

Arthropods Associated with Mammals. Their Importance as Part of the Richness in a Biosphere Reserve in Mexico

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Abstract

The Chamela Biological Station (ChBS) is located in the Pacific Coast of Mexico in the State of Jalisco. This represents one of the core areas of the Chamela-Cuixmala Biosphere Reserve, characterized by one of the most threatened ecosystems, the tropical dry forest. Although accumulated knowledge of biological diversity, only few studies have been focused on ectoparasites or ectodytes associated with mammals, only 23 arthropod taxa had been recorded. In order to increase knowledge about arthropods associated with Mexican mammals, the objective of this work was to record the richness of arthropods (mites, ticks, lice, and fleas) associated with small and medium-sized mammals in the ChBS. A total of 81 hosts belonging to four orders, six families and nine species were captured. From these hosts, 4,946 arthropods were recovered: 4,007 mites, 673 ticks, 230 lice, and 36 fleas. Among medium-sized mammals, *Nasua narica* (L.) and *Didelphis virginiana* Kerr showed the highest levels of richness, with six arthropod taxa; among rodents, *Heteromys pictus* (Thomas) had the highest number of associated species (five). Within the 22 arthropod taxa registered in the present work, 12 represent new records for the reserve, and 3 represent new records for Mexico. With this study, the arthropod fauna associated with mammals in the ChBS has been raised to 38 taxa. In terms of biological conservation, knowledge of the species that inhabit natural reserves must be a priority, since this represents the baseline for species protected, not only in Mexico but around the world.

Key words: Tick, lice, flea, Chamela, Mexico

Biosphere Reserves are protected areas circumscribed by legislation. The main purpose of these areas is to preserve biodiversity by protecting wildlife, traditional lifestyles of inhabitant, and domesticated plant/animal genetic resources (Jaisankar et al. 2018).

One of the first Biosphere Reserves decreed in the Mexican Pacific region was the Chamela-Cuixmala Biosphere Reserve (CCBR). This reserve is located in La Huerta Municipality in the state of Jalisco, and includes 13,142 ha of tropical dry forest, as well as, medium semievergreen forest, mangroves, and wetlands (Castillo et al. 2007). The CCBR, represents an area where a large proportion of the flora

and fauna are protected including 419 species of terrestrial vertebrates (69 species of mammals, 265 birds, 66 reptiles, 19 amphibians) (Ceballos and Miranda 2000).

One of the core areas of the CCBR, the Chamela Biological Station (ChBS), belonging to Universidad Nacional Autónoma de México (UNAM), was created in 1971 with the objective to provide services for scientific research, facilities for education and training, and the preservation of one of the most threatened ecosystems, the tropical dry forest. Although accumulated knowledge of biological diversity for the ChBS is available for different groups of animals,

only few studies have been focused on ectoparasites or ectodytes associated with mammals.

To date, only 23 arthropod taxa [including mites (14), ticks (6), lice (2), and one pseudoscorpion], associated with 9 wild mammals (representing only the 13% of the known species) have been recorded in the ChBS (Valenzuela et al. 2000, Gómez-Rodríguez et al. 2015, see Table 1).

As part of an ongoing project to evaluate the diversity of arthropods associated with vertebrates in Mexico, the objective of this work was to record the richness of arthropods (mites, ticks, lice, and fleas) associated with small and medium-sized mammals in the ChBS.

Materials and Methods

Field Collection

Collection of mammals

During April and November of 2018 and April of 2019, three field trips were made to the ChBS to collect arthropods associated with small and medium-sized mammals, under collection permits SGPA/DGVS/12771/16 and SGPA/DGVS/011184/18, issued to CGC by the Secretaría de Medio Ambiente y Recursos Naturales, Mexico. Rodents were collected using Sherman traps (Sherman Traps Inc., USA) in transects of 20 traps per site and set for 5 nights. Traps were baited with a mix of oat and vanilla. For medium-sized mammals,

Table 1. Chronological records of arthropods associated with mammals in the Chamela Biological Station, Jalisco, Mexico

Valenzuela et al. (2000)	Guzmán-Cornejo et al. (2011)	Gómez-Rodríguez et al. (2015)	This study
Mites			
-	-	<i>Androlaelaps casalis</i>	<i>Androlaelaps casalis</i>
-	-	-	<i>Androlaelaps fabrenholzi</i>
-	-	<i>Androlaelaps spinosus</i>	<i>Androlaelaps spinosus</i>
-	-	-	<i>Echynonyssus liomys</i>
-	-	<i>Laelaps nuttallii</i> Hirst, 1915	-
-	-	<i>Liponyssoides sanguineus</i> (Hirst, 1914)	-
-	-	<i>Ornithonyssus</i> sp.	-
-	-	-	<i>Ornithonyssus wernecki</i>
-	-	<i>Steptolaelaps liomydis</i>	<i>Steptolaelaps liomydis</i>
-	-	<i>Cordiseta hoffmanae</i> (Brennan, 1960)	-
-	-	<i>Ectonyx fuscicornis</i> Brennan, 1960	-
-	-	<i>Euchoengastoides</i> sp.	-
-	-	-	<i>Eutrombicula alfreddugesi</i>
-	-	<i>Sasacarus whartoni</i> (Hoffmann, 1951)	-
-	-	-	Myobiidae n. gen., n. sp.
-	-	-	<i>Didelphilichus</i> sp.
-	-	<i>Geomylichus postscutatus</i>	<i>Geomylichus postscutatus</i>
-	-	-	<i>Leporacarus sylvilagi</i>
-	-	<i>Prolistrophorus sclerobursatus</i>	<i>Prolistrophorus sclerobursatus</i>
-	-	<i>Dermacarus liomys</i> Fain and Ide, 1978	-
-	-	-	-
<i>Notoedres cati</i>			
Ticks			
-	-	<i>Amblyomma</i> sp.1	-
-	-	<i>Amblyomma</i> sp. 2	-
-	<i>Amblyomma mixtum</i> (=A. cajennense)	<i>Amblyomma mixtum</i> (=A. cajennense)	<i>Amblyomma mixtum</i>
-	-	-	<i>Amblyomma ovale</i>
-	-	-	<i>Amblyomma parvum</i>
-	-	-	<i>Amblyomma</i> cf. <i>oblongoguttatum</i>
-	-	<i>Ixodes</i> sp.	-
-	-	<i>Ixodes sinaloa</i>	<i>Ixodes sinaloa</i>
-	-	<i>Ornithodoros</i> sp.	-
-	-	-	<i>Ornithodoros talaje</i>
Lice			
-	-	-	<i>Fabrenholzia</i> sp.
-	-	<i>Fabrenholzia ehrlichi</i> Johnson, 1962	-
-	-	<i>Fabrenholzia texana</i> Stojanovich and Pratt, 1961	-
-	-	-	<i>Felicola (Loricicola) felis</i>
-	-	-	<i>Neotrichodectes pallidus</i>
Fleas			
-	-	-	<i>Pulex porcinus</i>
Pseudoscorpion			
-	-	<i>Epichernes aztecus</i> Muchmore and Hentschel, 1982	-

Table 2. Collection sites of mammals in the Chamela Biological Station (1–12), and outside the perimeter of the Chamela-Cuixmala Biosphere Reserve (A–C), Jalisco, Mexico

Sampling sites	1 ^c	2	3	4	5	6	7 ^a	8	9 ^c	10 ^a	11 ^c	12 ^c	A	B	C
April 2018	T(2)	S/T(1)	S	-	S/T(1)	-	S	-	S/T(1)	-	-	-	-	-	-
<i>Heteromys pictus</i>			•		•		•		•						
<i>Didelphis virginiana</i>	•				•										
<i>Nasua narica</i>									•						
November 2018	T(2)	S/T(2)	S/T(1)	T(1)	S/T(2)	T(1)	S	S	S/T(1)	-	-	-	-	-	-
<i>Heteromys pictus</i>		•	•		•		•	•							
<i>Osgoodomys banderanus</i>									•						
<i>Sigmodon</i> sp.					•										
<i>Didelphis virginiana</i>	•	•					•								
<i>Nasua narica</i>					•										
<i>Sylvilagus cunicularius</i>				•											
April 2019	T(1)	T(1)	-	-	S/T(2)	-	S	-	S/T(1)	S	T(1)	S/T(2)	-	-	T(2)
<i>Heteromys pictus</i>							•		•	•		•			
<i>Osgoodomys banderanus</i>							•		•			•			
<i>Oryzomys couesi</i>												•			
<i>Xenomys nelsoni</i>							•		•						
<i>Didelphis virginiana</i>	•				•								•		
<i>Leopardus pardalis</i>									•						
<i>Nasua narica</i>		•			•									•	

S= Sherman trap, T= Tomahawk trap, + Site partially marked as path, ^c=near a creek, •= sites with mammalian captures, ()= number of traps, A–B= road-killed mammals.

5–10 Tomahawk traps (Tomahawk Live Traps Inc., USA) were set randomly during the 3 surveys (Table 2). Traps were baited using canned sardines and were set for 5 d, and checked twice a day.

Traps were placed around 12 sampling points (1–12 see Fig. 1), 10 of them corresponded to delimited trails, while 2 were sites partially marked as paths where Sherman traps could be set. From these, four sampling points were set near creeks (Table 2). Additionally, two traps were set outside the ChBS where the presence of some carnivores (e.g., *Leopardus pardalis*) had been previously recorded (Cabrera-Garrido, personal communication) (Fig. 1, site C).

Captured animals were physically (e.g., rodents, opossums) and/or chemically restrained with intramuscular injection of ketamine (Anesket)/xylazine (Rompun) according to the dosage for medium-sized mammals (Kreeger et al. 2012). Rodents were examined for arthropods for 3–5 min, while medium-sized mammals for 20–30 min. Procedures for trapping and handling carnivores followed the guidelines of the American Society of Mammalogists (Sikes and Gannon 2011).

Body surfaces of hosts were screened for arthropods using forceps, and a special comb for lice and fleas. Rodents were brushed over a white tray to recover additional ectoparasites. All collected arthropods were preserved in vials with 96% ethanol. All hosts were measured and sexed, and identified following Burt and Grossenheider (1976), Ceballos and Miranda (2000) and Álvarez-Castañeda et al. (2017). Each mammal specimen was released at the same site of capture, after they had totally recovered from anesthesia.

Laboratory work

Collected arthropods were processed for further study according to their taxonomic group. Mites were cleared using lactophenol and mounted in semipermanent slides in Hoyer's medium, while fleas and lice were cleared using potassium hydroxide (KOH) and mounted in permanent slides using Canada balsam, following techniques referred by Guzmán-Cornejo et al. (2012).

Taxonomic and molecular determination

We used specialized taxonomic keys for each group of arthropods (e.g., Hopkins and Rothschild 1953, Fain 1973, Kim et al. 1986, Hoffmann 1990, Price et al. 2003, Martins et al. 2010, Guzmán-Cornejo et al. 2011). To confirm the specific identification for some ticks, we performed a molecular analysis using nymphs and adults randomly. Extractions were made using 500 µl of chelating resin Chelex 100 (Bio-rad, USA) at 10%, plus 20 µl of Proteinase K (Sigma); this was allowed to incubate at 56°C for 2 h. Samples were then centrifuged at 14,000 rpm for 15 min. The supernatant was transferred into new tubes and kept at –20°C until it was used. We obtained a partial fragment of the 16S rDNA gene using the primers 16S + 1 5'-CCGGTCTGAAGTCAAGT-3' and 16S –1-5'CTGCTCA ATGATTTTTAAATTGCTGTGG-3' (Norris et al. 1996). The PCR conditions were those referred by Trout et al. (2009). Positive PCR products were purified and sequenced at Laboratorio de Biología Molecular y de la Salud, Instituto de Biología, UNAM. Sequences obtained were compared with references available in GenBank using the Basic Local Alignment Search Tool (BLAST).

All ectoparasites were deposited at the Colección del Laboratorio de Acarología 'Anita Hoffmann' (LAFC), and some fleas at the Colección de Siphonaptera, Museo de Zoología 'Alfonso L. Herrera' (MZFC Siphon); both collections are housed at the Facultad de Ciencias, UNAM.

Results

A total of 81 mammal hosts, 46 in 2018 and 35 in 2019 were captured in the ChBS. Hosts belong to four orders and six families: Carnivora: Felidae [*Leopardus pardalis* (Linnaeus, 1758)], Procyonidae [*Nasua narica* (Linnaeus, 1776)]; Didelphimorphia: Didelphidae (*Didelphis virginiana* Kerr, 1792); Lagomorpha: Leporidae [*Sylvilagus cunicularius* (Waterhouse, 1848)]; Rodentia: Cricetidae [*Osgoodomys banderanus* (J.A. Allen, 1897), *Oryzomys couesi* (Alston, 1877), *Sigmodon* sp., *Xenomys nelsoni* Merriam, 1892];

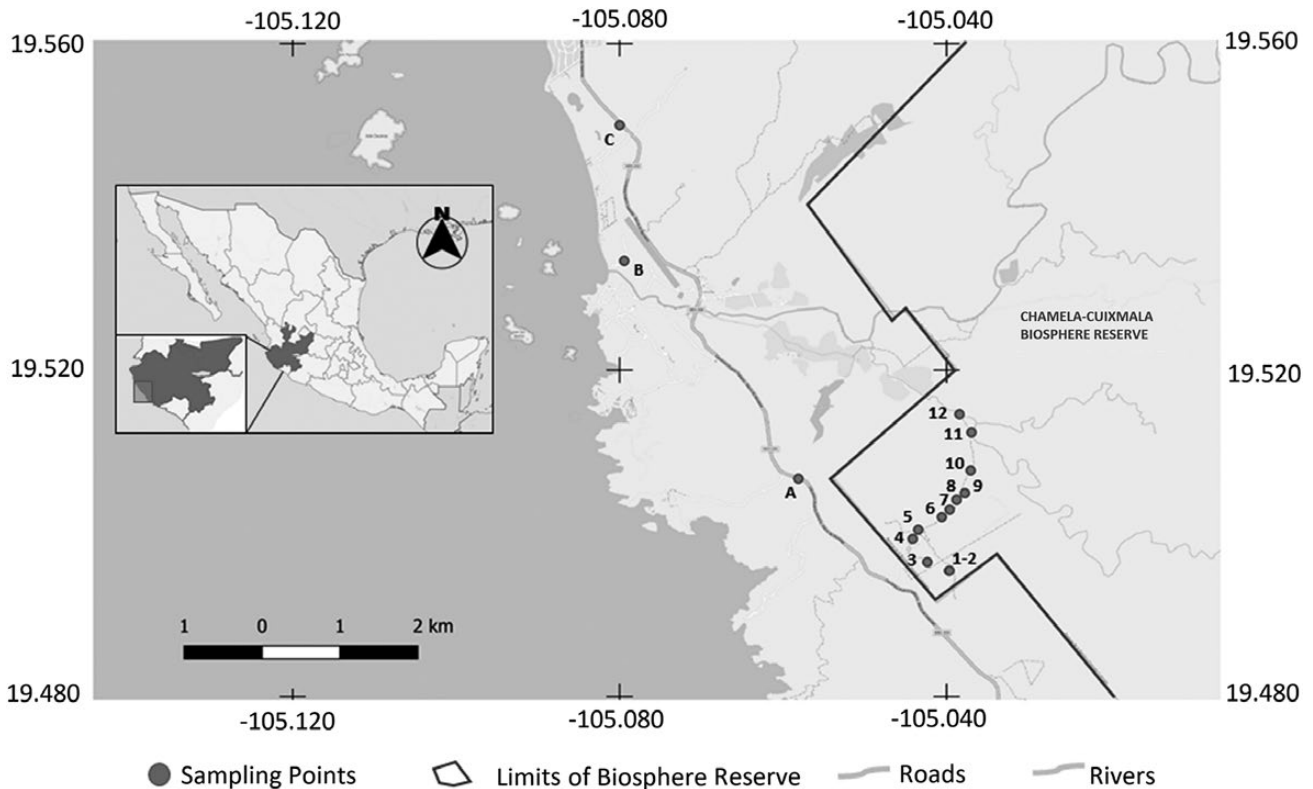


Fig. 1. Sampling sites in the Chamela Biological Station (1–12), and outside the perimeter of the Chamela-Cuixmala Biosphere Reserve (A–C), Jalisco, Mexico.

and Heteromyidae [*Heteromys pictus* (Thomas, 1893)]. In addition, we recovered two road-killed animals (one opossum, and one coati) on the Manzanillo-Puerto Vallarta highway inside the perimeter of La Huerta Municipality (Fig. 1, sites A, B).

Of total sampling sites, we captured rodents and medium-sized mammals in eight and seven points. In each field trip, three, six, and seven mammalian species were collected, respectively; being the sites nine and five those with the highest levels of captures with five and four species of mammals collected (Table 2). *Heteromys pictus* was collected in all sites where Sherman traps were set and among medium-sized mammals, *D. virginiana* was captured in four sites, while *N. narica* only in three, obtaining at least one specimen of each species in each field trip (Table 2).

We collected a total of 4,946 arthropods: 4,007 mites, 673 ticks, 230 lice, and 36 fleas. Mites were represented by 12 taxa, ticks by 6 species (including larvae of the genus *Amblyomma* that were collected from *D. virginiana*, *N. narica*, and *L. pardalis*), lice by three taxa, and fleas by one species (Table 3) (Supp Figs. S1–S3 [online only]).

Among mites, *Steptolaelaps liomydis* (Grant, 1947) (Mesostigmata: Laelapidae) was the most common species on *H. pictus*, while *Ornithonyssus wernecki* (Fonseca, 1935) (Mesostigmata: Macronyssidae) was only collected from *D. virginiana*. *Androlaelaps fahrenheiti* (Berlese, 1911) (Mesostigmata: Laelapidae) and *Androlaelaps spinosus* (Furman, 1955) (Mesostigmata: Laelapidae) were found in association with *O. banderanus*.

Although this study focused on analysis of arthropods associated with some species of small and medium-sized mammals, we noted that certain species of arthropods were present only on one host species, e.g., *S. liomydis* and *Echinonyssus liomys* (Herrin and Yunker, 1973 [Mesostigmata: Hirstionyssidae]) were on

H. pictus, *O. wernecki* on *D. virginiana*, *Leporacarus sylvilagi* Fain, Whitaker and Lukoschus, 1981 (Sarcoptiformes: Listrophoridae) on *S. cunicularius*, *Neotrichodectes pallidus* (Piaget, 1880) (Phthiraptera: Trichodectidae) on *N. narica*, and *Felicola (Lorisicola) cf. felis*. (Werneck, 1934) (Phthiraptera: Trichodectidae) on *L. pardalis*. In contrast, other groups such as ticks or the flea *Pulex porcinus* Jordan and Rothschild, 1923 (Siphonaptera: Pulicidae) were present on more than one host (generalist species) (Table 3).

Most of the species considered as fur mites were also collected on a specific species of host: *Didelphilichus* sp. (Sarcoptiformes: Atopomelidae), on *D. virginiana*; *Geomylichus postscutatus* Fain, 1976 (Sarcoptiformes: Listrophoridae) on *H. pictus*; *L. sylvilagi* on *S. cunicularius*, and the Myobiidae n. gen., n. sp., and *Prolistrophorus sclerobursatus* Fain and Estébanes, 1996 (Sarcoptiformes: Listrophoridae) were found on *X. nelsoni*. Four species of ticks of the genus *Amblyomma* were distributed among medium-sized mammals; only *Ixodes sinaloa* Kohls and Clifford, 1966 (Ixodida: Ixodidae) and *Ornithodoros talaje* (Guérin-Méneville, 1849) (Ixodida: Argasidae) were found parasitizing rodents. Lice were associated with two medium-sized mammals and one species of rodent, while the flea *P. porcinus* was recorded parasitizing three species of mammals (Table 3).

With regard to median-sized hosts, *N. narica* and *D. virginiana* presented the highest levels of richness, with six taxa each; while *L. pardalis* and *S. cunicularius* were infested by four and three species of arthropods respectively. The rodent species with the highest number of arthropod taxa (six) associated was *H. pictus*, followed by *O. banderanus* and *X. nelsoni* (with three), and *O. couesi* (with one) (Table 3). Conversely, *Sigmodon* sp. was the only species that was not parasitized; however, only one specimen was examined. We corroborated molecularly the morphological determination of some ticks; one male and a nymph determined as *Amblyomma* cf.

Table 3. Arthropods associated with small and medium-sized mammals (parasitized host (s)/ total of hosts) in April 2018, November 2018, April 2019 in the Chamela Biological Station, Jalisco, Mexico

	<i>Heteromys Pictus</i>	<i>Osgoodomys banderanus</i>	<i>Oryzomys couesi</i>	<i>Xenomys nelsoni</i>	<i>Didelphis virginiana</i>	<i>Leopardus pardalis</i>	<i>Nasua narica</i>	<i>Sylvilagus cunicularius</i>
Mesostigmata								
<i>Echynomyssus liomys</i>	1/6, -, 2/15							
<i>Septolaelaps liomydis</i>	6/6, 28/29, 15/15							
<i>Ornithomyssus wernecki</i>					1/2, -, 2/5			
<i>Androlaelaps casalis</i>		-, 1/1, 2/7						
<i>Androlaelaps fabrenholzi</i>		-, 1/1, 2/7						
<i>Androlaelaps spinosus</i>		-, 1/1, 7/7						
Ixodida								
<i>Amblyomma mixtum</i>					1/2, 1/3, 5/5		1/1, 1/2, 4/4	
<i>Amblyomma cf. oblongoguttatum</i>					-, -, 1/5	-, -, 1/1	1/1, 2/2, 3/4	
<i>Amblyomma ovale</i>					-, 1/3, -		1/1, -, 2/4	
<i>Amblyomma parvum</i>			-, -, 1/1		2/2, -, 4/5	-, -, 1/1	1/1, 1/2, 4/4	-, 1/1, -
<i>Ixodes sinaloa</i>	-, -, 1/15							
<i>Ornithodoros talaje</i>				-, -, 2/2				
Trombidiformes								
Myobiidae				-, -, 2/2				
n. gen., n. sp.								
<i>Eutrombicula alfreddugesi</i>								-, 1/1, -
Sarcoptiformes								
<i>Didelphilichus sp.</i>					-, -, 1/5			
<i>Geomylichus postscutatus</i>	2/6, 7/29, 7/15							
<i>Prolistophorus sclerobursatus</i>				-, -, 1/2				
<i>Leporacarus sylvilagi</i>								-, 1/1, -
Phthiraptera								
<i>Fahrenholzia sp.</i>	1/6, 1/29, 1/15							
<i>Felicola (Lorisicola) cf. felis</i>						-, -, 1/1		
<i>Neotrichodectes pallidus</i>							1/1, 2/2, 1/4	
Siphonaptera								
<i>Pulex porcinus</i>					1/2, -, -	-, -, 1/1	1/1, -, 2/4	

(-) = Not collected.

oblongoguttatum Koch, 1844 (Ixodida: Ixodidae) in this work were similar to sequences of *A. oblongoguttatum* in 92.42% and 93.43% (GenBank accession no. FJ424407.1 [Ogrzewalska et al. \[2009\]](#)), and to *Amblyomma* sp. (= *Amblyomma* cf. *oblongoguttatum* sensu [Lopes et al. \[2016\]](#)) (95.64% and 94.95%) (GenBank accession no. KU001161.1), respectively. One nymph of *Amblyomma mixtum* Koch, 1844 (Ixodida: Ixodidae) was similar to a sequence of *A. mixtum* in 98.43% (GenBank accession no. KM519935.1), while a nymph determined as *Amblyomma parvum* Aragão, 1908 (Ixodida: Ixodidae) was similar to a sequence of *A. parvum* (99.66%) (GenBank accession no. KT820314.1).

Discussion

The study of the fauna associated with vertebrates includes ecological interactions such as phoresy, commensalism, and parasitism. Rarely these organisms are considered to be part of the biodiversity

of a region, area or a Natural Reserve, without taking into account that many organisms that live in symbiosis have established a very close relationship with their hosts as a result of ecological interactions and/or coevolution. The aforementioned allows their use as indicators of the state of ecosystems, as key species in the taxonomic determination of hosts (e.g., species with a high degree of host specificity), and as indicators of migrations of their hosts, among others ([Greenbaum and Philips 1974](#); [Pérez-Ponce de León and García-Prieto 2001](#), [Gómez and Nichols 2013](#), [Herrera-Mares et al. 2017](#)). On the other hand, parasites are also important from a medical/veterinary perspective, since some species of arthropods can affect host fitness and cause scabies, dermatitis, rashes or act as vectors of microorganisms that can cause diseases. In this context, all diseases can affect conservation efforts, acting as threats for wild hosts ([Gómez and Nichols 2013](#)).

In terms of biological conservation, the knowledge of species that inhabit areas such as Biosphere Reserves must be a priority, because this

is essential for a better understanding for maintaining and preserving these areas. Although a large number of studies on the taxonomy of different groups of vertebrates have been undertaken at ChBS (e.g., Hutto et al. 1986, Ceballos and Miranda 2000, Arizmendi et al. 2002, Ramírez-Bautista and García 2002, Stoner 2002), studies about the fauna associated with these organisms are scarce. To the best of our knowledge, a total of 23 taxa of arthropods associated with mammals have been studied and documented from this area (Valenzuela et al. 2000, Guzmán-Cornejo et al. 2011, Gómez-Rodríguez et al. 2015). This study augments the number to 38 taxa (Table 1). The increase of taxa was mainly due to the study of other groups of mammals, besides mice. Among the 22 taxa recorded in this work, 12 (*A. fahrenbolzi*, *E. liomyis*, *Eutrombicula alfreddugesi* (Oudemans, 1910) (Trombidiformes: Trombiculidae), *Didelphilichus* sp., Myobiidae n. gen., n. sp., *A. cf. oblongoguttatum*, *A. ovale*, *A. parvum*, *O. talaje*, *Fahrenbolzia* sp., *N. pallidus*, and *P. porcinus*) are recorded for the first time (Table 1) while three species are reported for the first time in Mexico: *L. sylvilagi*, *O. wernecki* and *F. (Loricicola) cf. felis*.

Although *A. parvum* and *A. ovale* were previously reported by Guzmán-Cornejo et al. (2011), these species were collected on vegetation, and both were recorded directly on mammals for the first time in this survey.

Some of the arthropods we recorded include hematophagous species that also have been associated with humans, for example: *Androlaelaps casalis* (Berlese, 1887) (Rosen et al. 2002), *A. fahrenbolzi*, *A. mixtum*, *A. oblongoguttatum*, *A. ovale*, *A. parvum* (Moro et al. 2005, Guglielmo and Robbins 2018), and *E. alfreddugesi* (Hoffmann 1990, Santibañez et al. 2015). Due to their hematophagous habits, they could act as potential vectors of etiological agents of diseases. In this sense, most of the species of ticks recorded, have been associated with pathogenic bacteria, for example, *A. mixtum* has been positive for *Rickettsia rickettsii* (Rodaniche et al. 1953, Bermúdez et al. 2016), *Rickettsia amblyommatis* (= *Candidatus Rickettsia amblyommii*) (Eremeeva et al. 2009, Bermúdez et al. 2009, Sánchez-Montes et al. 2016), *Borrelia burgdorferi* s.l. (Solís-Hernández et al. 2018) and *Coxiella burnetii* (Noda et al. 2016). Pathogens associated with *A. ovale* include *Rickettsia amblyommatis* (Bermúdez et al. 2009, Troyo et al. 2016), *Rickettsia asebonensis* (Troyo et al. 2016), *Rickettsia* sp. strain Atlantic Rainforest (Londoño et al. 2014, Lopes et al. 2016), *Rickettsia africae* (Vogel et al. 2018), and *Rickettsia belli* (Pacheco et al. 2008). In *A. parvum*, the presence of *Candidatus Rickettsia* sp. Argentina (Tomassone et al. 2010), *Candidatus Rickettsia andeanae* (Labruna et al. 2011, Nieri-Bastos et al. 2014), *Rickettsia rickettsii* (Dzul-Rosado et al. 2013), and *Ehrlichia chaffeensis* (Tomassone et al. 2008) have been reported. Finally, the mite *A. fahrenbolzi* has been positive for *Rickettsia prowazekii* and *Coxiella burnetii*; however, its vectorial role for these two pathogens remains unlikely (Moro et al. 2005).

Although the pathogenicity of some of these bacteria remains unknown, for others it has been well studied; for example, *R. rickettsii* can cause Rocky Mountain Spotted Fever, *E. chaffeensis* can cause Human Monocytic Ehrlichiosis (Thomas et al. 2016), while *C. burnetii* is the etiological agent of Q fever (Piesman and Gage 2004). Virulence of many pathogens has been based on their effects on humans or domestic animals; however, little is known about the impact of these bacteria and other pathogens on wildlife.

The precise determination of potential vectors is crucial in biodiversity studies; the combined use of morphological and molecular characters promotes a better knowledge of species identities.

Among the listed mites, the Myobiidae and Listrophoridae include species well adapted for clasping to host hair, usually causing little or no apparent harm, even in high numbers. However, in

hosts under confinement or crowding, they can cause dermatitis, scratching and hair loss (Mullen and O'Connor 2019). The only specimen of *S. cunicularius* examined presented a high number of *L. sylvilagi* (1,952 mites); nonetheless, no apparent damage was observed. A similar situation was noticed for the ischnoceran louse *N. pallidus*; on one of the five coats collected, 143 lice specimens were found. In terms of strategies of feeding, the sucking lice are more important in transmitting pathogens than chewing lice (e.g., Ischnocera); however, the damage in this case would be caused by the number of lice involved that could produce dermatitis, an allergic response or secondary infections (Durden 2019).

Among rodents, *H. pictus* was the most abundant species which presented a strong association with the mite *S. liomydis* (Table 3); this parasite–host association was also reported by Gómez-Rodríguez et al. (2015), who mentioned that this rodent species was one of the most abundant in this tropical dry forest, and that *S. liomydis* had represented the 42% of all ectoparasites collected in their study.

Host such as: carnivores and probably *D. virginiana*, which were infested by ticks (Table 3), could play an important role in the dispersion of ticks or fleas in the ChBS, because these mammals have wide vagility. Males of *L. pardalis* can have home range between 3.5 and 17.7 km², while females can roam for 0.7–14.6 km² (Aranda 2005). *Nasua narica* can move near of 3.8 km² (Valenzuela 2002), while the activity area of *D. virginiana* goes from 0.01 to 0.23 km² (Ceballos and Miranda 2000). Also, *N. narica* is a very social animal that can form groups of up to 20 individuals (Valenzuela et al. 2000), a trait that can promote the transmission of ectoparasites, and in some cases cause epizootic events, such as the one produced by the mite *Notoedres cati* (Herring, 1838) in the coast of Jalisco state, which affected the population density of *N. narica* in the 1990's (Valenzuela et al. 2000).

Undoubtedly, the analysis of more species of mammals and other groups of hosts, as well as the exploration of other niches will increase the known diversity of arthropods in the ChBS. During this study, the use of Sherman traps was planned for forest-dwelling rodents and only few traps were set on branches of trees. This allowed us capture arboreal species, e.g., *X. nelsoni* which presented a particular group of mites associated (Table 3; see Supp Material [online only]). In the case of other vertebrate hosts, during field work in November 2018, we collected a single specimen of the turtle *Rhinoclemmys pulcherrima* (Gray, 1855) (Testudines: Geomydidae) parasitized by the tick *Amblyomma sabanerae* Stoll, 1894 (Ixodida: Ixodidae), representing a new record for the ChBS. On the other hand, most new species of Argasidae that have been recently described, came from reptile or amphibian hosts (Venzal et al. 2015, Barros-Battesti et al. 2015, Muñoz-Leal et al. 2016), so their study at the ChBS would surely result in establishing new records for the group or the description of new taxa. Similarly, sampling areas around the reserve would increase the richness of arthropods associated with mammals for the region, as shown through studies that have been conducted outside the perimeter of the CCBR; these included description of species (Hoffmann and Morales-Malacara 1986, Paredes-León et al. 2012); records of tick species and pathogens (Sánchez-Montes et al. 2016), and seasonal studies of ectoparasites associated with mammals (Salinas-Ramos et al. 2017, Salinas-Ramos et al. 2019).

The study of other groups of vertebrates would also provide knowledge on the life cycle of some tick species. For example, *A. oblongoguttatum* can use birds of the family Cracidae (Galliformes) as hosts for adults and nymphs (Guglielmo et al. 2014); in the ChBS this family is represented by two species: *Ortalis poliocephala* Wagler, 1830 and *Philortyx fasciatus* Gould, 1846 (Arizmendi et al. 1990); while larvae of *A. ovale* use the same

bird family (Guglielmone and Robbins 2018). Similarly, passeriform birds, represented in the area by 108 species (Arizmendi et al. 1990), can be hosts for immature stages of *A. parvum*.

We are still far from completing the inventory of arthropods associated with mammals and other vertebrates in the ChBS and in the CCBR in general. In this sense, present and futures studies provide an excellent opportunity to implement the 'One Health' approach (Destoumieux-Garzón et al. 2018) through the synergy of disciplines such as veterinary medicine, taxonomy, molecular biology, epidemiology, parasitology, among others, with the purpose of preserving these areas and their biological diversity, not only in Mexico but globally.

Supplementary Material

Supplementary data are available at Journal of Medical Entomology online.

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