



Molecular Detection of *Bartonella* sp. in *Psathyromyia shannoni* and *Lutzomyia cruciata* From Northeastern Mexico

Yokomi N. Lozano-Sardaneta¹, Nadia Joselyne Soto-Olguín¹, Jorge J. Rodríguez-Rojas², Sokani Sánchez-Montes^{1,3}, Eduardo A. Rebollar-Téllez^{4*} and Ingeborg Becker^{1*}

¹ Centro de Medicina Tropical, Unidad de Medicina Experimental, Facultad de Medicina, Universidad Nacional Autónoma de México, Ciudad de México, Mexico, ² Universidad Autónoma de Nuevo León, Centro de Investigación y Desarrollo en Ciencias de la Salud, Unidad de Patógenos y Vectores, Monterrey, Mexico, ³ Facultad de Ciencias Biológicas y Agropecuarias, Región Tuxpan, Universidad Veracruzana, Tuxpan de Rodríguez Cano, Mexico, ⁴ Universidad Autónoma de Nuevo León, Facultad de Ciencias Biológicas, Departamento de Zoología de Invertebrados, Laboratorio de Entomología Médica, San Nicolás de los Garza, Mexico

OPEN ACCESS

Edited by:

Yara M. Traub-Csekő,
Oswaldo Cruz Foundation (Fiocruz),
Brazil

Reviewed by:

Shih Keng Loong,
University of Malaya, Malaysia
Zubaidah Ya'cob,
University of Malaya, Malaysia

*Correspondence:

Ingeborg Becker
becker@unam.mx
Eduardo A. Rebollar-Téllez
eduardo.rebollart@uanl.edu.mx

Specialty section:

This article was submitted to
Vector Biology,
a section of the journal
Frontiers in Tropical Diseases

Received: 21 September 2021

Accepted: 25 October 2021

Published: 18 November 2021

Citation:

Lozano-Sardaneta YN, Soto-Olguín NJ, Rodríguez-Rojas JJ, Sánchez-Montes S, Rebollar-Téllez EA and Becker I (2021) Molecular Detection of *Bartonella* sp. in *Psathyromyia shannoni* and *Lutzomyia cruciata* From Northeastern Mexico. *Front. Trop. Dis.* 2:780808. doi: 10.3389/ftd.2021.780808

Phlebotomine sand flies are vectors of *Leishmania* spp., *Bartonella bacilliformis*, and several arboviruses worldwide. In Mexico, the presence of *Bartonella* species is associated sporadically with arthropods and little is known on the diversity of insects that could be incriminated with its transmission. The aim of this study was to perform a molecular detection of *Bartonella* DNA in sand fly species collected in northeastern Mexico. Sand flies were collected at the states of Nuevo Leon and Tamaulipas from June to August 2010, using 16 light traps per night. Sand fly species were morphologically identified, and for *Bartonella* detection, we amplified ~378 bp of the citrate synthase gene (*gltA*). DNA sequences were compared in a phylogenetic reconstruction based on maximum likelihood. A total of 532 specimens from seven sand fly species were morphologically identified, where 11 specimens from Tamaulipas tested positive for the presence of a new lineage of *Bartonella* sp. associated with *Psathyromyia shannoni* and *Lutzomyia cruciata*. This work represents the second record of *Bartonella*-associated with sand flies outside of the endemic area of Carrion's disease. More studies are necessary to understand their life cycle, transmission dynamics, and their relationship with sand fly species.

Keywords: *Bartonella* sp., sand flies, *Psathyromyia shannoni*, *Lutzomyia cruciata*, Mexico

INTRODUCTION

The phlebotomine sand flies (Diptera: Psychodidae: Phlebotominae) are insects of great relevance due to their role as vectors of several emerging and reemerging diseases caused by pathogens such as *Leishmania*, *Bartonella bacilliformis*, and some arboviruses worldwide (1).

The bacterium *Bartonella bacilliformis* is an endemic species of the Andean valleys of Peru, Colombia, and Ecuador and considered the causal agent of the Carrion's disease or human

bartonellosis, which is transmitted by several sand fly species (2). The genus *Bartonella* encompasses approximately 33 species of Gram-negative, facultative intracellular, and hemotropic bacteria, which can cause chronic intraerythrocytic infections in their hosts. These bacteria are transmitted by several taxa of hematophagous arthropods (fleas, sucking lice, and sand flies) worldwide (3–5). These pathogenic species are highly prevalent and can cause severe infection patterns, which could be related to the increasing number of emerging and reemerging diseases. Thus, it is important to elucidate the possible transmission routes to combat transmission and infections (3, 5).

In Mexico, *Bartonella* species have been reported in 10 states, and the record of new genetic lineages associated with louse, fleas, and rodents has increased over the last years (6, 7). Yet, studies of this bacterium associated with arthropods have been conducted sporadically and little is known on the insects involved in its transmission (8–10). Recently, our group reported the first study of *Bartonella* sp. in sand flies from the state of Veracruz, which is outside of the known endemic zone (11). Due to the relevance of the finding, more studies were warranted to detect this bacterium in sand flies and to elucidate whether it could be of relevance in the transmission of these pathogens in the country.

Until now, 54 sand fly species have been reported in Mexico, with Chiapas, Quintana Roo, Campeche, Yucatan, and Veracruz being the states with the highest number of species. Yet, the analysis for *Bartonella* detection was generally not performed (11, 12). The aim of this study was to perform a molecular detection and to determine the prevalence of *Bartonella* species in phlebotomine sand flies collected in the states of Nuevo Leon and Tamaulipas, Mexico.

MATERIAL AND METHODS

Study Area and Sampling Collection

The study sites were located in Santiago and Cadereyta Jiménez of the state of Nuevo Leon and in Gómez Fariás of the state of Tamaulipas (Figure 1). In the municipality of Santiago, the mean annual temperature is 20.9°C, with a mean annual precipitation of 1,015 mm. Its vegetation is characterized by pine and oak trees (e.g., *Quercus rysophylla*, *Quercus laeta*, *Pinus teocote*, and *Pinus pseudostrobus*). In contrast, in the municipality of Cadereyta Jiménez, the climate is a dry, warm steppe with an average annual temperature of 23°C and an average annual rainfall of 601–800 mm. The sampling place consisted of areas of abandoned crops, secondary vegetation (herbaceous and grasses), and primary vegetation composed of species of *Prosopis glandulosa*, *Acacia farnesiana*, *Ehretia anacua*, and *Pithecellobium ebano*. The municipality of Gómez Fariás is located in a transition zone in the state of Tamaulipas, where notable neotropical and Nearctic biotic elements overlap. It has a warm sub-humid climate and an average annual temperature of 25°C, with precipitation ranging from 1,558 to 1,778 mm. It is characterized by a tropical deciduous and sub-deciduous forest, with the predominance of *Mangifera indica*, *Ceiba pentandra*, *Brosimum alicastrum*, and *Mirandaceltis monoica* (13).

Sand flies were collected during three consecutive nights from June to August 2010. Sampling was carried out from 18:00 to 07:00 h, using 16 incandescent light traps (model 512; John W. Hock Co., Gainesville, FL, USA) per night. A transect of 300 m, with at least a 25-m distance between each trap, was used. Traps were hung from trees or branches, approximately 1.5 m above the ground. The specimens were collected daily and were killed

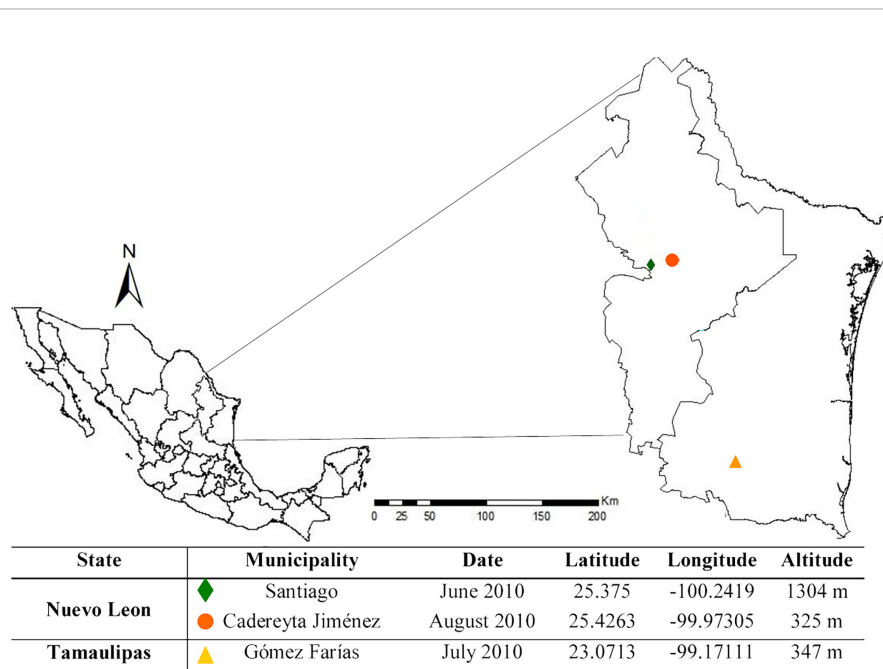


FIGURE 1 | Map showing the study areas of Nuevo Leon and Tamaulipas. The diamond, circle, and triangle depict the municipalities.

using ether vapors. The collected sand fly specimens were sorted from other insects, preserved in vials containing 70% ethanol, and kept at 4°C until their molecular analysis.

Identification of Sand Fly Species

The sand flies were mounted on microscope glass slides using Euparal® medium (BioQuip Products, Rancho Dominguez, CA, USA). The collected female sand flies were dissected, to separate the head from the rest of the body, while the last segments of the abdomen were also severed and preserved for later species identification. Male sand flies were slide-mounted laterally, the head was placed on the side, and the species were identified using morphological characters. Phlebotomine sand fly species were classified according to the classification proposal by Galati (14) and the abbreviation system proposed by Marcondes (15). All the sand fly specimens were deposited in the collection of the Laboratorio de Entomología Médica of the Universidad Autónoma de Nuevo León (UANL) (codes: RECL-NL-20-06-2010; RECL-NL-28-07-2010; RECL-NL-27-08-2010).

DNA Extraction and Polymerase Chain Reaction

Genomic DNA was extracted from the thorax and abdomen of each specimen analyzed, using the phenol chloroform isoamyl alcohol technique (16). For detection of *Bartonella* species, we amplified a segment of ~378 bp of the citrate synthase (*gltA*) gene, using the primers BhCS871.p and BhCS1137.n (17). The polymerase chain reactions (PCRs) were performed under the following conditions: initial denaturation at 95°C for 3 min, followed by 35 cycles at 95°C for 30 s, 51°C for 30 s, 72°C for 30 s, and a final extension at 72°C for 7 min (18). The reaction mixture was prepared in a final volume of 25 µl containing 12.5 µl GoTaq® Green Master Mix 2X Promega Corporation (Madison, WI, USA), 1 µl of each primer (100 ng each), 10 µl DNA template (~50 ng), and 0.5 µl nuclease-free water. For the positive control, we used DNA of *Bartonella vinsonni* obtained from *Hoplopleura hirsuta* (GenBank code KP9972050.1). The negative control consisted of ultrapure water instead of DNA. The amplified products were analyzed by electrophoresis in 1.5% agarose gels

stained with SYTO™ (Invitrogen, CA, USA). Positive PCR products were sequenced at the Laboratorio Nacional de Biodiversidad (Laboratorio de Secuenciación Genómica de la Biodiversidad y de la Salud, Instituto de Biología, UNAM).

Molecular Analysis

The electropherograms were visualized and edited in the Chromas software. Each sequence was compared with available sequences in the GenBank database using the BLASTn tool as a preliminary confirmation of *Bartonella* amplification. The DNA sequences were aligned with other reference sequences of *Bartonella* species deposited in GenBank using MEGA version 6.0. We made a phylogenetic reconstruction based on the maximum likelihood (ML) inference method in MEGA 6.0 with 1,000 non-parametric bootstraps, using the Tamura three-parameter model (T92) + gamma distribution and a BIC score of 3295.044. All alignment sites with less than 95% site coverage were eliminated from the analysis. We used sequences of *Rickettsia rickettsii* (KJ588069.1) as outgroup. The genetic distances were calculated in MEGA 6.0. The obtained sequences were deposited in GenBank under the following accession numbers MZ832303–MZ832304.

RESULTS

Specimens Collected

A total of 532 specimens from seven sand fly species were morphologically identified (Table 1). *Psathyromyia shannoni* and *Lutzomyia cruciata* were the most abundant species in the municipality of Gómez Farías in the state of Tamaulipas, Mexico, whereas for the state of Nuevo Leon, *Psathyromyia texana* was the most abundant species in the municipality Cadereyta Jiménez, and *Lutzomyia diabolica* in the municipality of Santiago. Only a total of 81 sand fly specimens were available for individual analysis by PCR (13 from Nuevo Leon and 68 from Tamaulipas) (Table 1).

Bartonella DNA Detection

A total of 11 specimens from Gómez Farías, Tamaulipas, Mexico, collected in July 2010, tested positive for *Bartonella* DNA using

TABLE 1 | Sand fly species collected in two states located at north of Mexico and *Bartonella* DNA detection.

Species	Tamaulipas		Nuevo Leon			DNA ^a	Gómez Farías <i>Bartonella</i>	
	Gómez Farías July		Cadereyta Jiménez August		Santiago June			
	♀	♂	♀	♂	♀			♂
<i>Dampfomyia (Dampfomyia) anthophora</i>	0	1	4	0	0	0	1	0/1
<i>Psathyromyia (Psathyromyia) cratifer</i>	5	2	0	0	0	0	1	0/1
<i>Lutzomyia (Tricholateralis) cruciata</i>	96	0	0	0	0	0	39	3/39 (7.7%)
<i>Lutzomyia (Tricholateralis) diabolica</i>	0	0	0	0	10	14	2	0/2
<i>Psathyromyia (Psathyromyia) shannoni</i>	69	306	0	0	0	1	27	8/27 (29.6%)
<i>Psathyromyia (Forattiniella) texana</i>	1	0	4	6	0	0	5	0/5
<i>Micropygomyia (Coquilletimyia) vindicator</i>	0	0	2	7	0	0	2	0/2
sp.	2	0	2	0	0	0	4	0/4
7 species	173	309	12	13	10	15	81	11/81 (13.6%)

^aFemale specimens available for *Bartonella* DNA detection.

the *gltA* gene (Table 1). The positive specimens were identified as *Pa. shannoni* (8/27 prevalence 29.62%) and *Lu. cruciata* (3/39 prevalence 7.7%). Although the 11 specimens were positive for *Bartonella* DNA, we only obtained three complete sequences to carry out the phylogenetic analysis (Figure 2).

The *gltA* sequences obtained in this study were 94% similar between each other and exhibited a 95% similarity with sequences of *Bartonella* sp. of *Rattus tanezumi flavipectus* from China (FJ589054.1 and FJ492799.1) and 93% of similarity with *Bartonella* sp. of *Lutzomyia* sp. from Veracruz, Mexico (MN325839.1 and MN325838.1). The ML analysis revealed the presence of a putative new lineage of a *Bartonella* sp., associated with *Pa. shannoni* and *Lu. cruciata*, with a bootstrap support value of 83%. According to the genetic distances, the nucleotides showed 89% similarities with the sequences of uncultivated *Bartonella* from Mexico and 92% with the sequences from China. Based on the proposal that *Bartonella* species can be classified as new, if they exhibit less than $\geq 96.0\%$ nucleotide similarity using the *gltA* gene with other validated species (19), the *Bartonella* detected in the current study represents a new lineage, although complementary studies are necessary.

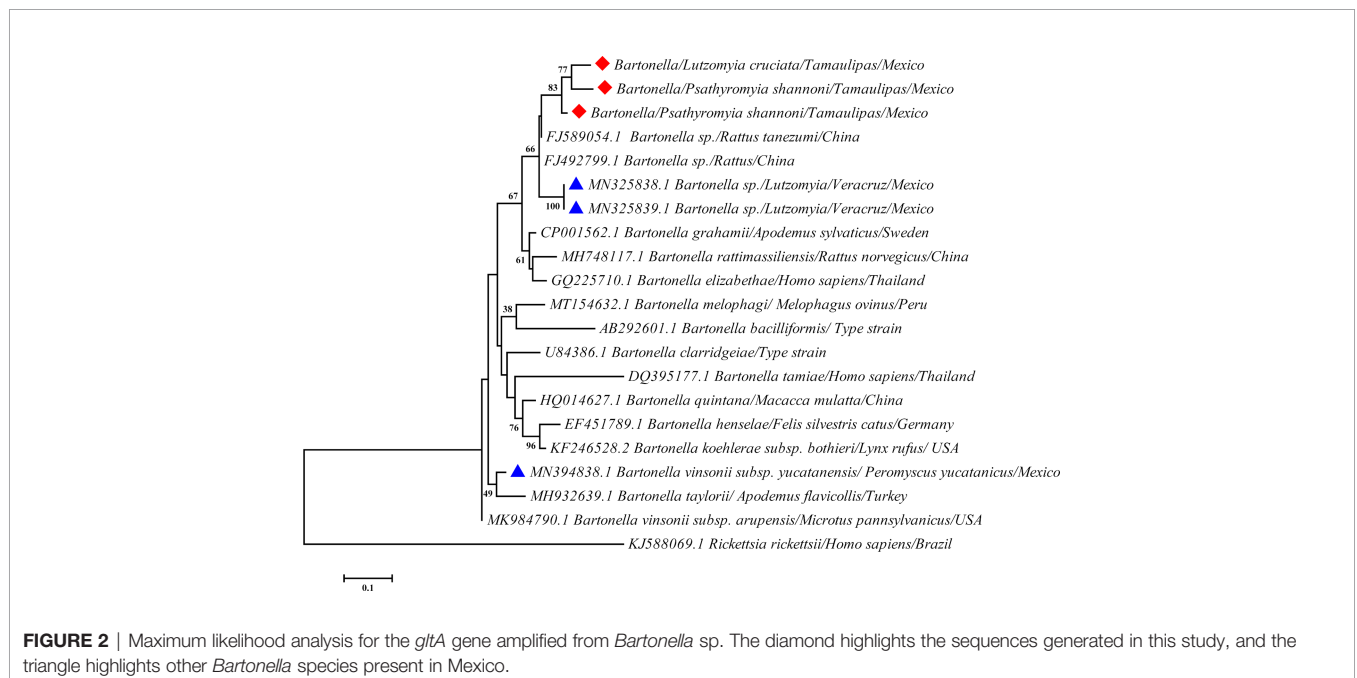
This lineage is related to other *Bartonella* species associated with rodents and humans such as *B. grahamii*, *B. elizabethae*, and *B. rattimassiliensis* (Figure 2). According to the analysis, there are probably three haplotypes (one associated with *Lu. cruciata* and two with *Pa. shannoni*) of this new lineage of *Bartonella* sp.

DISCUSSION

Apart from the Andean valleys, the detection of *Bartonella* species in sand flies from other parts of the American Continent is not recorded frequently. It could be possible that

climate changes may extend the distribution area of sand fly species and thereby also increase the spread of *Bartonella* (5). A recent study conducted in the state of Veracruz, Mexico, showed that this bacterium was related with sand fly species outside of the known endemic areas (11). Our current work now adds further evidence of this association and also shows the first record of a new strain of *Bartonella* sp. in the sand fly species *Lu. cruciata* and *Pa. shannoni* from Tamaulipas, Mexico.

These sand fly species have anthropophilic habits that are relevant due to their role as vectors of *Leishmania* spp., and their high abundance and dominance throughout the Gulf and Caribbean of Mexico (12, 13). In this study, the dominance of *Pa. shannoni* and *Lu. cruciata* over the other sand fly species was possibly related with the climatic conditions and the type of vegetation of Gómez Fariás, Tamaulipas, due to its being a transition zone of the Neotropical and Nearctic biotic provinces. The field work was carried out during the summer, with previous light rains, reporting an average temperature of 25°C and 88% average relative humidity. This characteristic agrees with previous records from Chiapas and Quintana Roo, which showed a positive correlation with the abundance of some sand fly species and these ranges of temperature (<25°C) and humidity (>88%) (20, 21). However, it is advisable to carry out a systematic study in an annual cycle to prove the population dynamic patterns of the phlebotomine sand fly assemblage and thus correlate with the type of vegetation and climatic variables, as well as identify their blood meal preferences to elucidate possible routes of transmission of *Bartonella* sp. in Gómez Fariás, Tamaulipas. Moreover, it is noteworthy that the same sand fly specimens analyzed in the current study had been previously examined for *Leishmania* DNA showing negative results (13). Due to the possibility of coinfection between both parasites (*Bartonella* and *Leishmania*), future studies should take into



account the interactions between sand fly species, their pathogens, their hosts, and the environment.

According to sequences obtained, the new strains of an uncultivated *Bartonella* sp. that we now report are similar to the sequences of *Bartonella* species detected in sand flies from Veracruz, Mexico (MN325839.1) and rats from China (FJ589054.1) (Figure 2). The identity of the obtained sequences and the phylogenetic analysis suggested that it could be a *Bartonella* species related to rodents or humans, such as *B. grahamii* and *B. elizabethae*. The prevalence of *Bartonella* sp. in this study was 13.58% (11/81), which could be considered high when compared with other areas (11, 22, 23). Nonetheless, more studies on this bacterium in arthropods and vertebrates are necessary, in order to understand their life cycle and their relationship with sand fly species.

With this report, the number of known sand fly species harboring *Bartonella* increases to five: *Pintomyia verrucarum*, *Lutzomyia noguchii*, *Lu. peruensis*, *Lu. Crucjata*, and *Pa. shannoni* (23). However, at present we do not have sufficient evidence to confirm whether *Lu. crucjata* or *Pa. shannoni* are competent vectors for the transmission of this pathogen, since the detection of *Bartonella* spp. in arthropods using PCR does not represent a confirmation of their vector competence (5). Since *Bartonella* spp. parasitizes the blood stream or erythrocytes of the infected hosts, their dissemination is facilitated through the blood meal ingestion by several hematophagous arthropods (5, 24, 25), as occurs when sand flies feed on infected blood from a vertebrate host (24).

The record of new sand flies species related to *Bartonella* sp. is not unexpected, since other studies have suggested that more sand fly species could be potential vectors of this bacterium in endemic and non-endemic areas (5, 22, 24). It is noteworthy that the 16 *Bartonella* species that have been confirmed as pathogenic were found to be ubiquitously distributed, whereas species adapted to a single host usually lack pathogenicity. It is therefore likely that the *Bartonella* species associated with sand flies are not necessarily pathogenic to their host (25).

We now showed that a higher diversity of *Bartonella* lineages (pathogenic or non-pathogenic) is to be expected in Mexico,

than previously reported (4), of which some could be related only with sand fly species. This information is very important, since still missing confirm their possible role as vectors of this bacterium in Mexico, to thereby avoid possible chronic or asymptomatic infections caused by this pathogen (5). To enable future classifications of new lineages of *Bartonella* species associated with sand flies, the parameters proposed by LaScola et al. (19) are recommended, as our study showed.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are publicly available. These data can be found here: MZ832303 and MZ832304.

AUTHOR CONTRIBUTIONS

All authors contributed to the study conception and design. Material preparation, data collection, and analysis were performed by YL-S, NS-O, JR-R, and SS. The first draft of the manuscript was written by YL-S, and all authors commented on previous versions of the manuscript. All authors contributed to the article and approved the submitted version.

FUNDING

Field work was conducted from grant PAICYT, UANL SA341-10. The sponsorship for this work was supported by grants CONACyT: 6682 and PAPIIT: AG201221.

ACKNOWLEDGMENTS

We thank Dr. Miriam Berzunza-Cruz for her valuable support in the molecular processing of the samples.

REFERENCES

- Akhoundi M, Kuhls K, Cannet A, Votýpka J, Marty P, Delaunay P, et al. Historical Overview of the Classification, Evolution, and Dispersion of *Leishmania* Parasites and Sandflies. *PloS Negl Trop Dis* (2016) 10:e0004349. doi: 10.1371/journal.pntd.0004349
- Serrano C, García E, León V, Rosiles M. Enfermedad De Carrión. *Rev Latinoam Patol Clin Med Lab* (2014) 61:246–52.
- Chomel BB, Boulouis H-J, Breitschwerdt EB, Kasten RW, Vayssier-Taussat M, Birtles RJ, et al. Ecological Fitness and Strategies of Adaptation of *Bartonella* Species to Their Hosts and Vectors. *Vet Res* (2009) 40:1–22. doi: 10.1051/vetres/2009011
- Kosoy M, Hayman DTS, Chan KS. *Bartonella* Bacteria in Nature: Where Does Population Variability End and a Species Start? *Infect Genet Evol* (2012) 12:894–904. doi: 10.1016/j.megid.2012.03.005
- Regier Y, O'Rourke F, Volkhard AJK. *Bartonella* Spp.- a Chance to Establish One Health Concepts in Veterinary and Human Medicine. *Parasit Vectors* (2016) 9:1–12. doi: 10.1186/s13071-016-1546-x
- Sánchez-Montes S, Cabrera-Garrido MY, Rios-Muñoz CA, Lira-Olguin AZ, Acosta-Gutiérrez R, Mata-Galindo M, et al. Detection of *Bartonella* and *Rickettsia* in Small Mammals and Their Ectoparasites in México. *THERYA* (2019) 10:69–79. doi: 10.12933/therya-19-722
- Zapata-Valdés C, Avila-Flores R, Gage K, Holmes J, Montenerri J, Kosoy M, et al. Mammalian Hosts, Vectors, and Bacterial Pathogens in Communities With and Without Black-Tailed Prairie Dogs (*Cynomys Ludovicianus*) in Northwestern Mexico. *J Wildl Dis* (2018) 54:26–33. doi: 10.7589/2016-09-214
- Sánchez-Montes S, Guzmán-Cornejo C, Herrera-Montalvo LG, Richman AD, Flores-Martínez JJ, García-Ruiz GF, et al. First Record of *Bartonella Vinsonii* in the Sucking Louse *Hoplopleura Hirsuta* Collected From Hispid Cotton Rats, *Sigmodon Hispidus*, in Mexico. *Southwest Entomol* (2016) 41:1031–6. doi: 10.3958/059.041.0403
- López-Pérez AM, Osikowicz L, Bai Y, Montenerri J, Rubio A, Moreno K, et al. Prevalence and Phylogenetic Analysis of *Bartonella* Species of Wild Carnivores and Their Fleas in Northwestern Mexico. *Ecohealth* (2017) 14:1–14. doi: 10.1007/s10393-017-1216-2

10. Moskaluk AE, Stuckey MJ, Jaffe DA, Kasten RW, Aguilar-Setién A, Olave-Leyva JI, et al. Molecular Detection of *Bartonella* Species in Blood-Feeding Bat Flies From Mexico. *Vector Borne Zoonotic* (2018) 18:258–65. doi: 10.1089/vbz.2017.2213
11. Lozano-Sardaneta YN, Colunga-Salas P, Sánchez-Montes S, Cáceres A, Becker I. First Report of *Bartonella* Sp. In Sand Flies (Diptera: Psychodidae: Phlebotominae) From Southern Mexico. *J Am Mosq Control Assoc* (2019) 35:224–7. doi: 10.2987/19-6854.1
12. Lozano-Sardaneta YN, Sánchez-Montes S, Sánchez-Cordero V, Becker I, Paternina L. Molecular Detection of *Leishmania Infantum* in Sand Flies (Diptera: Psychodidae: Phlebotominae) From Veracruz, Mexico. *Acta Trop* (2020) 207:1–7. doi: 10.1016/j.actatropica.2020.105492
13. Rodríguez-Rojas J, Rodríguez-Moreno Á, Berzunza-Cruz M, Gutiérrez-Granados G, Becker-Fausser I, Sánchez-Cordero V, et al. Ecology of Phlebotomine Sandflies and Putative Reservoir Hosts of Leishmaniasis in a Border Area in Northeastern Mexico: Implications for the Risk of Transmission of *Leishmania Mexicana* in Mexico and the USA. *Parasite* (2017) 24:1–17. doi: 10.1051/parasite/2017034
14. Galati E. Morfologia E Terminologia De Phlebotominae (Diptera: Psychodidae). In: *Classificação E Identificação De Tãxons Das Américas. Vol I Apostila Da Disciplina Bioecologia E Identificação De Phlebotominae do Programa De Pós-Graduação Em Saúde Pública*. São Paulo: Faculdade de Saúde Pública da Universidade de São Paulo (2019). p. 133p.
15. Marcondes B. A Proposal of Generic and Subgeneric Abbreviations for Phlebotomine Sandflies (Diptera: Psychodidae: Phlebotominae) of the World. *Entomol News* (2007) 118:351–6. doi: 10.3157/0013-872X(2007)118 [351:APOGAS]2.0.CO;2
16. Kato H, Uezato H, Katakura K, Calvopiña M, Marco JD, Barroso PA, et al. Detection and Identification of *Leishmania* Species Within Naturally Infected Sand Flies in the Andean Areas of Ecuador by a Polymerase Chain Reaction. *Am J Trop Med Hyg* (2005) 72:87–93. doi: 10.4269/ajtmh.2005.72.87
17. Norman F, Regnery R, Jameson P, Greene C, Krause DC. Differentiation of *Bartonella*-Like Isolates at the Species Level by PCR-Restriction Fragment Length Polymorphism in the Citrate Synthase Gene. *J Clin Microbiol* (1995) 33:1797–803. doi: 10.1128/jcm.33.7.1797-1803.1995
18. Rubio AV, Ávila-Flores R, Osikowicz LM, Bai Y, Suzán G, Kosoy MY. Prevalence and Genetic Diversity of *Bartonella* Strains in Rodents From Northwestern Mexico. *Vector-Borne Zoonotic Dis* (2014) 14:838–45. doi: 10.1089/vbz.2014.1673
19. La Scola B, Zeaiter Z, Khamis A, Raoult D. Gene-Sequence-Based Criteria for Species Definition in Bacteriology: The *Bartonella* Paradigm. *TRENDS Microbiol* (2003) 11:318–21. doi: 10.1016/S0966-842X(03)00143-4
20. Pérez J, Virgen A, Rojas J, Rebollar-Téllez E, Castillo A, Infante F, et al. Species Composition and Seasonal Abundance of Sandflies (Diptera: Psychodidae: Phlebotominae) in Coffee Agroecosystems. *Mem Inst Oswaldo Cruz* (2014) 109:80–6. doi: 10.1590/0074-0276130224
21. Rebollar-Téllez E, Reyes-Villanueva F, Fernandez-Salas I, Andrade-Narvaez F. Population Dynamics and Biting Rhythm of the Anthropophilic Sandfly *Lutzomyia Cruciana* (Diptera: Psychodidae) in Southeast, Mexico. *Rev Inst Med Trop Sao Paulo* (1996) 38:29–33. doi: 10.1590/S0036-46651996000100006
22. Ellis BA, Rotz LD, Leake JAD, Samalvides F, Bernable J, Ventura G, et al. An Outbreak of Acute Bartonellosis (Oroya Fever) in the Urubamba Region of Peru, 1998. *Am J Trop Med Hyg* (1999) 61:344–9. doi: 10.4269/ajtmh.1999.61.344
23. Villaseca P, Padilla C, Ventura G, Samalvides F, Yañez H, Chevarría L, et al. Importancia De La *Lutzomyia Peruensis* En La Transmisión De La Enfermedad De Carrion En El Valle Sagrado De Los Incas. Urubamba-Cusco, Perú. *Rev Peru Med Exp Salud Publica* (1999) 15:28–30.
24. Billeter SA, Levy MG, Chomel BB, Breitschwerdt TE. Vector Transmission of *Bartonella* Species With Emphasis on the Potential for Tick Transmission. *Med Vet Entomol* (2008) 22:1–15. doi: 10.1111/j.1365-2915.2008.00713.x
25. Breitschwerdt EB, Kordick DL. *Bartonella* Species and Vascular Pathology. In: Gavins FNE, Stokes KY, editors. *Vascular Responses to Pathogens*. LA, USA: Academic Press (2016). p. 61–74.

Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's Note: All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

Copyright © 2021 Lozano-Sardaneta, Soto-Olguín, Rodríguez-Rojas, Sánchez-Montes, Rebollar-Téllez and Becker. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.