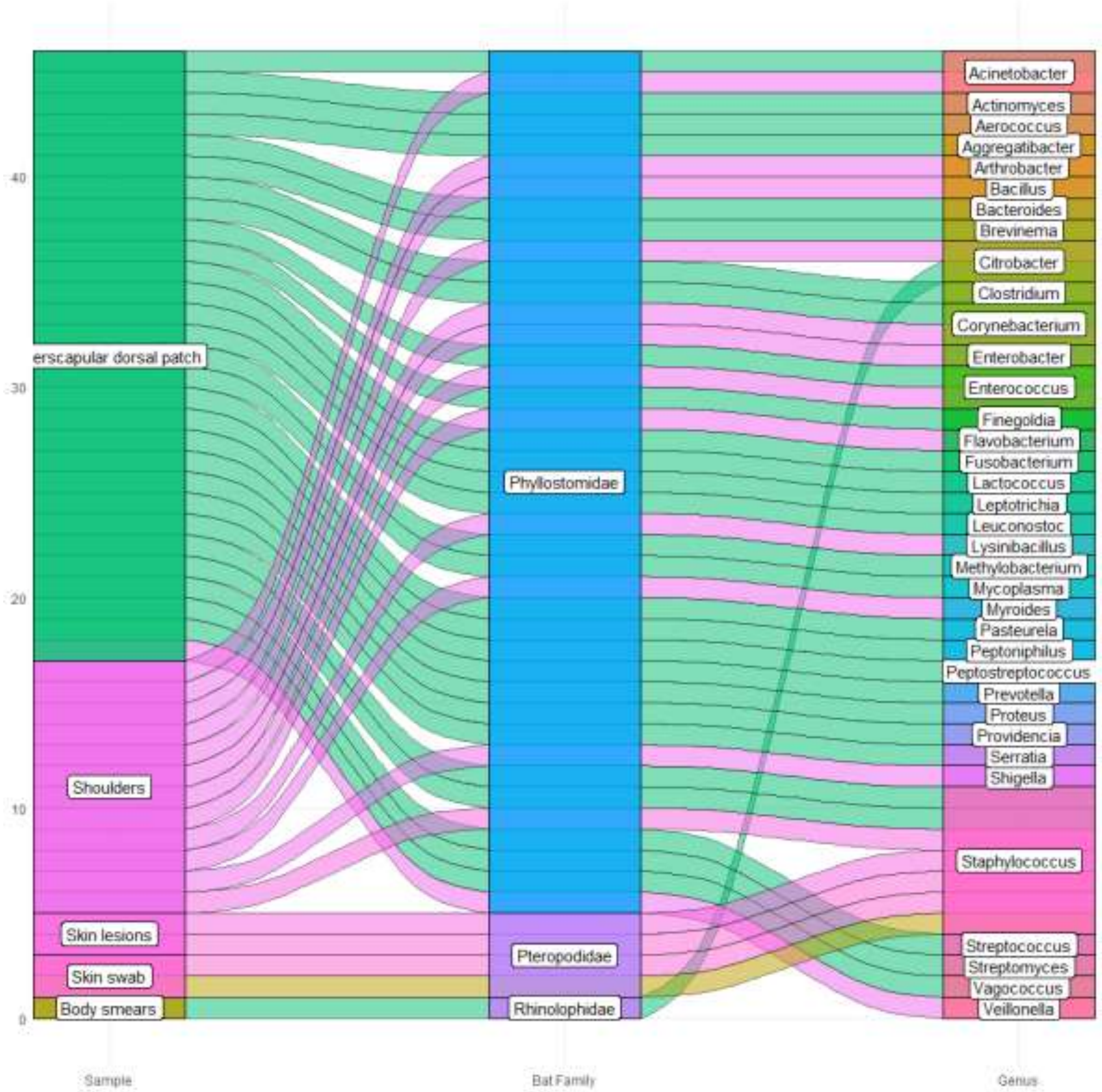


Figure 10: Genera of bacterial pathogens found according to bat family assessed in different skin samples

Pathogenic bacteria of the *Leptospira* genus

Among the studies that investigated *Leptospira* spp. in bats [30/31 (96.8%)] found positive animals. Frequency of positive animals/samples, local and year where and when the studies were performed and bat families in which *Lepstospira* spp. or anti-*Leptospira* spp. antibodies were identified are described in Table 1. Most studies found *Leptospira* spp. in renal samples and the frequency of positives ranged from 1.8% to 87.4 %.

Table 1: *Leptospira* spp. identified in bats sample, in different countries among the studies that found this pathogen in articles selected in this review.

First author, year	Country	Sample	% (N)	Bat family
Bai, 2017	Georgia	Kidney	11.5 (25/218)	Vespertilionidae
Ballados-González, 2018	Mexico	Kidney	30.8 (25/81)	Phyllostomidae
Bessa, 2010	Brazil	Kidney	1.7 (6/343)	Phyllostomidae
Bevans, 2020	India	Kidney	27.1 (47/173)	Phyllostomidae Molossidae
Bunnell, 2000	Peru	Kidney	35 (7/20)	Phyllostomidae
Cox, 2005	Australia	Kidney and urine	11 (19/173)	Pteropodidae
Desvars, 2012	Mayotte	Serum	10.2 (5/49)	Pteropodidae
Desvars, 2013	France	Urine	20 (2/10)	Molossidae
Dietrich, 2015	France	Urine	NI	Molossidae
Dietrich, 2017	South Africa	Urine	14.3 (1/7)	Vespertilionidae Pteropodidae
Dietrich, 2018a	South Africa	Kidney	UD	Vespertilionidae Pteropodidae Molossidae
Dietrich, 2018b	South Africa	Urine	NI	Vespertilionidae
Emanuel, 1964	Australia	Blood	8,9 (6/67)	Pteropodidae
Everard, 1983	Trinidad	Serum	87.3 (215/246)	Phyllostomidae Molossidae Mormoopidae.
Fennestad, 1972	Denmark	Kidney and urine	NI	Vespertilionidae
Gomard, 2016	Madagascar	Pool (kidney, spleen and lung)	21.5 (203/947)	Molossidae Pteropodidae Vespertilionidae
Han, 2018	China	Kidney	50 (62/124)	Vespertilionidae
Lagadec, 2012	Comoros	Pool (kidney, spleen and lung)	47.6 (61/129)	Vespertilionidae Pteropodidae Molossidae

Mateus, 2019	Colombia	Kidney	19.4 (7/26)	Phyllostomidae
Matthias, 2005	Peru	Kidney	3.4 (20/589)	Phyllostomidae
Mayer, 2017	Brazil	Kidney	39.2 (36/92)	Vespertilionidae Phyllostomidae Molossidae
Mgode, 2014	Tanzania	Serum	19.4 (7/36)	NI
Ogawa, 2015	Congo Zambia	Kidney	14.9 (79/529)	Pteropodidae
Smythe, 2002	Australia	Serum	16.2 (71/271)	Pteropodidae
Thayaparan, 2013	Malaysia	Serum	25 (5/20)	Pteropodidae
Thayaparan, 2015	Malaysia	Serum	40 (28/70)	Pteropodidae
Torres-Castro, 2020	Mexico	Kidney	21.7 (15/69)	Phyllostomidae Mormoopidae.
Tulsiani, 2011	Australia	Kidney and urine	76.9 (209/272)	Pteropodidae
Zetum, 2009	Brazil	Serum	7.8 (16/204)	Phyllostomidae
Zhao, 2019	China	Kidney	56.7 (34/60)	Vespertilionidae

N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed; UD: unextracted data.

Pathogenic bacteria transmitted by arthropods

In the group of bacteria transmitted by arthropods, the following pathogens were identified among bat samples: *Anaplasma* spp., *Borrelia* spp., *Bartonella* spp., *Erlichia* spp., and *Rickettsia* spp. The frequencies of positive animals varied from 1.6% to 89.8% (Table 2), being detected in 37 different countries. Vespertilionidae and Phyllostomidae were the bat families most frequent among the studies that detected pathogenic bacteria transmitted by arthropods in bat samples. *Bartonella* spp. was found in 100% (41/41) of the studies that researched this pathogen, and it was also the most frequent pathogen in the group (Table 2).

Table 2: Pathogenic bacterial species transmitted by arthropods identified in bats sample, in different countries among the studies that found this pathogen in articles selected in this review.

First author, year	Country	Bacteria	Sample	% (N)	Bat family
Afonso, 2018	France	*Anaplasma phagocytophilum*	Feces	22.6 (63/278)	Rhinolophidae
André, 2019	Brazil	*Bartonella* spp.	Liver	24.5 (51/208)	Phyllostomidae
Anh, 2015	Vietnam	*Bartonella* spp. *Bartonella grahamii* *Bartonella elizabethae*	Blood	35 (21/60)	Rhinolophidae Hipposideridae Pteropodidae Megadermatidae
Arinjay, 2020	Canada	*Borrelia* spp.	Serum	45.1 (14/31)	Vespertilionidae
Bai, 2011	Guatemala	*Bartonella* spp.	Blood	33 (39/118)	Phyllostomidae
Bai, 2012	Peru	*Bartonella* spp.	Blood	24.2 (27/112)	Phyllostomidae Vespertilionidae
Bai, 2017	Georgia	*Bartonella* spp.	Kidney	35.4 (77/218)	Vespertilionidae
Bai, 2018	Nigeria	*Bartonella* spp.	Blood	12.5 (22/177)	Pteropodidae
Becker, 2018	Peru	*Bartonella* spp.	Blood, oral swab and retal swab	NI	Phyllostomidae
Brook, 2015	Madagascar	*Bartonella* spp.	Blood	40.7 (31/76)	Pteropodidae
Cicuttin, 2017	Argentina	*Rickettsia* spp.	Pool (liver, spleen and lung)	1.6 (1/61)	Molossidae
Cicuttin, 2017	Argentina	*Bartonella* spp.	Pool (liver, spleen and lung)	4.9 (3/61)	Molossidae
Concannnon, 2005	United Kingdom	*Bartonella* spp.	Heart	8.3 (1/12)	Vespertilionidae
Corduneanu, 2018	Romania	*Bartonella* spp.	Heart	1.4 (6/435)	Vespertilionidae
D'Auria, 2010	Brazil	*Rickettsia rickettsia* *Rickettsia parkeri* *Rickettsia amblyommii* *Rickettsia rhipicephali* *Rickettsia belli*	Serum	10.2 (46/451)	Molossidae Phyllostomidae
Davoust, 2016	French Guiana	*Bartonella* spp.	Blood	16.9 (10/59)	Noctilionidae Molossidae

De Leon, 2018	Philippines	*Rickettsia* spp.	Feces	NI	NI
Dietrich, 2016	South Africa Swaziland	*Rickettsia* spp. *Bartonella* spp.	Blood	1.5 (6/384) 3.4 (13/384)	Pteropodidae Phyllostomidae Noctilionidae Mormoopidae Vespertilionidae
Dietrich, 2017	South Africa	*Rickettsia* spp. *Bartonella* spp.	Feces	NI	Nycteridae Vespertilionidae Rhinolophidae
Evans, 2009	United Kingdom	*Borrelia* spp.	Liver	100 (1/1)	Vespertilionidae
Ferreira, 2018	Brazil	*Bartonella* spp.	Spleen	18.5 (22/119)	Phyllostomidae
Gonçalves-Oliveira, 2020	Brazil	*Bartonella* spp.	Spleen	3.6 (4/110)	Phyllostomidae
Gulraiz, 2017	Pakistan	*Bartonella* spp.	Feces and bolus	NI	Pteropodidae
Han, 2017	China	*Bartonella* spp.	Blood	25.3 (27/107)	Pteropodidae Rhinolophidae Vespertilionidae
Hornok,2018	Netherlands	*Rickettsia* spp.	Feces	NI	Vespertilionidae
Hou, 2018	Malaysia	*Bartonella* spp.	Blood	6.7 (1/15)	Pteropodidae
Ikeda, 2017	Brazil	*Bartonella* spp.	Spleen, heart, liver and blood	NI	Natalidae Phyllostomidae Molossidae
Judson, 2015	Costa Rica	*Bartonella* spp.	Blood	33.3 (21/63)	Phyllostomidae, Vespertilionidae
Kamani, 2014	Nigeria	*Bartonella* spp.	Blood	51.3 (76/148)	Rhinolophidae Pteropodidae Molossidae
Kosoy, 2010	Kenyan	*Bartonella* spp.	Blood	32 (106/331)	Emballonuridae Hipposideridae Pteropodidae Vespertilionidae
Lilley, 2015	Finland	*Bartonella* spp.	Blood	37 (46/124)	Vespertilionidae
Lin, 2012	Taiwan	*Bartonella* spp.	Blood	11.1 (1/9)	Vespertilionidae
Marinkelle, 1968	Colombia	*Borrelia* spp.	Blood	0.1 (1/512)	Natalidae

McKee, 2017	Thailand	*Bartonella* spp.	Blood	36.5 (34/93)	Hipposideridae Emballonuridae Molossidae
Nabeshima, 2020	Japan	*Bartonella* spp.	Blood	24 (6/25)	Vespertilionidae
Olival, 2015	Puerto Rico	*Bartonella* spp.	Blood	13.3 (9/68)	Phyllostomidae
Pham, 2015	Vietnam	*Bartonella* spp.	Blood	35 (21/60)	Rhinolophidae Megadermatidae Hipposideridae
Qiu, 2019	Zambia	*Borrelia* spp.	Blood and pool (liver and spleen)	27 (64/237)	Pteropodidae
Qiu, 2020	Zambia	*Bartonella* spp.	Blood	16.7 (1/6)	Pteropodidae
Reeves, 2006	Georgea	*Borrelia* spp. *Rickettsia conorii* *Rickettsia rickettsii*	Serum	5.4 (3/56) 1.7 (1/56)	Phyllostomidae
Reeves, 2016	Saint Kitts Nevis	*Ehrlichia* spp. *Rickettsia africae*	Blood	3.6 (4/111) 2.7 (3/111)	Phyllostomidae
Selvin, 2019	India	*Rickettsia* spp. *Bartonella* spp.	Feces	NI	Rhinolophidae
Stuckey, 2017	Mexico	*Bartonella* spp.	Heart and blood	22.6 (54/238)	Emballonuridae Mormoopidae Phyllostomidae Vespertilionidae
Stuckey, 2017b	France Spain	*Bartonella* spp.	Heart	12/135	Vespertilionidae
Sun,2020	China	*Bartonella* spp.	Feces	NI	Pteropodidae Hipposideridae
Sunil, 2016	India	*Bartonella* spp.	Feces	NI	Pteropodidae
Szubert-Kruszynska, 2019	Poland	*Bartonella* spp.	Blood	8.9 (15/59)	Vespertilionidae
Urushadze, 2017	Georgia	*Bartonella* spp.	Blood	89.9 (212/236)	Rhinolophidae
Veikkolainen, 2014	Finland	*Bartonella mayotimonensis*	Blood	NI	Vespertilionidae
Wolkers-Rooijackers, 2018	Netherlands	*Rickettsia* spp.	Feces	NI	Vespertilionidae
Wray, 2016	Guatemala	*Bartonella* spp.	Serum, blood clot and fecal swab	NI	Phyllostomidae

Zhao, 2020	China	*Rickettsia parkeri* *Rickettsia lusitaniae* *Rickettsia slovaca* *Rickettsia raoultii*	Heart, lung, liver, intestine and kidney	1.1 (6/54)	Vespertilionidae

279 N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed.

Enterobacteriaceae family pathogens

The presence of several pathogenic bacterial genera belonged to Enterobacteriaceae family were identified in bat samples: *Cedecea, Citrobacter, Edwardisiella, Enterobacter, Erwinia, Escherichia, Ewingella, Hafnia, Klebsiella, Kluyvera, Leclercia, Moellerella, Morganella, Pantoea, Plesiomonas, Proteus, Providencia, Rahnella, Raoutella, Salmonella, Shigella, Serratia, Tatumella*, and *Yersinia* (Appendix S5). Bat families with most positive samples were Vespertilionidae and Pteropotidae, among studies were carried out in 30 different countries (Table 3). Details of the clinical samples, countries and families of bats in which the bacteria were identified are in Table 3.

Table 3: Enterobacteriaceae family pathogens identified in bats sample, in different countries among the studies that found this pathogen in articles selected in this review.

First author, year	Country	Sample	% (N)	Bat Family
Adesiyun, 2009	Trinidade	Gastrointestinal tract	1.2 (4/377)	Molossidae Noctilionidae
Apun, 2011	Sarawak and Malaysia	Anal swab	10.7 (9/84)	NI
Arata, 1968	Colombia	Feces	0.04 (1/2112)	Phyllostomidae Molossidae
Ausraful, 2013	Bangladesh	Rectal swab	0.3 (1/302)	Pteropodidae
Bilung, 2014	Malaysia	Anal swab	13.6 (42/308)	NI
Blehert, 2014	United States	Liver	20 (1/5)	Vespertilionidae
Cabal, 2015	Brazil	Feces	21.95 (18/82)	NI
Childs-Sanford, 2009	United States	Pool: liver, lymph nodes mesenteric and gastrointestinal tract	13.3 (4/30)	Pteropodidae
Claudio, 2014	Brazil	Oral and retal swabs	95.5 108/113	Phyllostomidae Vespertilionidae Molossidae
Collins, 2019	Australia	Feces	100 (1/1)	Vespertilionidae Rhinolophidae
Daniel, 2013	Malaysia	Stomach and intestine	100 (7/7)	Pteropodidae
Dietrich, 2017	South Africa	Feces	NI	Vespertilionidae Rhinolophidae
Dimkić, 2020	Serbia	Feces	NI	Vespertilionidae
Fajri, 2018	Indonesia	Feces	25	Hipposideridae Rhinolophidae Pteropodidae
Gaona, 2019	Mexico	Interscapular dorsal patch	NI	Phyllostomidae
Garces, 2019	Portugal	Feces	9.5 (14/146)	Molossidae
Gerbacova, 2020	Slovakia	Feces	UD	Vespertilionidae Rhinolophidae
Gharout-Sait, 2019	Algeria	Feces	1.8 (2/110)	NI
González-Quiñonez, 2014	Venezuela	Shoulders	NI	Phyllostomidae
Gulraiz, 2017	Paquistão	Feces	NI	Pteropodidae
Han, 2010	Coreia	Blood	1/1	Pteropodidae
Henry, 2018	Australia	Feces	NI	Pteropodidae
Imnadze, 2020	Georgia	Intestine	100 (20/20)	Vespertilionidae Rhinolophidae
Ingala, 2019	Belize	Rectal swab	NI	Phyllostomidae

Islam, 2013	Bangladesh	Rectal swab	0.3 (1/312)	Pteropodidae
Italia, 2012	Filiphine	Intestine	60.7 (34/56)	Pteropodidae Vespertilionidae
Kholik, 2019	Indonesia	Anal swab	10 (2/20)	Pteropodidae Emballonuridae
Mühldorfer, 2010	Germany	Lung, heart, kidney and pool: liver, spleen and intestine	1 (2/200)	Vespertilionidae
Mühldorfer, 2011b	Germany	NI	NI	NI
Mühldorfer, 2011c	Germany	Brain	NI	NI
Nakamura, 2013	Japan	Liver	NI	Pteropodidae
Newman, 2018	United States	Feces	NI	Pteropodidae
Nowak, 2017	Congo [Republic]	NI	60 (30/50)	Pteropodidae
Reyes, 2011	Philippines	Small intestine	2 (2/96)	Vespertilionidae
Selvin, 2019	India	Feces	NI	Rhinolophidae
Sens, 2018	Brazil	Oral and perianal swabs	NI	Phyllostomidae
Sun, 2019	China	Intestinal and stomach contents	NI	Rhinolophidae Vespertilionidae
Sun, 2020	China	Feces	NI	Emballonuridae Rhinolophidae Vespertilionidae Hipposideridae Pteropodidae
Sunil, 2016	China	Feces	NI	Pteropodidae
Vandzurova, 2013	China	Feces	NI	Vespertilionidae
Vengust, 2018	China	Feces	NI	Vespertilionidae Rhinolophidae
Wolkers-Rooijackers, 2018	China	Feces	NI	Vespertilionidae
Wu, 2019	China	Feces and large intestine	NI	Vespertilionidae Rhinolophidae
Xiao, 2019	China	Intestinal contents	NI	Rhinolophidae

N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed; UD: unextracted data.

Other Gram-positive pathogens

Other Gram-positive bacterial pathogens other than those mentioned described above were also identified in bat samples: *Actinomyces* spp., *Aerococcus* spp., *Arthrobacter* spp., *Bacillus* spp., *Brachybacterium* spp., *Brevibacterium* spp., *Carnobacterium* spp., *Corynebacterium* spp., *Enterococcus* spp., *Finegoldia* spp., *Kurthia* spp., *Lactococcus* spp., *Leucobacter* spp., *Leuconostoc* spp., *Listeria* spp., *Lysinibacillus* spp., *Micrococcus* spp., *Nocardia* spp., *Paenibacillus* spp., *Peptoclostridium* spp., *Peptoniphilus* spp., *Peptostreptococcus* spp., *Rhodococcus* spp., *Staphylococcus* spp., *Streptococcus* spp., *Streptococcus* spp. and *Weisella* spp. These bacterial genera were detected mainly in bats from Vespertilionidae, Pteropotidae and Phyllostomidae families, in studies carried out in 22 different countries (Table 4).

Table 4: Pathogenic Gram-positive bacteria identified in bats sample, in different countries among the studies that found this pathogen in articles selected in this review.

First author, year	Country	Bacteria	Sample	% (N)	Bat family
Akobi, 2012	Nigeria	*Staphylococcus aureus*	Feces	UD	Pteropodidae
Claudio, 2018	Brazil	*Stapylococcus* spp. *Staphylococcus aureus* *Staphylococcus hominis* *Staphylococcus xylosus* *Streptococcus* spp. *Enterococcus* spp. *Acinetobacter* spp. *Brevundimonas* spp. *Lactococcus* spp.	Oral and rectal swabs	95.6 (108/113)	Phyllostomidae Vespertilionidae Molossidae
Daniel, 2013	Malaysia	*Enterococcus* spp.	Intestine	14.3 (1/7)	Pteropodidae
De Leon, 2018	Philippines	*Legionella* spp. *Corynebacterium* spp.	Feces	UD	NI
Dietrich, 2017	South Africa	*Nocardia* spp. *Micrococcus* spp.	Urine, feces and spittler	UD	Vespertilionidae
Dimkić, 2020	Serbia	*Staphylococcus aureus* *Staphylococcus epidermidis* *Enterococcus* spp. *Brevibacterium* spp. *Rhodococcus* spp. *Paenibacillus* spp.	Feces	NI	NI
Fajri, 2018	Indonesia	*Staphylococcus aureus*	Mouth	25 (1/4)	Rhinopomatidae
Fountain, 2019	United Kingdom	Coagulase-negative Staphylococci	Skin swab, oropharynx, material ejected into the mouth and skin lesions	NI	Pteropodidae

Gaona, 2018	Mexico	*Lysinibacillus* spp. *Peptostreptococcus* spp. *Peptoniphilus* spp. *Finegoldia* spp. *Actinomyces* spp. *Leuconostoc* spp. *Lactococcus* spp. *Aerococcus* spp. *Enterococcus* spp. *Corynebacterium* spp. *Streptococcus* spp. *Staphylococcus epidermidis* *Staphylococcus* spp.	Interscapular dorsal patch	UD	Phyllostomidae
Gerbacova, 2020	Slovakia	*Enterococcus mundtii* *Enterobacter ludwigii* *Enterococcus casseliflavus* *Enterococcus faecium* *Leuconostoc* spp. *Lactococcus garvieae* *Brevundimonas diminuta* *Aerococcus viridans* *Paenibacillus* spp	Feces	NI	Rhinolophidae
González-Quiñonez, 2014	Venezuela	*Brevundimonas* spp. *Acinetobacter* spp. *Enterococcus* spp. *Staphylococcus* spp.	Shoulders	UD	Phyllostomidae
Gulraiz, 2017	Pakistan	*Corynebacterium* spp. *Nocardia* spp. *Listeria* spp.	Feces and bolus	NI	Phyllostomidae
Held, 2017	Gabon	*Staphylococcus chweitzer* *Staphylococcus aureus*	Pharyngeal swab	4.5 (6/133)	Pteropodidae Vespertilionidae
Henry, 2018	Australia	*Acinetobacter calcoaceticus*	Feces	UD	Pteropodidae
Imnadze, 2020	Georgia	*Enterococcus faecalis*	Intestine	100 (11/11)	Vespertilionidae

Ingala, 2019	Belize	*Staphylococcus* spp. *Streptococcus* spp.	Rectal swabs	100 (30/30) 10 (3/30)	Phyllostomidae
Mioni, 2018	Brazil	*Streptococcus dysgalactiae*	Lung, liver and intestine	100 (5/5)	Phyllostomidae
Mühldorfer, 2011b	Germany	Coagulase-negative Staphylococci *Staphylococcus aureus* *Staphylococcuintermedius* *Leucobacter* spp. *Aerococcus viridans* *Enterococcus* spp.	NI	NI	NI
Newman, 2018	United States	*Streptococcus* spp. *Peptoclostridium* spp. *Weisella* spp. *Lactococcus* spp. *Enterococcus* spp. *Paenibacillus* spp.	Feces	NI	Pteropodidae
Olatimehin, 2018	Nigeria	*Staphylococcus aureus* *Staphylococcus schweitzeri* *Staphylococcus argenteus*	Feces	NI	Pteropodidae
Selvin, 2019	India	*Staphylococcus* spp. *Rhodococcus* spp. *Enterococcus* spp. *Corynebacterium diptheriae*	Feces	UD	Rhinolophidae
Sun, 2019	China	*Staphylococcus* spp. *Acinetobacter* spp.	Intestinal and stomach contents	UD	Vespertilionidae Rhinolophidae
Sun, 2020	China	*Staphylococcus* spp. *Enterococcus* spp. *Streptococcus* spp.	Feces	NI	Vespertilionidae Rhinolophidae Pteropodidae Emballonuridae

Sunil, 2016	India	*Staphylococcus aureus* *Kurthia* spp. *Acinetobacter* spp. *Enterococcus* spp. *Corynebacterium* spp. *Streptococcus pneumoniae* *Brevibacterium* spp. *Weisella* spp. *Brachybacterium* spp.	Feces	UD	Pteropodidae
Vandzurova, 2012	Slovakia	*Staphylococcus sciuri* *Staphylococcus lentus*	Feces	UD	Vespertilionidae
Vengust, 2018	Slovenia	*Staphylococcus* spp. *Acinetobacter* spp. *Enterococcus* spp.	Feces	UD	Vespertilionidae Rhinolophidae
Walther, 2008	Germany	*Staphylococcus aureus*	Wounds	1/1	NI
Wolkers-Rooijackers, 2018	Holanda	*Staphylococcus capitis* *Enterococcus faecalis* *Leucobacter* spp. *Leuconostoc* spp. *Lactococcus* spp. *Acinetobacter* spp.	Feces	UD	Vespertilionidae
Wu, 2019	China	*Staphylococcus* spp.	Feces and intestine	UD	Vespertilionidae Rhinolophidae
Xiao, 2019	China	*Enterococcus* spp. *Lactococcus* spp.	Intestinal contents	UD	Rhinolophidae
Yuan, 2019	China	*Enterococcus* spp. *Lactococcus* spp.	Stomach and intestine	UD	Vespertilionidae

N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed; UD: unextracted data.

Other Gram-negative pathogens

Other Gram-negative bacterial pathogens other than those mentioned described above were also identified in bat samples: *Acinetobacter* spp., *Advenella* spp., *Aeromonas* spp., *Aggregatilbacter* spp., *Alcaligenes* spp., *Alistipes* spp., *Bacteroides* spp., *Bordetella* spp., *Brevinema* spp., *Brevundimonas* spp., *Brucella* spp., *Burkholderia* spp., *Clostridium* spp., *Comamonas* spp., *Coxiella* spp., *Cronobacter* spp., *Flavobacterium* spp., *Francisella* spp., *Fusobacterium* spp., *Haemophilis* spp., *Helicobacter* spp., *Legionella* spp., *Leptotrichia* spp., *Methylobacterium* spp., *Myroides* spp., *Neisseria* spp., *Neorickettsia* spp., *Ochrobactrum* spp., *Paracoccus* spp., *Pasteurella* spp., *Prevotella* spp., *Pseudomonas* spp., *Sphingomonas* spp., *Stenotrophomonas* spp., *Veilonella* spp., *Vibrio* spp., *Wauterisiella* spp. and *Yokenella* spp. These bacterial genera were detected mainly in bats from Vespertilionidae and Rhinopomatidae families, in studies carried out in 21 different countries (Table 5).

Table 5: Pathogenic Gram-negative bacteria identified in bats sample, in different countries among the studies that found this pathogen in articles selected in this review.

First author, year	**Country**	**Bacteria**	**Sample**	**% (N)**	**Bat family**
Bai, 2017	Georgia	*Brucella* spp.	Spleen	1.8 (4/218)	Vespertilionidae
Blehert, 2014	United States	*Pasteurella multocida*	Lung, liver, spleen, heart and mammary gland	80 (4/5)	Vespertilionidae
Bandelj, 2019	Slovenia	*Clostridium difficile*	Feces	19.3 (18/93)	Vespertilionidae Rhinolophidae
Cicuttin, 2013	Argentina	*Neorickettsia risticii*	NI	10 (3/30)	Molossidae
Cicuttin, 2017	Argentina	*Neorickettsia risticii*	Pool (liver, spleen and lung)	8.1 (5/61)	Molossidae
Claudio, 2018	Brazil	*Burkrolderia* spp. *Aeromonas* spp. *Neisseria* spp. *Yokenella* spp. *Ochrobactrum* spp. *Pseudomonas* spp.	Swab oral	NI	Phyllostomidae Vespertilionidae Molossidae
Daniel, 2013	Malaysia	*Pseudomonas* spp.	Intestine	14.3 (1/7)	Pteropodidae
De Leon, 2018	Philippines	*Burkrolderia* spp. *Francisella* spp. *Pseudomonas* spp.	Feces	NI	NI
Dietrich, 2017	South Africa	*Pasteurella* spp. *Coxiella* spp. *Burkrolderia* spp. *Helicobacter* spp. *Aeromonas* spp. *Haemophilis* spp. *Vagococcus* spp.	NI	NI	Vespertilionidae Rhinolophidae
Dimkić, 2020	Serbia	*Comamonas* spp.	Feces	NI	NI

		Pseudomonas spp.			
Fajri, 2018	Indonesia	Alcaligenes xylosoxidans Aeromonas caviae Neisseria sicca	Feces	25 1/4 25 1/4 25 (1/4)	Hipposideridae Pteropodidae
Ferreira, 2018	Brazil	*Coxiella burnetii*	Spleen, liver and heart	3.4 (4/119)	Vespertilionidae
Gaona, 2019	Mexico	*Aggregatibacter segnis* *Brevinema* spp. *Fusobacterium* spp. *Flavobacterium* spp. *Bacteroides* spp. *Leptotrichia* spp. *Prevotella* spp. *Vagococcus* spp. *Pasteurella multocida* *Pasteurela* spp. *Provetela* spp. *Clostridium perfringens,* *Clostridium* spp. *Methylobacterium* spp.	Interscapular dorsal patch	NI	Phyllostomidae
Gerbacova, 2020	Slovakia	*Brevundimonas diminuta* *Pseudomonas* spp.	Feces	NI	Rhinopomatidae
González-Quiñonez, 2014	Venezuela	*Myroides* spp.	Shoulders	UD	Phyllostomidae
Gulraiz, 2017	Pakistan	*Alcaligenes* spp.	Feces	NI	Pteropodidae
Henry, 2018	Australia	*Cronobacter* spp. *Haemophilis* spp. *Fusobacterium* spp. *Pseudomonas* spp. *Clostridium disporicum,* *Clostridium perfringens,* *Clostridium sordellii,*	Feces	UD	Pteropodidae
Imnadze, 2020	Georgia	Enterococcus faecalis *Pseudomonas* spp.	Intestine	100 (11/11)	Vespertilionidae

Ingala, 2019	Belize	*Helicobacter* spp. *Pseudomonas* spp.	Rectal swabs	NI	Phyllostomidae
Maliničová, 2017	Hungary	*Comamonas* spp. *Pseudomonas* spp.	Feces	NI	Rhinopomatidae
Muhldorfer, 2011b	Germany	*Pasteurela multocida* *Pasteurela* species B *Pasteurela pneumotropica* *Burkrolderia* spp. *Aeromonas* spp. *Myroides* spp. *Moerella* spp. *Clostridium sordellii* *Vibrio* spp.	Lung, heart, liver, spleen, kidney and tong		NI
Newman, 2018	United States	*Helicobacter* spp. *Clostridium spp.*	Feces	NI	Pteropodidae Molossidae
Selvin, 2019	India	*Burkrolderia* spp. *Pseudomonas* spp. *Clostridium* spp.	Feces	NI	Rhinopomatidae Phyllostomidae
Sun, 2019	China	*Burkrolderia* spp. *Pseudomonas* spp.	Intestinal and stomach contents	UD	Rhinopomatidae Vespertilionidae
Sun, 2020	China	*Brucella* spp. *Bordetella* spp. *Vibrio* spp.	Intestinal and stomach contents	NI	Emballonuridae Hipposideridae
Sunil, 2016	India	*Brucella* spp. *Aeromonas* spp. *Advenella* spp. *Wauterisiella* spp. *Paracoccus* spp. *Myroides* spp. *Pseudomonas* spp. *Clostridium* spp.	Feces	NI	Pteropodidae
Vandzurova, 2013	Slovakia	*Alcaligenes* spp.	Feces	UD	Vespertilionidae
Vengust, 2018	Slovenia	*Pseudomonas* spp.	Feces	UD	Vespertilionidae Rhinolophidae

Wolkers-Rooijackers, 2018	Netherlands	*Vagococcus* spp. *Moerella* spp. *Ochrobactrum* spp. *Pseudomonas* spp.	Feces and intestine	UD	Vespertilionidae
Wu, 2019	China	*Clostridium* spp.	Feces and large intestine	NI	Vespertilionidae Rhinolophidae
Xiao, 2019	China	*Helicobacter* spp. *Ochrobactrum* spp. *Pseudomonas* spp.	Intestinal contents	UD	Rhinopomatidae
Yuan, 2019	China	*Sphingomonas* spp. *Alistipes* spp. *Pseudomonas* spp. Sphingomonas spp.	Stomach and intestine	UD	Vespertilionidae

N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed; UD: unextracted data.

Other pathogenic bacteria

Other neither Gram-positive nor Gram-negative pathogenic bacteria that have not been classified in any other group described above identified in bat samples were: *Clamydia* spp., *Mycobacterium* spp, *Mycoplasma* spp., *Treponema* spp. and *Ureaplasma* spp. These bacterial genera were detected mainly in bats from Vespertilionidae and Phyllostomidae families, in studies carried out in 17 different countries (Table 6).

Table 6: Other neither Gram-positive nor Gram-negative pathogenic bacteria (atypical bacteria) identified in bats sample, in different countries among the studies that found this pathogen in articles selected in this review.

First author, year	**Country**	**Bacteria**	**Sample**	**% (N)**	**Bat family**
Becker, 2020	Belize	*Mycoplasma* spp.	Blood	50.9 (239/469)	Phyllostomidae Mormoopidae Vespertilionidae Natalidae Emballonuridae
Cataldo, 2020	Nigeria	Mycoplasma spp.	Blood	35.5 (32/90)	Pteropodidae Molossidae
De Leon, 2018	Philippines	*Mycobacterium* spp.	Feces	NI	NI
Dietrich, 2017	South Africa	*Treponema* spp.	Urine, feces and spittler	NI	NI
Fritschi, 2020	Germany	*Clamydia* spp. *Mycoplasma* spp.	Spleen, liver and intestine	31.4 (149/475) 3.1 (15/475)	Vespertilionidae
Gaona, 2019	Mexico	*Mycoplasma* spp.	Interscapular dorsal patch	NI	Phyllostomidae
Hokynar, 2017	Finland	*Clamydia* spp.	Feces	54 (108/200)	Vespertilionidae
Holz, 2019	Australia	*Mycoplasma* spp.	Blood	9.7 (8/83)	Vespertilionidae
Ikeda, 2017	Brazil	*Mycoplasma* spp.	Spleen, hert, liver and blood	UD	Phyllostomidae Molossidae Vespertilionidae
Ingala, 2019	Belize	*Mycoplasma* spp.	Rectal swab	UD	Phyllostomidae
Mascarelli, 2014	United States	*Mycoplasma* spp.	Spleen	47 (32/68)	Vespertilionidae
Millán, 2015	Spain	*Mycoplasma* spp.	Blood	96.7 (30/31)	Vespertilionidae
Millán, 2019	Chile	*Mycoplasma* spp.	NI	21.8 (12/55)	Vespertilionidae
Modra, 2017	Czech Republic	*Mycobacterium* spp.	Feces	73.3 (11/15)	NI
Newman, 2018	United States	*Mycoplasma* spp. *Ureaplasma* spp.	Feces	NI	Pteropodidae Molossidae
Santos, 2020	Brazil	*Mycoplasma* spp.	Blood	80 (8/10)	Molossidae Phyllostomidae
Selvin, 2019	Índia	*Mycobacterium* spp.	Feces	NI	Rhinolophidae

Sunil, 2016	India	*Mycobacterium* spp.	Feces	NI	NI
Volokhov, 2017	Peru	*Mycoplasma* spp.	Blood	67.3 (150/223)	Phyllostomidae
Xiao, 2019	China	*Mycoplasma* spp.	Intestinal contents	UD	Rhinolophidae
Yuan, 2019	China	*Mycobacterium* spp. *Mycoplasma* spp.	Stomach and intestine	NI	Vespertilionidae

N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed; UD: unextracted data.

Discussion

The synanthropic behavior of bats, their ability to fly, their immune system adapted to suppress some diseases, altogether contribute to these animals to be potential hosts of emerging bacterial pathogens. Therefore, in this review, we focused on compiling and describing the bacterial pathogens already reported in different bat families around the world, aiming to contribute to the understanding of the risks associated with the contact with these animals and to guide the formulation of surveillance policies. Our findings showed that more than 100 pathogenic bacterial genera have been described in 14 different bat families, being *Bartonella* spp., *Leptospira* spp. and *Staphylococcus* spp. the most researched and found pathogens among bat species, evidencing the importance of these mammals as a host of zoonotic pathogens.

The modification of a habitats as due to several factors such as environmental degradation by natural disasters or human action that increase the synanthropic behavior of bats, the discoveries of new research and diagnostic techniques, and the improvement of existing ones, as well as the implementation of One health perception on health issues, may have contributed to the emergence in recent years of studies that sought to unravel the role of bats in the epidemiology of zoonotic bacterial diseases, as observed in the present study (Figure 2). In fact, the identification of more than a hundred different bacterial genera in bats and the fact that most studies that have searched for these genera have found them, point to the great capacity of bats in harboring these zoonotic pathogens. Among the genera identified in this review, *Bartonella* spp., *Leptospira* spp. and *Staphylococcus* spp. were the most observed and with significant growth over the years since the first papers published on the subject (Table 1, 2 and 4). Previous knowledge and importance of these pathogens for human and animal populations probably have contributed to the high interest of the authors for these agents, as well as having motivated the investigation of other pathogens of known zoonotic importance, standing out *Borrelia* spp., *Brucella* spp., *Campylobacter* spp., *Coxiella* spp., *Escherichia* spp., *Listeria* spp., *Rickettsia* spp., *Salmonella* spp., *Shigella* spp., *Streptococcus* spp. and , *Yersinia* spp. (Figure 3). The presence of these agents in different clinical samples of bats in several countries around the world points to the need to implement epidemiological surveillance measures, considering bats as a potential source of infection. Furthermore, future studies should be carried out in order to clarify the possible role of bats in the diseases caused by these zoonotic pathogens, whether they act only as a host or they can be considered reservoirs or epidemiologicallyimportant sources of infection.

In addition, many opportunistic pathogens were also found in bats, as *Aggregatibacter* spp., *Arthrobacter* spp., *Enterobacter* spp., *Enterococcus* spp., *Methylobacterium* spp., *Ochrobactrum* spp., *Paenibacillus* spp., *Pantoea* spp., *Veillonella* spp. (Figure 3). The identification of bats as potential hosts for these pathogens gains importance taking into account the increasing longevity of the human population, with the elderly and immunosuppressed individuals the relevant group for these pathogens. The identification of potential risks gives epidemiologists and healthcare professionals more tools for investigating cases and outbreaks of bacterial diseases caused by these pathogens. Indeed, conducting a systematic review is a rational way of organizing this knowledge, generally dispersed in the literature, with the possibility of measuring the risks.

Another important result obtained from the studies compiled in this review showed that pathogenic bacteria were observed in 14 different bat families, encompassing 66.7% (14/21) of existing bat families (21, 22), which is a significant number considering the diversity of bat species found harbouring pathogens or with evidence of exposure to (antibodies) (Figure 4). Data such as these have impacts beyond public health, revealing a possible negative action of these pathogens also on bat populations, which may have important consequences from the point of view of species conservation, fauna health and environmental balance (23). Furthermore, it is important to mention that among the bat families in pathogens surveyed, at least one was identified (or evidence of exposure) in all (100%). The absence of species representatives of seven bat families (Cistugidae, Craseonycteridae, Frupteridae, Miniopteridae, Myzopodidae, Mystacinidae and Rhinonycteridae) can be justified considering factors such as habitat diversity, the difference in flight height and consequently in the capture strategy, which can make sampling difficult. Even more important, the very low number of species belonging to some families, such as Frupteridae, Myzopodidae and Mystacinidae (2 species each) (21, 22), must also be considered. Moreover, research involving wild animals also involves ethical and legal issues (conservation), and generally has high costs (24).

Also, data on the relationship between the clinical sample and the bacterial genus found revealed the potential risks that each clinical sample may represent in the transmission of pathogens to other wild or domestic animals and to humans. In this sense, samples from skin and TGI obtained the greatest diversity among the pathogenic genera found (Figure 5 and 10), which can be explained due to the very diverse microbial community usually present in TGI (25, 26). Also, the use of metagenomic by some studies selected by this review (27) allowed the simultaneous identification of several pathogens in these samples. Samples from skin, TGI and also urine (from which all papers that researched, found *Leptospira* spp.), possibly pose the greatest risks of transmission of bacterial pathogens due to a greater probability of contact. The bacterial genera found in blood and organ samples, such as *Bartonella, Rickettsia, Mycoplasma, Borrelia, Leptospira, Pasteurella, Chlamydia, Salmonella* and *Brucella* (Figure 7), suggest bacteremia and infection in organs, and that thereby these agents are causing pathologies in bats. Additionally, all these findings can drive future studies on which samples should be collected considering different bacterial genera.

The main limitation of this study was the impossibility of conducting a meta-analysis, which led to a descriptive analysis of most of the available information in the selected studies. Moreover, it is worth mentioning that use of pool samples in some studies prevented the identification of risks for individual clinical samples, and that samples of feces collected on the floor of caves did not allow the assessment of the frequency of the pathogen but their mere presence. However, the information generated by compiling all these studies is extremely valuable, especially for directing health surveillance and disease prevention actions for domestic animals and humans, as well as for the adoption of measures for the conservation of bats. In conclusion, this systematic review on bacterial pathogens in bats, revealed an alarming potential of bats of different species as hosts of more than a hundred bacterial pathogens.

Acknowledgments

ACRF thanks the Coordination for the Improvement of Higher Education Personnel and the National Council for Scientific and Technological Development for the fellowship.

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Appendix S1: PRISMA Checklist

Section/topic	#	Checklist item	Reported on paragraph number #
TITLE			
Title	1	Identify the report as a systematic review, meta-analysis, or both.	Paragraph 1
ABSTRACT			
Structured summary	2	Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number.	Paragraph 1
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known.	Paragraph 1 to 3
Objectives	4	Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS).	Paragraph 3
METHODS			
Protocol and registration	5	Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number.	Paragraph1
Eligibility criteria	6	Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale.	Paragraph 4 to 5
Information sources	7	Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched.	Paragraph 1
Search	8	Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated.	S2 Appendix
Study selection	9	State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis).	Paragraph 3 to 4

Data collection process	10	Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data from investigators.	Paragraph 5
Data items	11	List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made.	Paragraph 4
Risk of bias in individual studies	12	Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis.	Not done
Summary measures	13	State the principal summary measures (e.g., risk ratio, difference in means).	Not applicable
Synthesis of results	14	Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I^2) for each meta-analysis.	Paragraph 5
Risk of bias across studies	15	Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies).	Not done
Additional analyses	16	Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified.	Not done
RESULTS			
Study selection	17	Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram.	Paragraph 1
Study characteristics	18	For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations.	Paragraph 2 and 3
Risk of bias within studies	19	Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12).	Not done
Results of individual studies	20	For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot.	S4 Appendix
Synthesis of results	21	Present results of each meta-analysis done, including confidence intervals and measures of consistency.	Not done
Risk of bias across studies	22	Present results of any assessment of risk of bias across studies (see Item 15).	

Additional analysis	23	Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see Item 16]).	9
DISCUSSION			
Summary of evidence	24	Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers).	Paragraph 1 and 2
Limitations	25	Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias).	Paragraph 2
Conclusions	26	Provide a general interpretation of the results in the context of other evidence, and implications for future research.	Paragraph 4
FUNDING			
Funding	27	Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review.	Paragraph 1

Appendix S2: Combination of terms used at each database investigated within all the sections 9,930 from papers (title, abstract and full text) in the databases, as well as the number of articles found for the search performed on August 25th, 2020.

Database	***Conbination of words***	***Results***
Cabi	(bat OR bats OR flittermouse OR Chiroptera) AND (reservoirs OR carriers OR transmitters OR preval* OR incidenc* OR occur* OR detection) AND ((disease* AND (communicable OR animal ORemerging) OR (bacterial AND (pathogen* OR infect* OR diseas*)) OR bacter* OR Leptospira OR Salmonella OR Brucella OR Bartonella OR Campylobacter OR Clostridium OR Listeria OR Shigella OR Yersinia OR Borrelia OR Neorickettsia))	2,714 articles
Cochrane	(bat OR bats OR flittermouse OR Chiroptera) AND (reservoirs OR carriers OR transmitters OR preval* OR incidenc* OR occur* OR detection) AND ((disease* AND (communicable OR animal ORemerging) OR (bacterial AND (pathogen* OR infect* OR diseas*)) OR bacter* OR Leptospira OR Salmonella OR Brucella OR Bartonella OR Campylobacter OR Clostridium OR Listeria OR Shigella OR Yersinia OR Borrelia OR Neorickettsia))	88 articles
Pubmed	(((bat OR bats OR flittermouse OR Chiroptera)) AND (reservoirs OR carriers OR transmitters OR preval* OR incidenc* OR occur* OR detection)) AND ((disease* AND (communicable OR animal OR emerging) OR (bacterial AND (pathogen* OR infect* OR diseas*)) OR bacter* OR Leptospira OR Salmonella OR Brucella OR Bartonella OR Campylobacter OR Clostridium OR Listeria OR Shigella OR Yersinia OR Borrelia OR Neorickettsia)	2,462 articles
Scielo	(bat OR bats OR flittermouse OR Chiroptera) AND (reservoirs OR carriers OR transmitters OR preval* OR incidenc* OR occur* OR detection) AND ((disease* AND (communicable OR animal OR emerging) OR (bacterial AND (pathogen* OR infect* OR diseas*)) OR bacter* OR Leptospira OR Salmonella OR Brucella OR Bartonella OR Campylobacter OR Clostridium OR Listeria OR Shigella OR Yersinia OR Borrelia OR Neorickettsia)	0 articles
Scopus	TITLE-ABS-KEY (bat OR bats OR flittermouse OR chiroptera) AND (reservoirs OR carriers OR transmitters	6,738 articles

	OR preval* OR incidenc* OR occur* OR detection) AND ((disease* AND (communicable OR animal OR emerging)) OR (bacterial AND (pathogen* OR infect* OR diseas*)) OR bacter* OR leptospira OR salmonella OR brucella OR bartonella OR campylobacter OR clostridium OR listeria OR shigella OR yersinia OR borrelia OR neorickettsia)	
Web of Science	TS=((bat OR bats OR flittermouse OR Chiroptera) AND (reservoirs OR carriers OR transmitters OR preval* OR incidenc* OR occur* OR detection) AND ((disease* AND (communicable OR animal OR emerging)) OR (bacterial AND (pathogen* OR infect* OR diseas*)) OR bacter* OR leptospira OR salmonella OR brucella OR bartonella OR ampylobacter OR clostridium OR listeria OR shigella OR yersinia OR borrelia OR neorickettsia))	985 articles

Appendix S3: Inclusion and exclusion criteria for selection of studies in this systematic review.

Inclusion criteria	***Exclusion criteria***
Papers of all countries All years Portuguese Approach in bats Approach in bacterial zoonoses	Non-bacterial zoonosis Bacterial zoonosis in other species than bats Commensal microbiota study Ecology of bats Studies written in languages other than English, Spanish or Portuguese Reviews Full text not available Proceedings Books

Appendix S4: Data extracted from all the 146 articles selected by this systematic review from the exclusion/inclusion criteria, published between 1964 and 2020

First author, year	Enviroment	Year	Country	Source	Diagnostic	N tested animals	sp. Isolated (N positive animals)	Positive Bat species
Adesiyun, 2009	Wild	2006-2007	Trinidade	Gastrointestinal tract	Culture, Biochemical	377	*Salmonella* spp. (4)	*Molossus major* *Molossus ater* *Noctilio leporinus*
Afonso, 2018	Urban	2011	France	Feces	Conventional PCR, Sequencing	278	*Anaplasma* spp. (63)	*Rhinolophus hipposideros*
Akobi, 2012	Urban	2008 - 2010	Nigeria	Feces	Conventional PCR, Sequencing	560	*Staphylococcus* spp. (107)	*Eidolon helvum*
André, 2019	NI	NI	Brazil	Liver	Conventional PCR, Real time PCR Sequencing	208	*Bartonella* spp. (51)	*Desmodus rotundus,* *Diphylla ecaudata,* *Diaemus youngii*
Anh, 2015	Urban and Wild	2013	Vietnam	Blood	Conventional PCR	60	*Bartonella* spp. (21)	*Hipposideros armiger, Larvatui hipposideros, Megaerops niphanae, Megaderma espasma, Megaderma lyra, Rhinolophus acuminatus, Rhinolophus chaseli, Rhinolophus sinicus*
Apun_2011	Urban and Wild	2008	Malaysia	Anal swab	Conventional PCR	84	*Escherichia coli* (9)	NI
Apun_2011	Urban and Wild	2008	Malaysia	Anal swab	Conventional PCR	84	*Escherichia coli* (9)	NI
Arata_1968	Urban and Wild	1964 - 1966	Colombia	Feces	Culture UD	2112	*Salmonella blockley* (1), *Salmonella* anatum (1), *Salmonella* landoff (1), *Shigella boydii* (1)	*Molossus molossus, Artibeus lituratus,* *Sturnira lilium,* *Molossus bondae*
Arinjay_2020	NI	2012 a 2018	India	Blood	Culture, ELISA	31	*Borrelia burgdorferi* (14)	*Eptesicus fuscus*

Ausraful_2013	Wild	2010	Bangladesh	Rectal swabs	Culture, Biochemical	302	*Salmonella* Virchow (1)	*Pteropus giganteus*
Bai_2011	NI	2009	Guatemala	NI	Cultura, Conventional PCR	118	*Bartonella* spp. (39)	*Artibeus toltecus, Desmodus rotundus, Glossophaga soricina, Phyllostomus discolor, Sturnira lilium*
Bai_2012	Wild l	2010	Peru	Blood	Culture, Conventional PCR, Sequencing	112	*Bartonella* spp. (27)	*Artibeus obscurus, Artibeus planirostris, Carollia brevicauda, Carollia perspicillata, Desmodus rotundus, Glossophaga soricina, Myotis* spp., *Phyllostomus discolor, Phyllostomus hastatus, Platyrrhinus recifinus, Sturnira lilium, Vampyricus bidens*
Bai_2017	Urban and Wild	2012	Georgia	Kidney and spleen	Conventional PCR, Real time PCR, Sequencing	218	*Leptospira* spp. (25), *Bartonella* spp. (77), *Brucella* spp. (4)	*Miniopterus schreibersii, Myotis blythii*
Bai_2018	Rural	2010 e 2013	Nigeria	Blood	Cultura, Conventional PCR	177	*Bartonella* spp. (22)	*Rousettus aegyptiacus*
Ballados-González_2018	Wild	2016	Mexico	Kidney	Cultura, Conventional PCR	81	*Leptospira* spp.(25)	*Desmodus rotundus, Artibeus lituratus, Choeroniscus godmani*
Bandelj_2019	NI	2014-2015	Slovenia	Feces	Culture, Biochemical, Conventional PCR	93	*Clostridium difficile* (18)	*Barbastella barbastellus Miniopterus schreibersii ; Myotis bechsteinii ; Myotis blythii, Myotis daubentonii ; Myotis emarginatus ;*

								Myotis myotis ; Myotis nattererii, Nyctalus leisleri, Pipistrellus pipistrellus ; Plecotus auritus , Rhinolophus ferumequinum ; Rhinolophus hipposideros
Becker_2020	Wild	2017-2018	Belize	Blood	Conventional PCR, Sequencing	469	*Mycoplasma* spp. (239)	*Artibeus intermedius Artibeus jamaicensis Artibeus lituratus, Carollia perspicillata, Carollia sowelli, Dermanura phaeotis, Dermanura watsoni, Desmodus rotundus, Eptesicus furinalis, Glossophaga soricina, Lophostoma evotis, Molossus nigricans, Myotis elegans, Myotis pilosatibialis, Natalus mexicanus, Platyrrhinus helleri, Pteronotus fulvus, Rhynchonycteris naso, Pteronotus mesoamericanus, Saccopteryx bilineata, Sturnira parvidens, Trachops cirrhosus, Uroderma convexum*
Becker_2018	NI	2015-2016	Peru	Blood, oral swab and rectal swab	Conventional PCR, Real time PCR, Sequencing	NI	*Bartonella* spp. (NI)	*Desmodus rotundus*
Bessa_2010	Urban and	2008	Brazil	Kidney	Cultura,	343	*Leptospira* spp. (6)	*Glossophaga soricina;*

	Wild				MAT, Conventional PCR, Sequencing			*Platyrrhinus lineatus*
Bevans_2020	Wild	2015-2017	India	Kidney	Conventional PCR, Sequencing	173	*Leptospira* spp. (47)	*Artibeus* spp., *Glossophaga longirostris*
Bilung_2014	Wild	2008-2009	Malaysia	Anal swab	Culture, Biochemical, Conventional PCR, Sequencing, Virulence test	308	*Escherichia coli* (42)	NI
Blehert_2014	Urban	2008	United States	Lung, liver, spleen, heart, mammary gland and faces	Culture, Biochemical	5	*Salmonella* spp. (0), *Pasteurella multocida* (4), *Klebsiella oxytoca* (1)	*Eptesicus fuscus*, NI
Brook_2015	Wild	2013	Madagascar	Blood	Conventional PCR, Sequencing	76	*Bartonella* spp. (31)	*Eidolon dupreanum*
Bunnell_2000	Wild	1997-198	Peru	Kidney	Conventional PCR, Sequencing	20	*Leptospira* spp.(7)	NI
Cabal_2015	Wild	2012-2013	Brazil	Feces	Real time PCR, Virulence test	412	*Escherichia coli* (NI)	NI
Cataldo_2020	Urban	2018-2019	Nigeria	Blood	Conventional PCR, Sequencing	90	*Candidatus M. haemohominis* (32)	*Eidolon* sp., *Micropteropus* sp., *Querofonte* sp., *Rhinolophus* sp., *Rousettus* sp., *Tadarida nigeriae,*
Childs-Sanford_2009	Urban	NI	United States	Pool: liver, lymph nodes mesenteric, gastrointestinal tract	Culture, Biochemical, Histopathology	30	*Yersinia pseudotuberculosis* (0)	*Rousettus aegyptiacus*
Cicuttin_2013	Urban	2011	Argentina	Liver spleen and lung	Conventional PCR, Real time PCR, Sequencing	30	*Neorickettsia risticii* (3)	*Tadarida brasiliensis*

Cicuttin_2017	Urban	2012-2013	Argentina	UD	Conventional PCR,Sequencing	61	*Neorickettsia risticii* (5); *Bartonella* spp. (3); *Rickettsia* sp. (1); *Borrelia* spp. (0)	*Tadarida brasiliensis*
Claudio_2018	Wild	2016-2017	Brazil	Oral swabs and rectal swabs	Culture, MALD TOF,	113	*Burkrolderia* spp (UD), *Aeromonas* spp. (UD), *Neisseria* spp. (UD), *Yokenella* spp. (UD), *Ochrobactrum* spp. (UD), *Pseudomonas* spp. (UD), *Stapylococcus* spp. (UD), *Staphylococcus aureus* (UD), *Staphylococcus hominis* (UD), *Staphylococcus xylosus* (UD), *Streptococcus* spp. (UD), *Enterococcus* spp. (UD), *Acinetobacter* spp. (UD), *Brevundimonas* spp. (UD), *Lactococcus* spp. (UD), *Salmonella* spp. (UD), *Proteus* spp. (UD), *Serratia* spp. (UD), *Serratia liquefaciens* (UD),	*Artibeus lituratus, Molossus rufus*

							Serratia marcescens (UD), *Klebsiella oxytoca* (UD), *Klebisiella* spp. (UD), *Kluyvera* spp. (UD), *Kluyvera ascorbate* (UD), *Enterobacter* spp. (UD), *Pantoea* spp. (UD), *Providencia* spp. (UD), *Citrobacter* spp. (UD), *Cedecea* spp. (UD), *Edwardisiella* spp. (UD), *Raoutella* spp. (UD), *Leclercia* spp. (UD), *Erwinia* spp. (UD), *Ewingella* spp (UD),	
Collins_2019	Urban	2016–2017	Australia	Feces	Culture, Biochemical	1	*Salmonella* Bovismorbificans (1)	*Nyctophilus gouldi*
Concannon_2005	NI	NI	United Kingdom	heart	Cultura, Conventional PCR, Sequencing	60	*Bartonella* spp. (5)	*Myotis mystacinus;* *Pipistrellus* sp.; *Myotis. daubentonii;* *Nyctalus noctula*
Corduneanu_2018	NI	2011-2016	Romania	Heart	Conventional PCR, Sequencing	435	*Bartonella* spp. (6)	*Myotis cf. alcathoe,* *Nyctalus noctula,* *Pipistrellus pipistrellus*
Cox_2005	NI	NI	Australia	Kidney and urine	Conventional PCR	173	*Leptospira* spp. (19)	*Pteropus alecto* *Pteropus conspicillatus* *Pteropus poliocephalus* *Pteropus scapulatus*
Daniel_2013	Wild	NI	Malaysia	Stomach and intestine	Culture, Biochemical,	NI	*Escherichia hermannii*(NI),	*Cynopterus brachyotis brachyotis*

					ELISA, PCR,		*Serratia marcescens* (NI), *Klebsiella pneumonia* (NI), *Klebsiella oxytoca* (NI), *Enterobacter* spp (NI).; *Enterococcus* spp. (NI). *Pseudomonas* spp. (NI).	
D'Auria_2010	Urban	2007-2008	Brazil	Serum	IFA	451	*Rickettsia rickettsii,* *Rickettsia parkeri,* *Rickettsia. amblyommii,* *Rickettsia. rhipicephali,* *Rickettsia belli* (46)	*Eumops auripendulus* *Eumops perotis* *Molossus molossus* *Molossus Rufus* *Nyctinomops laticaudatus* *Nyctinomops macrotis* *Tadarida brasiliensis* *Artibeus lituratus Platyrrhinus lineatus Histiotus velatus* *Myotis nigricans*
Davoust_2016	Urban	2013	French Guiana	Blood	Cultura, Real time PCR, Sequencing	59	*Bartonella* spp. (10)	*Eumops auripendulus* *Noctilio albiventris Pteronotus parnellii* *Noctilio albiventris*
De Leon_2018	Wild	NI	Philippines	Feces	IFA, Conventional PCR	NI	*Rickettsia* spp. (NI); *Burkrolderia* spp. (NI); *Francisella* spp. (NI); *Mycobacterium* spp. (NI); *Corynebacterium* spp. (NI); *Pseudomonas* spp. (NI); *Legionella* spp. (NI)	NI
Desvars_2013	Wild	2009	France	Urine	qPCR	10	*Leptospira* spp. (2)	*Mormopterus francoismoutoui*
Desvars_2012	Urban	2007	Mayotte	Serum	MAT	49	*Leptospira* Pyrogenes	*Pteropus seychellensis*

							and Grippotyphosa (5)	
Dietrich_2015	Wild	2012-2013	France	Urine	Real time PCR	420	*Leptospira* spp. (221)	*Mormopterus francoismoutoui*
Dietrich_2016	Wild	2007-2012	South Africa and Swaziland	Blood	Conventional PCR, Sequencing	384	*Bartonella* spp. (13); *Rickettsia conorii* (3); *Rickettsia* spp. (3)	*Miniopterus natalensis, Nycteris thebaica, Epomophorus wahlbergi, Rousettus aegyptiacus,*
Dietrich_2017	Wild	2015	South Africa	Urine	Conventional PCR, Sequencing	7	*Leptospira* spp. (2); *Treponema* spp. (NI)	*Miniopterus natalensis* *Nycteris thebaica*
Dietrich_2018a	Wild	NI	South Africa	Kidney	Cultura, Conventional PCR, Sequencing	55	*Leptospira* spp. (55)	*Myotis goudoti, Miniopterus gleni, Miniopterus griffithsi, Miniopterus mahafaliensis, Miniopterus majori, Miniopterus sororculus, Molossidae Otomops madagascariensis, Mormopterus jugularis, Pteropus rufus, Triaenops menamena*
Dietrich_2018b	Wild	2015-2016	South Africa	N.I.	Conventional PCR, Sequencing	NI	Leptospira spp. (NI)	*Miniopterus natalensis* *Rousettus aegyptiacus*
Dimkić_2020	Wild	NI	Serbia	Feces	Culture, Biochemical, Conventional PCR, Sequencing, Antimicrobial test	NI	*Staphylococcus aureus* (NI), *Staphylococcus epidermidis* (NI); *Kluyvera intermedia* (NI); *Serratia quinivorans* (NI); *Pseudomonas* spp. (NI);	NI

							Escherichia furgusonii (NI); *Bacillus* spp. (NI); *Citrobacter* spp. (NI); *Paenibacillus amylolyticus* (NI); *Comamonas* spp. (NI); *Rhodococcus* spp. (NI); *Brevibacterium* spp. (NI); *Enterococccus* spp. (NI)	
Duignan_2003	Urban	1998	New Zeland	UD.	Culture	38	*Salmonella* spp. (0), *Yersinia* spp. (0)	N. A.
Emanuel_1964	Wild	1953-1963	Australia	Blood	MAT	67	*Leptospira serovar. Australis* (6)	*Pteropus alecto gouldii*
Evans_2009	Urban	2008	United Kingdon	Liver	Conventional PCR, Sequencing	1	*Borrelia* spp. (1)	*Pipistrellus* spp.
Everard_1983	Wild	NI	Trinidad and Grenada	Serum	Culture, MAT	246	*Leptospira* serovar Autommalis, Cynopteri, Hebdomadis, Javanica, Panama, Pyrogenes, Ballum, Bataviae, Tarassovi, Grenada: *Leptospira* serovar Icterohaemorrhagiae, Shermani, Grippothyphosa) (215)	*Carollia persilata,* *Phyllostomus hastatus,* *Pteronotus davyi,* *Molossus major,* *Anoura* sp., *Glossophaga* spp.
Fajri_2018	NI	2017-	Indonesia	Mouth	Culture,	4	*Staphylococcus aureus*	*Rhinophoma microphyllum*

		2018			Biochemical		(4); *Klebsiella oxytoca* (1); *Serratia ribidaca(*1); *Acinetobacter calcoaceticus* (1); *Providencia penneri*, *Providencia stuartii* (1); *Alcaligenes xylosoxidans* (1); *Neisseria sicca* (1); *Citrobacter freundii* (1); *Aeromonas caviae* (1);	
Fennestad_1972	Wild	NI	Danish	Urine and kidney	Culture, MAT	NI	*Leptospira* spp. (31)	*Myotis daubentoni*, *Pipistrellus pipistrellus*, *Nyctalus noctula* *Epitesicus serotinus*
Ferreira_2018	Wild	2013-2015	Brazil	Spleen, lunger, liver, heart and kidney	ELISA, Conventional PCR, Sequencing	119	*Coxiella* spp. (0), *Bartonella* spp. (22)	*Carollia perspicillata*, *Rhinophylla pumilio*, *Desmodus rotundos*, *Phyllostomus discolor*, *Artibeus fimbriatus*, *Artibeus lituratus*, *Artibeus obscurus*, *Sturnira lillium*
Fountain_2019	NI	2014-2016	United Kingdom	Skin swab, oropharynx, material ejected into the mouth, and skin lesions	Culture, Isolation, MALDI TOF, Conventional PCR, Sequencing,	44	Coagulase-negative Staphylococci, *Staphylococcus aureus* (NI)	*Pteropus livingstonii*
Fritschi_2020	Wild	2014-2017	Germany	Spleen	Conventional PCR, Real time PCR, Sequencing	462	*Mycoplasma* spp. (15); *Clamydia* spp. (149)	*Nyctalus noctula*, *Vespertilio murinus*, *Glossopha gacomissarisi*
Gaona_2019	Wild	2015	Mexico	Interscapular	Conventional PCR,	11	*Staphylococcus*	*Leptonycteris yerbabuenae*

	dorsal patch	Sequencing	*epidermidis;* *Staphylococcus* spp. (NI); *Clostridium perfringens* (N.I); *Clostridium* spp. (NI); *Pasteurella multocida* (NI); *Pasteurela* spp. (NI); *Mycoplasma* spp. (NI); *Serratia marcescens* (NI); *Serratia* spp. (NI); *Streptococcus* spp. (NI); *Corynebacterium* spp. (NI); *Aggregatibacter segnis* (NI); *Brevinema andersonii* (NI); *Methylobacterium adhaesivim* (NI); *Veillonella pasvula* (NI); *Morganella morganii* (NI); *Enterococcus* spp. (NI); *Acinetobacter* spp. (NI) *Providencia* spp. (NI); *Aerococcus* spp. (NI); *Lactococcus* spp. (NI); *Leuconostoc* spp. (NI); *Fusobacterium* spp. (NI);

							Proteus spp. (NI); *Bacteroides* spp.(NI); *Actinomyves* spp. (NI); *Finegoldia* spp. (NI); *Peptoniphilus* spp. (NI); *Leptotrichia* spp. (NI); *Peptostreptococcus* spp. (NI); *Prevotella* spp. (NI); *Vagococcus* spp. (NI)	
Garces_2019	Urban	2014-2016	Portugal	Feces	Culture, Biochemical tests, Conventional PCR, Sequencing,	NI	*Escherichia coli (34)*	*Tadarida teniotis*
Garcês_2020	Urban and Wild	2014-2016	Portugal	Feces	Culture, Biochemical tests,	NI	*Escherichia coli (NI)*	*Tadarida teniotis*
Gerbacova_2020	NI	2017	Slovakia	Feces	Culture, Isolation, Biochemical tests, Conventional PCR, Real time PCR,	NI	*Serratia liquefaciens* (NI); *Serratia fonticola* (NI); *Pseudomonas* spp. (NI); *Enterococcus mundtii* (NI); *Enterobacter ludwigii* (NI); *Enterococcus casseliflavus* (NI); *Pantoea aglomerans* (NI); *Enterococcus faecium* (NI); *Bacillus cereus* (NI); *Bacillus simplex* (NI); *Aerococcus viridans*	*Myotis myotis,* *Rhinolophus hipposideros*

							(NI); *Brevundimonas diminuta* (NI); *Artrobacter* spp. (NI); *Lactococcus* spp. (NI); *Lactococcus garvieae* (NI); *Paenibacillus amylolyticus* (NI); *Cedecea davisae* (NI); *Hafnia alvei* (NI)	
Gharout-Sait_2019	Wild	2016	Algeria	Feces	Culture, Isolation, Biochemical tests, MALDI-TOF, Conventional PCR, Sequencing, Antimicrobial test, Resistent genes	110	*Klebsiella pneumoniae* (2)	N.I
Gomard_2016	Urban and Wild	2012-2013	Madagascar	Pool: kidney spleen and lung	Real time PCR, Sequencing	947	*Leptospira* spp. (203)	*Coleura kibomalandy*, *Hipposideros commersoni*, *Miniopterus manavi*, *Chaerephon leucogaster*, *Rousettus madagascariensis*, *Miniopterus griffithsi*, *Mormopterus jugularis*, *Otomops madagascariensis*, *Paratriaenops furculus*, *Triaenops menamena*, *Myotis goudotii*, *Neoromicia malagasyensis*, *Neoromicia matroka*, *Neoromicia robertsi*,

								Pteropus rufus, *Scotophilus marovaza*, *Miniopterus griveaudi*, *Miniopterus mahafaliensis*, *Miniopterus majori*, *Miniopterus sororculus*, *Miniopterus manavi*
Gonçalves-Oliveira_2020	Urban and wil	2015-2018	Brazil	Spleen	Conventional PCR, Sequencing	110	*Bartonella* spp. (4)	*Artibeus lituratus* *Carollia perspicillata*
González-Quiñonez_2014	Wild	2010	Venezuela	Shoulders	Culture, MALDI TOF, Conventional PCR,	89	*Staphylococcus* spp. (NI); *Shigella sonnei* (NI); *Enterococcus* spp. (NI); *Bacillus* spp. (NI); *Enterobacter* spp. (NI); *Acinetobacter* spp. (NI); *Arthrobacte*r spp. (NI); *Myroides* spp. (NI); *Lysinibacillus* spp. (NI); *Flavobacterium* spp. (NI)	*Sturnira lilium*
Gulraiz_2017	Urban	2011	Pakistan	Feces	Culture	N.I	*Salmonella* spp. (NI); *Bartonella* spp. (NI); *Klebsiella* spp. (NI); *Corynebacterium* spp. (NI); *Listeria* spp. (NI); *Bacillus* spp. (NI); *Pseudomonas* spp. (NI); *Alcaligenes* ssp. (NI); *Nocardia* spp.(NI)	*Pteropus giganteus*, *Cynopterus brachyotis brachyotis*
Han_2017	Urban and wil	2015	China	Blood	Conventional PCR, Sequencing	107	*Bartonella* spp. (27)	*Rhinolophus ferrumequinum*, *Rhinolophus pusillus*,

								Myotis fimbriatus, *Myotis ricketti*, *Myotis pequinius*
Han_2018	Urban and Wild	2015	China	Kidney	Conventional PCR, Sequencing,	124	*Leptospira* spp. (62)	*Myotis fimbriatus*, *Myotis ricketti*, *Myotis pequinius*
Han_2010	Urban	NI	South Korea	Blood	Culture, Isolation, Biochemical tests, Conventional PCR, Sequencing,	1	*Kluyvera ascorbata* (1)	*Rousettus aegyptiacus*
Harkin_2014	Urban	2012	United States	Kidney	Conventional PCR, Real time PCR, Sequencing	98	*Leptospira* spp. (0)	UD
Hatta_2016	Wild	NI	Philippines	Swab retal	ELISA, Sequencing	91	*Campylobacter jejuni* (5)	NI
Hazeleger_2018	Wild	2007-2008	Holanda	UD	Culture, Conventional PCR	631	*Salmonella* spp. (0)	UD
Held_2017	Wild	2015	Gabon	Pharyngeal swab	Culture, Conventional PCR, Sequencing, Antimicrobial test, Virulence test	133	*Staphylococcus chweitzer* (2), *Staphylococcus aureus* (4)	*Rousettus aegyptiacus*, *Miniopterus pusillus*
Henry_2018	Urban	NI	Australia	Feces	Conventional PCR, Sequencing	18	*Salmonella* spp. (NI); *Shigella* spp. (NI); *Yersinia* spp. (NI); *Clostridium disporicum* (NI); *Clostridium perfringens* (NI); *Clostridium sordellii* (NI); *Klebsiella* spp. (NI);	*Pteropus poliocephalus*

							Streptococcus spp. (NI); *Acinetobacter* spp. (NI); *Citrobacter* spp. (NI); *Cronobacter* spp. (NI); *Haemophilis* spp. (NI); *Fusobacterium* spp. (NI)	
Hokynar_2017	NI	2008-2013	Finland	Feces	Conventional PCR, Real time PCR, Sequencing	200	*Chlamydia* spp. (108)	*Myotis daubentonii*
Holz_2019	Wild	2015-2017	Australia	Blood	Conventional PCR, Sequencing	83	*Mycoplasma* spp. (8)	*Miniopterus fuliginosus,* *Miniopterus orianae bassanii*
Hornok_2018	NI	2014	Hungary and Netherlands	Feces	Conventional PCR, Sequencing	UD	*Rickettsia spp.*(UD) *Neorickettsia* spp. (UD) *Mycoplasma* spp. (UD)	*Myotis dasycneme* *Myotis daubentonii* *Myotis alcathoe* *Pipistrellus pipistrellus* *Barbastella barbastellus*
Hou_2018	Wild	2016	Malaysia	Blood	Culture, Conventional PCR, Sequencing	30	*Bartonella* spp. (2)	*Pteropus hypomelanus*
Ikeda_2017	Wild	2015-2016	Brazil	Spleen, heart, liver and whole blood	Conventional PCR, Sequencing	162	*Bartonella* spp. (NI); *Mycoplasma* spp. (NI)	*Sturnira lilium,* *Carollia perspicillata,* *Glossophaga soricina,* *Carollia perspicillata,* *Natalus espiritosantensis,* *Phyllostomus discolor*
Imnadze_2020	Wild	2018	Georgia	Spleen, liver, intestine	Culture, Isolamento	11	*Yersinia enterocolitica* (NI); *Serratia liquefaciens* (NI); *Pseudomonas aeroginosa* (NI); *Enterococcus faecalis* (NI);	NI

Ingala_2019	Wild	2015	Belize	Rectal swab	Conventional PCR, Sequencing	30	*Helicobacter* spp. *Pseudomonas* spp. *Bacillus cereus* (NI); *Bacillus subtilis* (NI); *Hafnia* spp. (2 NI) *Staphylococcus* spp. (30); *Mycoplasma* spp. (NI); *Streptococcus* spp. (3); *Pseudomonas* spp. (NI); *Helicobacter* spp. (NI); *Proteus* spp. (NI); *Edwardsiella* spp. (NI)	*Desmodus rotundus*
Islam_2013	NI	2010	Bangladesh	Retal swabs	Culture, Biochemical, Antimicrobial test	312	*Salmonella Vrchow* (1)	*Pteropus giganteus*
Italia_2012	Urban and Wild	NI	Filiphine	Intestine	Culture, Biochemical, Conventional PCR, Virulence test	56	*Escherichia coli* (34)	*Ptenochirus jagori*, *Cynopterus brachyotis*, *Eonycteris spelaea*, *Rousettus amplexicaudatus*, *Scotophilus kuhlii*,
Judson_2015	Wild	2012-2013	Costa Rican	Blood	Conventional PCR, Sequencing	63	*Bartonella* spp. (21)	*Micronycteris microtus*, *Myotis keaysi*, *Carollia sowelli*, *Artibeus lituratus*, *Anoura geoffroyi*, *Artibeus jamaicensis*, *Platyrrhinus vittatus*, *Vampyressa thyone*, *Carollia perspicillata*, *Sturnira mordax*, *Phyllostomus discolor*, *Sturnira lilium*, *Carollia castanea*,
Kamani_2014	NI	2010	Nigeria	Blood	Culture,	148	*Bartonella* spp. (76)	*Eidolon helvum*,

					Conventional PCR, Real time PCR, Sequencing			*Epomorphorus* spp., *Micropterus* spp., *Chaerephon nigeriae,* *Rhinolophus* spp.
Kholik_2019	Wild	2017	Indonesia	Anal swab	Culture, Biochemical	20	*Salmonella* spp.(2); *Klebsiella ozaenae* (1)	*Eonycteris speleae,* *Achates taphozous*
Kosoy_2010	Urban and wil	NI	Kenyan	Blood	Culture, Conventional PCR, Sequencing	331	*Bartonell*a spp. (106)	*Miniopterus* spp., *Eidolon helvum, Rousettus aegyptiacus , Coleura Afra , Triaenops persicus , Hipposideros commersoni*
Lagadec_2012	Wild	NI	Madagascar and Comoros	Pool:kidney, spleen and lung	Conventional PCR, Real time PCR, Sequencing	129	*Leptospira* spp. (61)	*Mormopterus jugularis,* *Otomops madagascariensis,* *Triaenops furculus,* *Triaenops menamena,* *Miniopterus gleni, Miniopterus mahafaliensis, Myotis goudoti* *Rousettus obliviosus,* *Chaerephon pusillus,* *Miniopterus griveaudi*
Liang_2015	NI	NI	China	NI.	Culture, Isolation, Conventional PCR	368	*Yersinia* spp. (0)	UD
Lilley_2015	NI	2010	Finland	Blood	Conventional PCR, Sequencing	124	*Bartonella* spp. (46)	*Myotis daubentonii*
Lin_2012	Wild	2009-2010	Taiwan	Blood	Culture, Conventional PCR, Sequencing	54	*Bartonella* spp. (6)	*Miniopterus schreibersii*
Maliničová_2017	NI	2014-2015	Hungary	Feces	Conventional PCR, Sequencing	NI	*Pseudomonas* spp. (NI); *Comamonas* spp. (NI)	*Rhinolophus euryale*
Marinkelle_1968	Wild	NI	Colombia	Blood	N.I.	512	*Borrelia* spp. (1)	*Natalus tumidirostris*
Mascarelli_2014	Wild	NI	USA	Spleen	Conventional PCR, Sequencing	68	*Mycoplasma haemomuris* (32)	*Myotis lucifugus*

Mateus_2019	NI	NI	Colombia	Kidney	Conventional PCR, Sequencing	26	*Leptospira* spp. (7)	*Carollia perspicillata, Glossophaga soricina, Dermanura phaeotis, Uroderma bilobatum, Desmodus rotundus, Lophostoma silvicolum*
Matthias_2005	Wild and Urban	2004		Kidney	Cultura, Conventional PCR, Sequencing	589	*L. interrogans* serovar Icterohaemorragia, *L. kirschneri* serovar Grippotyphosa (20)	*Artibeus obscurus, Aribeus planirostris, Carollia perspicillata, Desmodus rotundus Glossophaga soricina, Lonchophylla thomasi, Mimon crenulado, Myotis riparius Phyllostomus hastatus, Promops nasutus, Rhinophylla pumilio, Sturnira lilium, Sturnira tildae, Uroderma bilobatum*
Mayer_2017	NI	2010-2012	Brazil	Kidney	Conventional PCR, Real time PCR	92	*Leptospira* spp. *(36)*	*Eptesicus diminutus , Eumops auripendulus, Glossophaga soricina, Histiotus velatus, Lasiurus ega, Molossus molossus, Molossus rufus, Myotis nigricans, Tadarida brasiliensis*
McKee_2017	Wild	NI	Thailand	Blood	Culture, Isolation, Conventional PCR, Sequencing	93	*Bartonella* spp. (34)	*Hipposideros fulvus, Hipposideros larvatus, Melanopogon taphozous, Chaerephon plicatus, Hipposideros armiger*
Mgode_2014	Urban	NI	Tanzania	Serum	MAT	36	*Leptospir*a serovar	NI

							Sokoine, sorovar Quênia, sorovar Lora (7)	
Millán_2019	Urban	2014	Chile	NI	Conventional PCR, Nested PCR, Sequencing	55	*Mycoplasma* spp. (12)	*Myotis chiloensis, Histiotus montanus, Histiotus macrotus*
Millán_2015	NI	NI	Spain	Blood	Conventional PCR, Nested PCR, Sequencing	31	*Mycoplasma* spp. (30)	*Miniopterus schreibersii*
Mioni_2018	Wild	2015	Brazil	Lung, liver and intestine,	Culture, ELISA	5	*Streptococcus dysgalactiae* (5);	*Desmodus rotundus*
Modra_2017	Wild	NI	Czech Republic	Feces	Culture, Isolation, Conventional PCR	15	*Mycobacterium* spp. (11)	NI
Mühldorfer_2010	NI	2006-2008	Germany	Lung, heart, kidney and pool: liver, spleen, and intestine	Culture, Biochemical, Conventional PCR, Sequencing	200	*Yersinia pseudotuberculosis Yersinia enterocolítica* (2)	*Myotis myotis; Pipitsrellus pipistrellus*
Mühldorfer_2011a	Urban	2002-2009	Germany	Liver, lung, heart, kidney, spleen and smear of the chest cavity	Culture, Biochemical, Conventional PCR, Sequencing	29	*Pasteurella multocida* (NI)	NI
Muhldorfer_2011b	Urban	2002-2009	Germany	NI	Culture, Biochemical	430	*Morganella* spp., *Enterobacter cancerogenus, Enterobacter faecium, Enterobacter fecalis, Providencia* spp., *Citrobacter* spp., *Cedecea davisae, Hafnia* spp., *Hafnia alvei, Proteus* spp., *Erwinia* spp.,	NI

							Rahnella spp., *Moellerella* spp., *Aeromonas* spp., *Myroides* spp., *Moerell*a spp., *Clostridium sordellii,* *Vibrio* spp., Coagulase-negative Staphylococci, *Staphylococcus aureus,* *Staphylococcuintermedius,* *Leucobacter* spp., *Aerococcus viridans,* *Enterococcus* spp.,	
Mühldorfer_2011c	Wild	2003-2009	Germany	Lung, heart, liver, spleen, kidney and tong	Culture, Biochemical	486	*Salmonella* Typhimurium, *Yersinia*spp., *Pasteurella* spp., *Bacilus* spp.,	NI
Nabeshima_2020	Urban	2013	Japan	Blood	Culture, Isolation, Conventional PCR, Sequencing	50	*Bartonella* spp. (12)	*Miniopterus fuliginosus*
Nakamura_2013	Urban	2008-2009	Japan	Liver	Culture, Histopathological, Conventional PCR, Virulence test	1	*Yersinia pseudotuberculosis* (1)	*Rousettus aegyptiacus*
Newman_2018	Wild	2016	United States	Feces	Conventional PCR,	NI	*Shigella* spp. (NI), *Clostridium* spp. (NI)	*Tadarida brasiliensis*
Nowak_2017	Wild	NI	Congo Republic	NI	Culture, Isolation, Conventional PCR, Sequencing	50	*Escherichia coli,* *Escherichia albertii (30)*	*Eidolon helvum,* *Epomops franqueti,* *Hypsignathus monstrosus,*

								Myonycteris torquata, *Rousettus aegyptiacus*
Ogawa_2015	Wild	2008-2013	Democratic Republic of Congo and Zambia	Kidney	Conventional PCR, Sequencing	529	*Leptospira* spp. (79)	*Eidolon helvum*
Olatimehin_2018	Urban	2015-2016	Nigeria	Feces	Culture, Biochemical, Conventional PCR, Sequencing, Antimicrobial test	NI	*S. aureus*, *S. schweitzeri*, *S. argenteus* (NI)	*Eidolon helvum*
Olival_2015	Wild	2012	Puerto Rico	Blood	Culture, Conventional PCR, Sequencing	68	*Bartonella* spp. (9)	*Artibeus jamaicensis* *Brachyphylla cavernarum*, *Monophyllus redmani*
Pham Hong_2015	Wild	2013	Vietnam	Blood	Conventional PCR, Sequencing	60	*Bartonella* spp. (21)	*Hipposideros armiger*, *Larvatui hipposideros* *Megaerops niphanae* *Megaderma espasma* *Megaderma lyra Rhinolophus acuminatus Rhinolophus chaseli Rhinolophus sinicus*
Qiu_2020	Wild	2017-2018	Zambia	Blood	Culture, Isolamento, Conventional PCR, Sequencing	36	*Bartonella* spp. (6)	*Rousettus aegyptiacus*, *Macronycteris vittatus*
Qiu_2019	Wild	201-2016	Zambia	Blood, pool: liver and spleen	Culture, Isolamento, Conventional PCR, Sequencing	38	*Borrelia* spp. *(NI)*	*Rousettus aegyptiacus*, *Hipposideros* spp., *Miniopterus* spp.
Reeves_2006	Urban	2005 2006	Georgia	Serum	Culture, Isolamento, ELISA, Conventional PCR,	56	*Bartonella* spp. (0); *Bartonella hermsi*i (3); *Rickettsia conorii*(1); *Rickettsia rickettsii* (1);	*Eptesicus fuscus*

					Sequencing			
Reeves_2016	Wild	2010-2011	Saint Kitts and Nevis	Blood	Conventional PCR, Sequencing	318	*Bartonella* spp. (41); *Rickettsia africae* (3); *Ehrlichia* spp. (3)	*Artibeus jamaicensis;* *Brachyphylla cavernarum*
Reyes_2011	Urban and Wild	NI	Felipinas	Small intestine	Culture, Biochemical, Conventional PCR	96	*Salmonella* spp. (2)	*Miniopterus australis* *Miniopterus schreibersii*
Sanseverino_2019	Urban and Wild	2013-2014	Brazil	UD	Conventional PCR	330	*Borrelia* spp. (0)	UD
Santos_2020	Wild	2015	Brazil	Blood	Conventional PCR, Sequencing	10	*Mycoplasma* spp. *(8)*	*Diphylla ecaudata,* *Molossus* sp., *Desmodus rotundus,*
Selvin_2019	Wild	NI	Meghalaya, India	Feces	Culture, Isolamento, Biochemical tests, ELISA, Sequencing	3	*Escherichia furgusonii* (NI); *Sthaphylococcus* spp. (NI); *Bartonella* spp. (NI); *Rickettsia* spp. (NI); *Serratia marcescens* (NI); *Serratia liquefaciens* (NI); *Serratia quinivorans* (NI); *Mycobacterium* spp. (NI); *Corynebacterium diptheria* (NI); *Pseudomonas stutzeri* (NI); *Pseudomonas aeruginosa* (NI); *Enterococcus* spp. (NI);	*Rhinolophus monoceros*

Sens_2018	Wild	NI	Brazil	Oral swab	Culture, Isolamento, Biochemical tests	1	*Bacillus* spp. (NI); *Enterobacter* spp. (NI); *Hafnia* spp. (NI); *Rhodococcus* spp. (NI) *Shigella* spp. (0); *Kluyvera* spp. (68); *Serratia liquefaciens* (9); *Serratia rubidae* (9); *Morganella morganii* (NI); *Enterobacter aerogenes* (NI); *Enterobacter cloacae* (NI); *Pantoea aglomerans* (NI); *Proteus* spp. (NI); *Ewingella americana* (NI); *Yokenella* spp. (NI); *Erwinia* spp. (NI); *Burkrolderia* spp. (NI)	*Carollia perspicillata*
Smythe_2002	Wild	1997-1999	Australia	Serum	MAT	271	Leptospira Austalis, Cynopteri, Hardjo, Bulgarica, Tarassovi, Pomona (71);	*Pteropus poliocephalus* *Pteropus scapulatus* *Pteropus alecto* *Pteropus conspicillatus*
Stuckey_2017	NI	2011-2013	Mexico	Heart and blood	Culture, conventional PCR, Sequencing	238	*Bartonella* spp. (54)	*Desmodus rotundus,* *Artibeus jamaicensis,* *Stirnira* spp. *Balantiopteryx plicata* *Pteronotus parnelli*
Stuckey_2017	NI	NI	France and Spain	Heart	Conventional PCR, Sequencing	135	*Bartonella* spp. (12)	*Myotis daubentonii,* *Myotis mystacinus, Pipistrellus*

								nathusii, *Nyctalus noctula*
Sun_2020	NI	NI	China	Feces	Conventional PCR, Sequencing	NI	*Salmonella* spp. (NI); Staphylococcus spp. (NI); *Bartonell*a spp. (NI); *Shigella* spp. (NI); *Brucella* spp. (NI); *Yersinia pestis* (N.I); *Yersinia pseudotuberculosis* (N.I); *Streptococcus* spp. (NI); *Bordetella* spp. (NI); *Enterococcus* spp. (NI); *Bacillus* spp. (NI); *Vibrio* spp. (NI)	*Eonycteris spelaea,* *Hipposideros armiger,* *Myotis petax,* *Taphozous melanopogon*
Sun_2019	NI	2018	China	Intestinal contentes and, stomach contents	Conventional PCR,	0	*Staphylococcus* spp. (NI); *Shigella* spp. (NI); *Burkrolderia* spp. (NI); *Pseudomonas* spp. (NI); *Acinetobacter* spp. (NI) *Brucella* spp. (NI);	*Rhinolophus luctus,* *Murina leucogaster*
Sunil_2016	Wild	NI	India	Feces	Culture, MALDI-TOF, Conventional PCR, Sequencing	NI	*Campylobacter* spp. (17); *Staphylococcus aureus* (NI); *Bartonella* spp. (NI); *Shigella flexneri* (NI); *Yersinia pestis* (NI); *Clostridium perfringens* (NI);	*Rousettus leschenaultii*

							Pseudomonas aeroginosa (NI); *Acinetobacter* spp. (NI); *Serratia rubidaea* (0); *Serratia spp.* (0); *Enterobacter* spp. (NI);	
Szubert-Kruszynska_2019	Urban and Wild	2007-2008	Poland	Blood	Conventional PCR, Sequencing	59	*Bartonella* spp. (15)	*Myotis myotis*
Thayaparan_2015	Urban and Wild	2011-2012	Malaysia	Serum	Cultura, MAT, Conventional PCR, Sequencing	70	NI	*Penthetor lucasi,* *Cynopterus brachotis,* *Balionycteris maculate* *Hipposideros cervinus*
Thayaparan_2013	Wild	NI	Malaysia	Serum	MAT	20	*Leptospira* serovar Copenhegeni, Lai, Pomona, Pyrogenes, lepto175 (5)	*Cynopterus brachyotis* *Penthetor lucasi* *Nycteris tragata* *Hipposideros cervinus*
Torres-Castro_2020	Wild	2017	México	Kidney	Conventional PCR, Sequencing	69	*Leptospira* spp. (15)	*Artibeus jamaicensis,* *Pteronotus parnellii* *Chiroderma villosum.*
Tulsiani_2011	Wild	2007-2008	Australia	Urine and kidney	Cultura, MAT, Conventional PCR	272	*Leptospira* spp. (209)	*Pteropus conspicillatus,* *Pteropus alecto,* *Pteropus poliocefalia* *Pteropus scapulatus*
Urushadze_2017	Not informed	2012	Georgia	Blood	Culture, Isolamento, Conventional PCR, Sequencing	236	*Bartonella* spp. (212)	*Eptesicus serotinus* *Miniopterus schreibersii* *Myotis blythii* *Myotis emarginatus* *Pipistrellus pygmaeus* *Rhinolophus euryale* *Rhinolophus ferrumequinum*
Vandžurová_2013	Urban	2010	Slovakia	Feces	Culture, Biochemical, MALDI TOF	NI	*Staphylococcus scuri* (NI); *Staphylococcus lentus*	*Myotis blythii,* *Myotis myotis*

							(NI); *Providencia* spp. (NI); *Alcaligenes* spp. (NI);	
Veikkolainen_2014	NI	2012	Finland	Blood	Culture, Isolamento, Conventional PCR, Sequencing	NI	*Bartonella mayotimonensis* (NI)	*Myotis daubentonii*
Vengust_2018	Wild	2014	Slovenia	Feces	MALDI TOF Sequencing	92	*Staphylococcus* spp. (NI); *Serratia* spp. (NI), *Providencia* spp. (NI), *Yersinia* spp. (NI); *Acinetobacter* spp (NI), *Enterococcus* spp. (NI), *Pseudomonas* spp. (NI),	*Myotis blythii*, *Myotis emarginatus*, *Myotis miotis*, *Rhinolophus hipposideros*
Volokhov_2017	Wild	2015-2016	Peru	Blood	Conventional PCR, Sequencing	223	*Mycoplasma* spp. (150)	*Desmodos rotundus*
Walther_2008	NI	2003-2004	Germany	Wounds	Culture, Biochemical, Conventional PCR	1	*Staphyloccoccus aureus* (1)	NI
Wolkers-Rooijackers_2018	Wild	2008	Holanda	Feces	MALDI TOF	37	*Serratia* spp. (NI), *Serratia fonticola* (NI), *Serratia liquefaciens* (NI), *Moellerella* spp. (NI), *Rahnella* spp. (NI), *Erwinia* spp. (NI), *Yersinia* spp. (NI), *Providencia* spp. (NI), *Citrobacter* spp. (NI), *Cedecea* spp. (NI), *Staphylococcus capitis* (NI),	NI

							Enterococcus faecalis (NI), *Leucobacter* spp. (NI), *Leuconostoc* spp. (NI), *Lactococcus* spp. (NI), *Acinetobacter* spp (NI) *Vagococcus* spp. (NI), *Moerella* spp. (NI), *Ochrobactrum* spp. (NI)	
Wray_2016	NI	2013	Guatemala	Serum; blood clot; fecal swab	Conventional PCR, Sequencing	39	*Bartonella* spp. (NI)	*Desmodus rotundus*
Wu_2019	Wild	2016	China	Feces and intestine	Conventional PCR, Antimicrobial test	0	*Staphylococcus* spp. (6); *Clostridium* spp. (NI); *Serratia* spp. (NI)	*Rhinolophus sinicus*, *Myotis altarium*
Xiao_2019	NI	2017-2018	China	Intestinal contents	Conventional PCR, Real time PCR	39	*Mycoplasma* spp. (NI); *Serratia* spp. (NI); *Pseudomonas* spp. (NI); *Helicobacter* spp.(NI); *Morganella* spp. (NI); *Enterococcus* spp. (NI); *Lactococcus* spp. (NI); *Ochrobactrum* spp.(NI);	*Rhinolophus ferrumequinum*
Yuan_2019	Wild	2015	China	Stomach and intestine	qPCR, Nested PCR	NI	*Mycoplasma* spp. (NI); *Mycobacterium* spp. (NI); *Pseudomonas* spp. (NI); *Enterococcus* spp. (NI); *Bacillus spp.* (NI); *Lactococcus* spp. (NI); *Bacteroides* spp. (NI); *Alistipes* spp. (NI); *Sphingomonas* spp. (NI)	*Hypsugo alaschanicus*
Zetun_2009	Urban and	Not	Brazil	Serum	MAT	204	*Leptospira* sorovar	*Desmodus rotundus*

	Wild	informed					Pyrogenes, Shermani e Javanica (16)	
Zhao_2019	Wild	2018	China	Kidney	Conventional PCR	60	*Leptospira* spp. (34)	*Miniopterus schrebersii Myotis adversus* *Myotis davidii,*
Zhao_2020	Urban	2015	China	Heart, lung,liver, intestine and kidney	Conventional PCR, Sequencing	54	*Leptospira* ssp. (34); *Rickettsia parkeri,* *Rickettsia lusitaniae,* *Rickettsia slovaca* *Rickettsia raoultii* (6)	*Pipistrellus pipistrellus*

N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed; UD: unextracted data.

Appendix S5: Enterobacteriaceae genus pathogens identified in bats sample, in different countries among the studies that found this pathogen in articles selected in this review.

Reference	**Location**	**Bacteria**	**Source**	**% (N)**	**Family of bats**
Adesiyun, 2009	Trinidade	*Salmonella spp.*	Gastrointestinal tract	1 (4/377)	Molossidae Noctilionidae
Apun, 2011	Sarawak and Malaysia	*Escherichia coli*	Anal swabs	10.7 (9/84)	N. I.
Arata, 1968	Colombia	*Shigella boydii; Salmonella blockley, Salmonella anatum, Salmonella sandiego and Salmonella landoff*	Feces	0.04 (1/2112)	Phyllostomidae Molossidae
Ausraful, 2013	Bangladesh	*Salmonella* Virchow	Rectal swabs	0, 3 (1/302)	Pteropodidae
Bandelj, 2019	Slovenia	*Clostridium difficile*	Feces	19.3 (18/93)	Vespertilionidae Rhinolophidae
Bilung, 2014	Malaysia	*Escherichia coli*	Anal swab	13.6 (42/308)	NI
Blehert, 2014	United States	*Klebsiella oxytoca, Salmonella spp.*	Liver	20 (1/5)	Vespertilionidae
Cabal, 2015	Brazil	*Escherichia coli*	Feces	21.9 (18/82)	NI

Childs-Sanford, 2009	United States	*Yersinia pseudotuberculosis*	Liver, lymph nodes mesenteric, gastrointestinal tract (pool)	13.3 (4/30)	Pteropodidae
Claudio, 2014	Brazil	*Salmonella* spp.; Proteus spp.; Serratia spp. S. liquefaciens, S. marcescens; Klebsiella oxytoca, Klebisiella spp.; Kluyvera spp., Kluyvera ascorbata; Enterobacter ssp.; Pantoea spp.; Providencia spp.; Citrobacter spp.; Cedecea ssp.; Edwardisiella spp.; Raoutella spp.; Leclercia spp.; Erwinia spp.,	Oral swabs retal swabs	15.9 (18/113)	Phyllostomidae Vespertilionidae Molossidae
Collins, 2019	Australia	*Salmonella* Bovismorbificans	Feces	100 (1/1)	Vespertilionidae Rhinolophidae
Daniel, 2013	Malaysia	*Escherichia hermannii;* *Serratia marcescens;* *Klebsiella pneumoniae,* *Klebsiella oxytoca;* *Enterobacter spp.;*	Stomach and intestine	100 (7/7)	Pteropodidae

Dietrich, 2017	South Africa	*Morganella* spp.	Feces	NI	Vespertilionidae Rhinolophidae
Dimkić, 2020	Serbia	*Escherichia furgusonii;* *Serratia quinivorans;* *Kluyvera intermedia;* *Citrobacter spp.*	Feces	NI	Vespertilionidae
Fajri, 2018	Indonesia	*Serratia ribidaca;* *Klebsiella oxytoca;* *Providencia penneri,* *Providencia stuartii;* *Citrobacter freundii;*	Feces	25	Hipposideridae Rhinolophidae Pteropodidae
Gaona, 2019	Mexico	*Serratia marcescens,* *Serratia* spp.*;* *Clostridium perfringens,* *Clostridium* spp.*;* *Morganella morganii;* *Providencia* spp.; *Citrobacter* spp.; *Proteus* spp.;	Interscapular dorsal patch	NI	Phyllostomidae
Garces, 2019	Portugal	*Escherichia coli*	Feces	9.6 (14/146)	Molossidae
Gerbacova, 2020	Slovakia	*Serratia liquefaciens,* *Serratia fonticola;* *Enterobacter;* *Pantoea aglomerans;* *Cedecea davisae;* *Hafnia alvei*	Feces	UD	Vespertilionidae Rhinolophidae
Gharout-Sait, 2019	Algeria	*Klebsiella pneumoniae*	Feces	1.8 (2/110)	NI

González-Quiñonez, 2014	Venezuela	*Shigella sonnei and Enterobacter* ssp.	Shoulders	NI	Phyllostomidae
Gulraiz, 2017	Paquistão	*Salmonella* spp.; *Listeria* spp.; *Klebsiella* sp.	Feces	NI	Pteropodidae
Han, 2010	Coreia	*Kluyvera ascorbata*	Blood	100 (1/1)	Pteropodidae
Hatta, 2016	Filiphine	*Campylobacter jejuni*	Rectal swabs	5.5 (5/91)	
Henry, 2018	Australia	*Shigella spp.;* *Citrobacter spp.;* *Klebsiella sp.;* *Clostridium disporicum* *Clostridium perfringens* *Clostridium sordellii;* *Yersinia spp,* *E.albertii;* *Salmonella spp.*	Feces	NI	Pteropodidae
Hezeleger, 2018	Netherlands	*Campylobacter jejuni* *Clostridium coli* *Clostridium lari*	Feces	2.7 (17/631)	Vespertilionidae
Imnadze, 2020	Georgia	*Serratia liquefaciens;* *Hafnia alvei;* *Yersinia enterocolitica*	Intestine	100 (20/20)	Vespertilionidae Rhinolophidae
Ingala, 2019	Belize	Proteus; Edwardisiella	Rectal swab		Phyllostomidae
Islam, 2013	Bangladesh	*Salmonella* Virchow	Rectal swab	0.3 (1/312)	Pteropodidae
Italia, 2012	Filiphine	*Escherichia coli*	Intestine	60.7 (34/56)	Pteropodidae Vespertilionidae

Kholik, 2019	Indonesia	*Salmonella spp.; Klebsiella ozaenae*	Anal swab	2/20	Pteropodidae Emballonuridae
Mühldorfer, 2010	Germany	*Yersinia pseudotuberculosis, Yersinia enterocolítica.*	Lung, heart, kidney; pool liver, spleen and intestino	1 (2/200)	Vespertilionidae
Mühldorfer, 2011b	Germany	*Serratia liquefaciens, Serratia fonticola, Serratia marcescens, Serratia plymuthica, Serratia proteamaculans; Yersinia pseudotuberculosis, Yersinia enterocolitica; Clostridium sordellii; Vibrio spp.; Klebsiella oxytoca; Klebsiella mobilis; Klebsiella pneumoniae; Kluyvera spp.; Morganella spp.; Enterobacter cancerogenus, Enterobacter faecium , Enterobacter fecalis; Providencia spp.; Citrobacter spp.; Cedecea davisae; Hafnia spp.*	NI	NI	NI

		Hafnia alvei; *Proteus spp.;* *Erwinia spp.;* *Rahnella spp.;* *Moellerella spp.*			
Mühldorfer, 2011c	Germany	*Salmonella* Typhimurium	Brain	NI	NI
Nakamura, 2013	Japan	*Yersinia pseudotuberculosis*	Liver	NI	Pteropodidae
Newman, 2018	United States	*Shigella spp.;* *Clostridium spp.;* *Plesiomonas spp.*	Feces	NI	Pteropodidae
Nowak, 2017	Congo [Republic]	*Escherichia coli,* *Escherichia albertii*	NI	60 (30/50)	Pteropodidae
Reyes, 2011	Philippines	*Salmonella* spp.	Small intestine	2 (2/96)	Vespertilionidae
Selvin, 2019	India	*Escherichia furgusonii;* *Serratia marcescens,* *Serratia liquefaciens,* *Serratia quinivorans;* *Clostridium spp.;* *Enterobacter spp.;* *Hafnia alvei*	Feces	NI	Rhinolophidae
Sens, 2018	Brazil	*Shigella spp.;* *Proteus spp.;* *Pantoea aglomerans;* *Enterobacter aerogenes,* *Enterobacter cloacae;* *Morganella morganii;*	Oral swab and perianal swab	NI	Phyllostomidae

		Kluyvera sp.; *Serratia liquefaciens,* *Serratia rubidae;* *Erwinia spp.*			
Sun, 2019	China	*Shigella spp.*	Intestinal contentes and stomach contents	NI	Rhinolophidae Vespertilionidae
Sun, 2020	China	*Shigella spp.;* *Salmonella spp.;* *Yersinia pestis,* *Yersinia pseudotuberculosis;* *Vibrio spp.*	Feces	NI	Emballonuridae Rhinolophidae Vespertilionidae Hipposideridae Pteropodidae
Sunil, 2016	China	*Campylobacter ssp.;* *Tatumella spp.;* *Leclercia spp.;* *Raoutella spp.;* *Proteus spp.;* *Hafnia alvei;* *Citrobacter spp.;* *Providencia spp.;* *Enterobacter spp.;* *Kluyvera ascorbata;* *Klebsiella spp.;* *Vibrio spp.;* *Clostridium spp.;* *Yersinia pestis;* *Serratia rubidaea,* *Serratia spp.;* *Escherichia coli;* *Salmonela enterica;*	Feces	NI	Pteropodidae

		Shigella flexneri;			
Vandzurova, 2013	China	Providencia spp	Feces	NI	Vespertilionidae
Vengust, 2018	China	Serratia spp.; Providencia spp.; Yersinia spp.	Feces	NI	Vespertilionidae Rhinolophidae
Wolkers-Rooijackers, 2018	China	Serratia spp, Serratia fonticola, Serratia liquefaciens; Moellerella spp.; Rahnella spp.; Erwinia spp.; Yersinia spp.; Providencia spp.; Citrobacter spp.; Cedecea spp.;	Feces	NI	Vespertilionidae
Wu, 2019	China	*Serratia spp.;* *Clostridium spp.*	Feces and large intestine	NI	Vespertilionidae Rhinolophidae
Xiao, 2019	China	*Serratia spp.;* *Morganella spp.;*	Intestinal contents	NI	Rhinolophidae

N*: number of positive animals or samples/number of animals or samples tested; NI: Not Informed; UD: unextracted data.

CHAPTER 2: Formatted according to the submission guidelines Comparative Immunology, Microbiology & Infectious Diseases (Published article)

Cross-sectional study on *Brucella* spp., *Leptospira* spp. and *Salmonella* spp. in bats from Montes Claros, Minas Gerais, Brazil

Abstract

The understanding on the role of bats in the ecology of zoonotic diseases, especially its relevance as a carrier of pathogens, is important for the determination of preventive measures considering the One Health context. The present study aimed to investigate the presence of *Brucella* spp., *Leptospira* spp. and *Salmonella* spp. in blood (n = 163), liver (n = 35) and spleen (n = 62) samples from bats captured in Montes Claros, Minas Gerais, Brazil. Only *Salmonella* spp. was found in a blood sample of an insectivorous female bat of the species *Lasiurus blossevilli*, evidencing the capacity of this animal species to host this pathogen. In conclusion, our results in bats from Montes Claros indicate that they do not act as hosts for *Brucella* spp. and *Leptospira* spp., although being potential carriers of *Salmonella* spp. in a low prevalence.

Key words: *Brucella* spp., *Salmonella* spp., *Leptospira* spp., PCR, zoonotic diseases, One Health.

1. Introduction

Some bacterial species from the genus *Brucella*, *Leptospira* and *Salmonella* are known as important zoonotic pathogens that cause disease in humans and animals [1]. Brucellosis is caused by *Brucella* spp., which can infect cattle, goats, sheep, buffaloes, pigs and dogs, besides wildlife animals and humans [2]. *Leptospira* spp. is eliminated through the urine of infected animals, being the rodents the main carriers of the agent for humans. Leptospirosis affect wild, synanthropic and domestic animals, such as sheep, goats, dogs, pigs, cattle and horses, with humans being accidental hosts [3]. Salmonellosis, in turn, is caused by *Salmonella* spp., being foodborne disease with enteric or systemic manifestation that affect humans, domestic animals and also reptiles, amphibians and fishes [4]. The knowledge about the ability of these zoonotic pathogens to infect bats is limited, mainly in South America, although evidence of infection was observed in different countries and species of bats for *Leptospira* spp. and *Salmonella* spp. [5], and more recently also for *Brucella* spp. [6].

Bats (Order: Chiroptera) are widely distributed across the world, except for the coldest regions, being some of the most evolutionarily and ecologically diverse animal species known [7]. Their ability to fly allows bats to travel long distances, occupy different habitats, and serve important roles in ecosystem function (e.g., seed dispersal, pollination) [8]; however, this same characteristic makes bats important disseminators of pathogens. Moreover, the increase in forest fragmentation together with the synanthropic behavior of some bat species also contributes to their importance as hosts of diseases [5]. Therefore, the aim of this study was to investigate the occurrence of *Brucella* spp., *Leptospira* spp. and *Salmonella* spp. in bats captured in Montes Claros, Minas Gerais, Southeastern Brazil, and thereby shed some light on their potential as potential carriers of these important zoonotic agents.

2. Material and methods

2.1 Ethics statement

The study was approved by the Brazilian Ministry of Environment (protocols 41709-1 and 41245-1), by the Ethics Committee for Animal Research of Universidade Federal de Minas Gerais (UFMG) (333/2013) and by state laws (IEF-MG 012/2014).

2.2 Sampling

Samplings were performed in Montes Claros, a municipality in north of Minas Gerais state, for 13 consecutive months, from April 2014 to April 2015 [9] in four regions: two neighborhoods, one urbanized (Vila Luiza) and another peri-urban (Nossa Senhora das Graças); and two parks, one more (Lapa Grande State Park) and the other less (Sapucaia Municipal Park) preserved. At each sampling point, a fog net was installed to aid in capture. The captured bats were placed in individualized cotton bags and later the animals were identified using taxonomic keys; sex, dietary niche and habitat (urban or wild), according to the place of capture [10, 11]. A total of 1,100 bats were captured, after their identification, up to five individuals per capture were randomly selected to compose the sampling, totaling 247 bat specimens [9].

The selected animals were anesthetized using Ketamine Hydrochloride intramuscularly in the pectoral muscle for the extraction of blood samples by cardiac puncture [12]. Subsequently, the animals were euthanized with an overdose of the anesthetic, and fragments of skin, spleen, blood, liver and bone marrow were collected from each bat. The samples were stored with RNAlater® (Qiagen, Germany) and preserved at -20ºC. DNA was extracted from all samples using the kit PureLink ™ Genomic DNA Mini Kit (Invitrogen, USA). The bat carcasses were deposited in the Collection of Mammals of the Center for Taxonomic Collections of the UFMG.

2.3 Molecular detection of *Brucella* spp., *Salmonella* spp. and *Leptospira* spp.

Brucella spp., *Salmonella* spp. and *Leptospira* spp. DNA detection in bat samples was performed using conventional PCR. All reagents of the PCR mix without template DNA were routinely used in each assay, as negative control. Visualization of the amplified PCR products was performed in 1.0% agarose gel in tris-borate-EDTA buffer (TBE) (89 mM Tris Base, 89 mM boric acid, and 2 mM EDTA; pH 8.0; all from Sigma-Aldrich, USA) and stained with ethidium bromide (0.5 mg/mL) (Ludwig Biotecnologia Ltda, Brazil). Following electrophoresis, the gels were visualized under ultraviolet light and photographed (L-PIX EX, Loccus Biotechnology, Brazil). The 100 bp DNA ladder (Ludwig Biotec, Brazil) was used in all electrophoresis assays.

2.3.1 Molecular detection of Brucella spp.

The search for *Brucella* spp. DNA was carried out by amplification of the gene *bscp31*, using the primers B4- 5’-TGGCTCGGTTGCCAATATCAA-3’ and B5- 3’-CGCGCTTGCCTTTCAAGGTCTG-5’ [13]. PCR conditions were as previously described by Richtzenhain et al. [14]. The expected amplicon size was 223bp and DNA from *Brucella abortus* 544 (ATCC 23448) was used as positive control in all assays.

2.3.2 Molecular detection of Salmonella spp.

Amplification of the gene *ompC* was performed for detection *Salmonella* spp. DNA, using the primers S18- 5’- ACCGCTAACGCTCGCCTGTAT-3’ and S19- 3’-AGAGGTGGACGGGTTGCTGCCGTT-5’ [15]. PCR conditions were as previously described by Malorny et al. [16]. DNA from *Salmonella* Typhimurium (ATCC 14028) was used as positive control in all assays and the expected amplicon size was 159bp.

2.3.3 Molecular detection of Leptospira spp.

For the search of *Leptospira* spp., a duplex PCR was performed using the *16S rRNA* gene (Lep1 5´ GGAACTGAGACACGGTCCAT 3´ and Lep2 5´ GCCTCAGCGTCAGTTTTAGG 3´) and *lipL32* gene (Lep3 5´ AAGAATGTCGGCGATTATGC 3´and Lep4 5´ CCAACAGATGCAACGAAAGA 3´) that amplify a product of 430 bp and 279 bp, respectively [17]. PCR conditions were as previously described by Tansuphasiri et al [17]. A pathogenic *Leptospira interrogans* serovar Hardjo-prajitno strain belonged to the collection of the Laboratório de Zoonoses Bacterianas, Universidade de São Paulo, was used as positive control in all assays.

2.4 Sequencing of PCR-positive samples

Amplicon from PCR-positive samples were purified using a PCR purification kit (Invitek, USA), and sequenced using Big Dye™ 3.1 (Applied Biosystems, USA) on an ABI-3500 automatic sequencer (Applied Biosystems, USA). The sequences obtained were submitted to quality evaluation by the Phred (reliability index > 20) [18], grouped in a consensus using Bioedit 7.2 [19], and compared with those deposited in the National Center for Biotechnology Information (NCBI) (https://blast.ncbi.nlm.nih.gov/Blast.cgi).

3 Results

Not all samples from all individuals had sufficient DNA volume to be analyzed, thereby, the screening of *Brucella* spp., *Leptospira* spp. and *Salmonella* spp. DNA was performed in 263 bat samples, belonging to 196 individuals, representing 79.35% (196/247) of the total specimens collected; including blood (n = 166), spleen (n = 62) and liver (n = 35) samples. The 196 individuals included 23 species, 17 genera and 3 families, 90.82% were from the family Phyllostomidae, 8.16% from Vespertilionidae and only 1.02% from

Molossidae (Table 1; Supplementary file 1). There was a greater diversity of species and dietary niche belonging to the Phyllostomidae family, the other families were composed of predominantly insectivorous species. Frugivores, followed by insectivores, were the most prevalent bats captured. Males were more frequent (61.74%) than females (38.26%), and there was a similarity in the frequency of urban (47.45%) and wild (52.55%) habitat individuals (Table 1; Supplementary Table S1). No lesions or signs of disease were found in any of the sampled animals and no organs were enlarged or apparently injured. The animals were captured during natural flight and considered healthy. The DNA of *Brucella* spp. and *Leptospira* spp. was not detected in any of the analyzed samples. *Salmonella* spp. DNA was detected in a blood sample from an insectivorous female bat of the species *Lasiurus blossevilli* captured in the urbanized neighborhood of Vila Luiza in March 2015, at the rainy season (Figure 1; Supplementary file 1). The sequencing of the *Salmonella* spp.-positive sample showed 98.34% of identity with sequences of *Salmonella* spp. strains deposited in NCBI (ACCGCTAACGCTCGCCTGTATGGTAACGGCGATCGCGCCACGGTTTA CACCGGCGGCTTGGAATACGATGCGAACAACATCTATCTGGCAGCGCAGTATTCT CAGACCTATAACGCAACCCGTTTTGGTACCTCTAACGGCAGCAACCCGTC CACCTCT). Blood was the only sample analyzed for this individual.

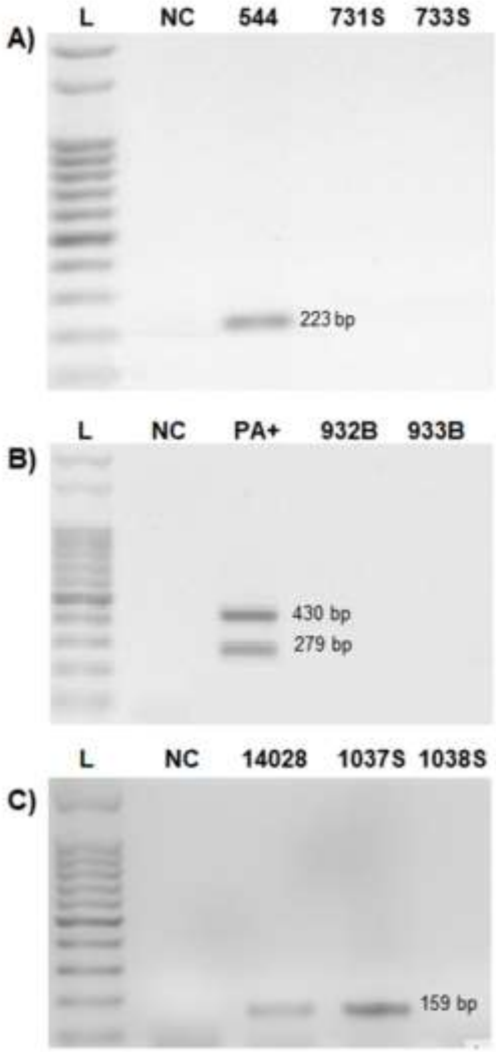

Figure 1: Agarose gel 1% (w / v) stained with ethidium bromide (0.5 mg / mL) of *Brucella* spp., *Leptospira* spp. and *Salmonella* spp. PCR performed in bat samples from Montes Claros, Minas Gerais state, Brazil. A) *Brucella* spp. PCR: *Brucella abortus* 544 -ATCC 23448 (544) used as positive control and negative tested samples (731S and 733S). B) *Leptospira* spp. PCR: *Leptospira interrogans* serovar Hardjo-prajitno (PA+) used as positive control and negative tested samples (932B and 933B). C) *Salmonella* spp. PCR: *Salmonella* Typhimurium - ATCC 14028 (14028) used as positive control, the positive sample (1037S) and a negative sample (1038S). 100 bp DNA Ladder (Ludwig Biotec, Brazil) (L); Negative control (NC).

4. Discussion

Sampling wildlife species for infectious diseases investigations is a complex task due to its ethical, conservational and economical (high costs) implications, which raises the scientific and public health relevance of studies with this objective [20]. Furthermore, it is important to consider that the identification of pathogens that cause brucellosis, leptospirosis and salmonellosis in bats may also have implications for the conservation of the species as well. In addition, the present sampling included 12.70% (23/181) of the bat species already reported in Brazil [21], which can be considered an important step in the knowledge of the role these species in the transmission of zoonotic diseases. However, in the present study, only *Salmonella* spp. was identified and in just one blood sample, suggesting the apparent low relevance of bats as hosts for this agent in Montes Claros and an absence of infection by *Brucella* spp. and *Leptospira* spp. in the evaluated organs. These results contrast with those observed in bats captured in Georgia, in 2017 that demonstrated an 11% prevalence of *Leptospira* spp. and a 2% prevalence of *Brucella* spp. by PCR [6]. On the other hand, studies conducted in bats from São Paulo, Santa Catarina and Rio Grande do Sul, Brazil and Peruvian Amazon have observed a rate of renal colonization by *Leptospira* spp., between 2% and 39.13% [22-24]. The differences between the results of the present study and others may be related to the very different ecology of bats, variation of the species evaluated and also of the sampled ecosystems, since all the controls used in the tests provide reliability of the results obtained. Moreover, all PCR assays used were reported to have high sensitivity [14,15, 17, 25]. On the other hand, the absence of *Leptospira* spp. may have been due to the evaluated organs, since kidneys and urine would be the organs of choice for the evaluation of this pathogen. The identification of *Salmonella* spp., even at a low prevalence [0.5% (1/196)], indicates the potential ability of bats from Montes Claros to be carriers of this pathogen. The prevalence of infection by *Salmonella* spp. in bats observed in previous studies varies from

0.2% to 12.6% [5], being similarly low in the study carried out in Bangladesh on fruit bats (1/320), from fecal samples [26]. Studies on bat microbiota revealed that *Salmonella* spp. is commonly found as part of the commensal microbiota [27, 28], but once isolated from blood samples, as observed in the present study, it suggests bacteremia and possible acute disease.

This study pioneers the search of these pathogens in bats from Brazil and is essential to determine surveillance policies in relation to these synanthropic animals, which are increasingly adapted to the urban environment and in constant contact with domestic animals and humans, as a result of the imbalance environmental. Furthermore, studies that show these animals as hosts of zoonotic pathogens are relevant in the context of One Health approach that seeks to unify animal, human and environmental health. Bats provide us with important ecosystem services, and the study also expands the knowledge about urban and wild fish fauna in a scarce area of bat studies [29].

5. Conclusions

In conclusion, our results in bats from Montes Claros, Minas Gerais, Brazil, indicate that they do not act as hosts of *Brucella* spp. and *Leptospira* spp., although being potential carriers of *Salmonella* spp. at low prevalence. Further studies are needed to elucidate the importance of bats as potential transmitters of *Salmonella* spp. in Brazil.

Conflicts of interests

The authors declare that they have no conflict of interest.

Acknowledgements

ACRF and APL are grateful to Coordenação de Aperfeiçoamento de Pessoal de Nível Superior and Conselho Nacional de Desenvolvimento Científico e Tecnológico for their fellowships. TMV, CMFG and MNM are grateful to Fundação de Amparo à Pesquisa do Estado de Minas Gerais (APQ-00606-14).

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Table 1: Family distribution, dietary niche (diet), species, regional identity and sex, of the 196 bats studied, captured between 2014 and 2015 in the municipality of Montes Claros, Minas Gerais

Family	**Diet**[a]	**Species**	**NS**[b]	**Habitat**		**Sex**	
				Urban	**Wild**	**Female**	**Male**
Molossidae	I	*Cynomops planirostris*	1	1	0	0	1
	I	*Molossus temminckii*	1	0	1	0	1
Phyllostomidae	F	*Anoura caudifer*	1	1	0	1	0
	F	*Anoura geoffroiy*	4	3	1	1	3
	F	*Artibeus lituratus*	50	26	24	16	34
	F	*Artibeus obscurus*	1	1	0	1	0
	F	*Artibeus planirostris*	33	13	20	9	24
	F	*Carollia brevicauda*	9	4	5	4	5
	F	*Carollia perspicillata*	12	6	6	2	10
	F	*Chiroderma villosum*	2	1	1	2	0
	F	*Chrotopterus auritus*	1	1	0	1	0
	F	*Dermanura cinerea*	1	1	0	1	0
	H	*Desmodus rotundus*	12	8	4	2	10
	I	*Glossophaga soricina*	17	3	14	6	11
	C	*Micronycteris microtis*	1	0	1	1	0
	F	*Platyrrhinus lineatus*	30	10	20	17	13
	N	*Platyrrhinus recifinus*	1	0	1	1	0
	F	*Sturnira lilium*	2	2	0	1	1
	F	*Urodema cf. magnirostrum*	1	0	1	0	1
Vespertilionidae	I	*Eptesicus brasiliensis*	1	0	1	1	0
	I	*Eptesicus furinalis*	1	0	1	0	1
	I	*Lasiurus blossevilli*	2	2	0	1	1
	I	*Myotis nigricans*	12	10	2	7	5
		Total	**196**	**93**	**103**	**75**	**121**

[a] I= insetivore, F= frugivore, H= hematophage, C= carnivore, N= nectarivore; [b] NS= number of individuals per species

GENERAL CONCLUSIONS

In the midst of pandemic situations, the knowledge generated from studies taking the One health approach is indispensable. Thinking and understanding that humans, animals and the environment in which we live interact and that this interaction can often favor the emergence or reappearance of epidemic and pandemic diseases is the initial step to propose control and preventive measures. Studies such as the present one are one step forward to guide health surveillance policies, which, when carried out by a multidisciplinary team, can positively impact an entire community, since the contact of the general population with bats has become increasingly frequent.

The identification of numerous bacterial pathogens in bats demonstrated in this dissertation confirms the ability of these animals to harbor pathogens. Moreover, the relationship of pathogenic genera detected in different clinical samples contributes to the understanding of risk in the face of different situations that the synanthropy of bats can represent to the general population. A variety of questions regarding the real role of bats in the epidemiology of bacterial zoonoses still needs to be better elucidated, however the imminent risk that contact with these animals without proper protection offers, directs us to think about preventive measures to promote human health and animal.