Bacteria related to tick-borne pathogen assemblages in *Ornithodoros* cf. *hasei* (Acari: *Argasidae*) and blood of the wild mammal hosts in the Orinoquia region, Colombia

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Received: 21 October 2021 / Accepted: 16 June 2022 / Published online: 13 July 2022
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**Abstract**

Interest in research on soft ticks has increased in recent decades, leading to valuable insight into their role as disease vectors. The use of metagenomics-based analyses have helped to elucidate ecological factors involved in pathogen, vector, and host dynamics. To understand the main bacterial assemblages present in *Ornithodoros* cf. *hasei* and its mammalian hosts, 84 ticks and 13 blood samples from bat hosts (Chiroptera) were selected, and the 16S rRNA gene V4 region was sequenced in five pools (each one related to each host-tick pairing). Bacterial taxonomic assignment analyses were performed by comparing operational taxonomic units (OTUs) shared between ticks and their host blood. This analysis showed the presence of Proteobacteria (38.8%), Enterobacteriaceae (25%), Firmicutes (12.3%), and Actinobacteria (10.9%) within blood samples, and Rickettsiaceae (39%), Firmicutes (25%), Actinobacteria (13.1%), and Proteobacteria (9%) within ticks. Species related to potentially pathogenic genera were detected in ticks, such as *Borrelia* sp., *Bartonella* tamiae, *Ehrlichia* sp. and *Rickettsia*-like endosymbiont, and the presence of these organisms was found in all analyzed bat species (*Cynomops planirostris, Molossus pretiosus, Noctilio albiventris*), and *O. cf. hasei*. About 41–48.6% of bacterial OTUs (genera and species) were shared between ticks and the blood of bat hosts. Targeted metagenomic screening techniques allowed the detection of tick-associated pathogens for *O. cf. hasei* and small mammals for the first time, enabling future research on many of these pathogens.

**Keywords** *Borrelia* · Chiroptera · Endosymbiont · Microbiome · Soft tick · *Rickettsia*
Introduction

Globally, ticks comprise about 955 species from three families: Ixodidae (ca. 736 species), Argasidae (ca. 218 species) and Nuttalliellidae (1 species), and about a quarter of all species are found within the Neotropical region (Dantas-Torres et al. 2019). Common methods to investigate the role of ticks as a disease vector involve DNA-based diagnostic molecular methods (i.e., PCR-based), but these methods alone are unable to provide insight into other ecological factors (e.g., transmission of organisms between tick species and hosts, detection of other microorganisms, parasite loads, etc. (Estrada-Peña et al. 2013; Tijsse-Klasen et al. 2014; Cabezas-Cruz et al. 2018). Targeted microbiome analysis enables the detection and identification of bacteria assemblages by metagenomic profiling (Cabezas-Cruz et al. 2018; Greay et al. 2018; Thoendel 2020) and has allowed for increased detection of new microorganism species, strains, and genetic variation within ticks (Tokarz and Lipkin 2021). The list of potential tick-borne pathogens is growing (Shapiro et al. 2010; Subramanian et al. 2012; Wu-Chuang et al. 2021) and microbiome studies are beginning to take on a critical role in the functional investigation of microbial communities; this is largely due to the understanding of vector-borne diseases in relation to their pathogenicity, ecology, reproduction, potential hosts, and the implication in human and animal public health (Vílcins et al. 2009; Rynkiewicz et al. 2015; Bonnet et al. 2017). For hard ticks from the genus Amblyomma (A. americanum, A. maculatum, A. tuberculatum), Ixodes rici-nus, and Rhipicephalus microplus, microbiome analyses have been successfully used to characterize bacterial communities involving pathogenic bacteria species such as Borrelia, Anaplasma, Rickettsia and Ehrlichia (Andreotti et al. 2011; Carpi et al. 2011; Menchaca et al. 2013; Budachetri et al. 2014, 2016; Wu-Chuang et al. 2021), whereas other studies have focused on complete pathobiome analysis involving ticks (Vayssier-Taussat et al. 2015; Bennett 2017; Zhuang et al. 2018; Tufts et al. 2020). Similarly, research on soft ticks (Argasidae) has gained importance in recent decades and has provided considerable information on the ecology, taxonomy, systematics, and their role as vectors of pathogens (Wen and Chen 2016; Nava et al. 2017). Nonetheless, studies focusing on bacterial assemblages of soft ticks are known for limited species such as Argas japonicus with special interest in pathogens such as Rickettsia (Yan et al. 2019); Ornithodoros muesebecki with interest in pathogenic groups such as Borrelia, Coxiella, and Rickettsia (Alkayyoomi 2018); and Ornithodoros turicata and its general microbiome (Barraza-Guerrero et al. 2020). In Latin America, studies on soft ticks have focused on the role as vectors of Anaplasma, Borrelia, and Rickettsia (Loftis et al. 2005; Tahir et al. 2016; Muñoz-Leal et al. 2019; Luz et al. 2019; de Oliveira et al. 2020). Nonetheless, other epidemiological groups of argasid-related organisms such as Coxiella, responsible for Crimean-Congo hemorrhagic fever, West Nile virus, and Royal Farm virus, have re-emerged as common pathogens (Manzano-Román et al. 2012; Sarwar 2017; Diaz 2021; Hanafi-Bojd et al. 2021; Kazim et al. 2021).

In Colombia, studies involving ticks, bacterial assemblages and pathogens related to soft ticks are incipient and fragmented. Within the 58 tick species found, 51 are associated with wild mammals Hidalgo et al. 2011; Esser et al. 2016; Faccini-Martínez et al. 2016; Rivera-Páez et al. 2018a; Guglielmon 2021; Ortíz-Giraldo et al. 2021): 43 of these species belong to Ixodidae and 15 to Argasidae. For the latter, 12 species (Antricola mexicanus and 11 species of the genus Ornithodoros: O. azteci, O. brodyi, O. hasei, O. marmosae, O. peropteryx, O. puertoricensis, O. rossi, O. rudis, O. talaje and O. yumatensis) are related to mammals (Ortíz-Giraldo et al. 2021). Some species distributed in Colombia such as O. rudis have been related to recurrent fevers in the 20th century
In particular, *Ornithodoros hasei* (Schulze), is one of the most widely distributed soft ticks in South America and is present in about 20 countries (Nava et al. 2017) where it has been primarily associated with bats (Marinkelle and Grose 1981; Ortíz-Giraldo et al. 2021). Molecular detection of *Rickettsia* has been verified in *O. hasei* in Argentina (Colombo et al. 2020), French Guyana (Tahir et al. 2016) and *Borrelia* in Brazil (Muñoz-Leal et al. 2021a). In Colombia, *O. hasei* has been recorded mainly in bats (Marinkelle and Grose 1981; Tarquino-Carbonell et al. 2015; Ortíz-Giraldo et al. 2021); however, to date there are no reports of the presence of associated pathogens. Given this, the objective of this study is to describe the main bacterial and the related to tick-borne pathogens assemblages present in *Ornithodoros cf. hasei* and its mammalian hosts in the Orinoquia region of Colombia.

**Materials and methods**

**Collection of samples and identification of specimens**

Samples were obtained in the municipalities of Arauca, Cravo Norte, Tame, Department of Arauca (Orinoquia region of Colombia), between November and December 2018, and March, July, and August 2019 (Table S1). Bats (Chiroptera) were captured and sampled using standard protocols (Bazán-León 2011). The collected ticks were stored in 2-mL Eppendorf tubes with 96% ethanol. Blood samples were taken from mammal samples hosting argasids via axillary venipuncture, and deposited in 5-mL heparinized tubes mixed at a 1:9 ratios with DNA/RNA Shield reagent (Zymo Research, Irvine, CA, USA) according to the manufacturer’s instructions and stored at −80 °C.

Sample collection was conducted under the framework permit granted by the National Environmental Licensing Authority (ANLA) to the Universidad de Caldas as stipulated in resolution 02497 of December 31, 2018. Additionally, no species registered in the list of threatened wild species of Colombian biological diversity consigned in resolution nr. 1912 of 2017 were collected. All samples and specimens collected were deposited in the mammal collection of the Museum of Natural History of the Universidad de Caldas (MHN-UCa), and identified using taxonomic keys (e.g., Gardner 2008).

Morphological identification of soft ticks to species level was performed following clarification in 25% KOH and fixation in Hoyer medium (Muñoz-Leal et al. 2019). The dichotomous keys of Filippova (1966), Hoogstraal (1985), Klompen and Oliver (1993), Camicas et al. (1998) and Battesti et al. (2006) were used. After morphological identification, individuals were processed for DNA extraction using the DNeasy Blood and Tissue kit (Qiagen) according to the manufacturer’s suggested protocol. DNA extracted from each tick was amplified via PCR targeting an approximate 460 bp fragment corresponding to the mitochondrial 16S rDNA gene using primers F 5′-CCG GTC TGA ACT CAG ATC AAG-3′ and R 5′-GCT CAA TGA TTT TTT AAA TTG CTG-3′ (Mangold et al. 1998). The amplicons were used for Sanger sequencing at Macrogen (Seoul, South Korea). Confirmation of soft tick species was performed using BLAST and comparison of a maximum likelihood (ML) similarity analysis with 1000 iterations in MEGA X and a Bayesian (BY) analysis using MrBayes v.3.2.7 (Ronquist et al. 2012) via CIPRES tool (Miller et al. 2011), employing four independent Markov chains, 15,000000 generations and sampling every 1000 generations. The first 25% of the trees
were discarded and the remaining trees were used to calculate posterior probability values. The trees were edited using the iTOL tool (Letunic and Bork 2019). Identification and analysis of ticks were performed based on similarity comparisons with public sequences in GenBank and BOLD (Barcode of Life Data Systems) databases. The sequences obtained in this study were deposited in GenBank (accessions MZ773894–MZ773899).

Sample selection, preparation, and sequencing

All ticks selected were attached to the hosts (feeding stage). For tick pools, a selection was made on the abundance of ticks found on the hosts, and only the samples that contained ticks and the mammalian blood collected on RNA/DNA-shield were used. This selection included five pools of ticks, as well as blood pools from bat species such as *Cynomops planirostris*, *Molossus pretiosus*, *Myotis handleyi*, and two pools from *Noctilio albiventris* (Table 1). Ticks were sterilized using 1% sodium hypochlorite followed by washes with 70% ethanol and distilled water (Binetruy et al. 2019). DNA from ticks and blood of wild mammals was obtained using ZymoBIOMICS DNA/RNA Miniprep Kit (Zymo Research), according to the specific instructions that involve the maceration of all samples through bead beating (30 min), and specifically for blood, 750 µL of sampled blood (blood + RNA/DNA shield) were used to the whole process according to the specific instructions. Samples were prepared in argasid and mammalian blood pools. Samples were sent for sequencing to amplify the V4 region of the 16S gene (ca. 250 bp) bacterial rRNA (fusion primers/515F-806R) using the targeted sequencing service at BGI Genomics (Hong Kong, China). This includes quality control to verify the viability of the sequencing process, 16S gene library preparation and use of the Illumina HiSeq2500 sequencing platform to obtain amplified reads.

Bioinformatics analysis

Sequences were individually filtered to obtain high quality clean sequences using fqtools software; fqcheck (v.0.25), readfq (v.1.0) (removal of truncated reads and reads below 75% length) (Fadrosh et al. 2014; Droop 2016); and cutadapt (v.2.6) (Martin 2011), to remove reads contaminated with adapter sequences, ambiguous bases (N bases), and low complexity. Sequence consensus of paired-end reads was performed using FLASH v.1.2.11 (Magoč and Salzberg 2011). Clustering, chimera removal, rarefaction curves, Shannon index, and sequence identification at 97% identity was performed in QIIME 2 (v.2021.04) (Estaki et al. 2020). Operational taxonomic units (OTUs) were generated using the VSEARCH tool (Rognes et al. 2016) and the Greengenes database (Kaehler et al. 2019). The MEGAN v4 program was used to compare the readings with NCBI (Huson and Mitra, 2012). To relate the shared bacterial communities between ticks and hosts, a Venn diagram was made using the taxonomic classification of OTUs (genus and species) by means of the vegan package (Oksanen et al. 2013), in the R v.4.0 program. Sequences are available under the BioProject ID PRJNA767818.

Results

In total, 169 soft ticks of the genus *Ornithodoros* were collected from 19 bats: 163 larvae and 6 nymphs (Table S1). The ticks involved in the study were morphologically and molecularly assigned to *O. cf. hasei*, based on the following combination of traits: 19 pairs of
Table 1 Conformation of the pools used in the study for *Ornithodoros cf. hasei* ticks and blood from wild mammals of Arauca, Orinoquia region, Colombia (all ticks used in the study were in the larval stage)

| Pool ID | Museum code            | No. ticks | Host             | Locality                                              | Coordinates            |
|---------|------------------------|-----------|------------------|-------------------------------------------------------|------------------------|
| 3AS     | MHN-UCa-M 2808         | 1         | *Molossus pretiosus* | Arauca, Vereda El Socorro, Finca Los Trompillos      | 06°47'3.23" N 70°42'8.2" W |
|         | MHN-UCa-M 2863         | 1         | *Molossus pretiosus* | Arauca, Vereda El Socorro, Finca Los Trompillos      | 06°47'3.23" N 70°42'8.2" W |
|         | MHN-UCa-M 2822         | 10        | *Molossus pretiosus* | Arauca, Vereda El Socorro, Finca Los Trompillos      | 06°47'3.23" N 70°42'8.2" W |
|         | MHN-UCa-M 2869         | 2         | *Molossus pretiosus* | Arauca, Vereda El Socorro, Finca Los Trompillos      | 06°47'3.23" N 70°42'8.2" W |
| 5AS     | MHN-UCa-M 2327         | 1         | *Cynomops planirostris* | Cravo Norte, Vereda El Deleite                      | 06°32'25.2" N 70°31'23.6" W |
|         | MHN-UCa-M 2328         | 1         | *Cynomops planirostris* | Cravo Norte, Vereda El Deleite                      | 06°32'25.2" N 70°31'23.6" W |
|         | MHN-UCa-M 2317         | 1         | *Cynomops planirostris* | Arauca, Vereda Las Plumas, Sitio Los Cunaguaro       | 06°36'15" N 70°29'52" W |
|         | MHN-UCa-M 2323         | 1         | *Cynomops planirostris* | Arauca, Vereda Las Plumas, Sitio Los Cunaguaro       | 06°36'15" N 70°29'52" W |
| 6AS*    | MHN-UCa-M 2265         | 3         | *Noctilio albiventris* | Cravo Norte, Vereda El Deleite                      | 06°32'25.2" N 70°31'23.6" W |
|         | MHN-UCa-M 2253         | 6         | *Noctilio albiventris* | Cravo Norte, Vereda El Deleite                      | 06°32'25.2" N 70°31'23.6" W |
|         | MHN-UCa-M 2262         | 1         | *Noctilio albiventris* | Cravo Norte, Vereda El Deleite                      | 06°32'25.2" N 70°31'23.6" W |
| 7AS     | MHN-UCa-M 2806         | 50        | *Noctilio albiventris* | Arauca, Vereda El Socorro, Finca Los Trompillos     | 06°47'3.23" N 70°42'8.2" W |
| 8AS     | MHN-UCa-M 2928         | 6         | *Myotis handleyi* | Arauca, Campus Universidad Nacional Sede Orinoquia, Vereda Mategallina, road to Caño Limón | 07°0'8.47" N 70°44'44.2" W |

*The 6SAN pool belongs to the *N. albiventris* marked in all the document as *
setae on the dorsal, three pair sternal setae (ventral), three pair circumananal setae (ventral), four central setae (dorsal), seven pairs of anterolateral setae (dorsal), eight pairs of posterolateral setae (dorsal) and pointed end hypostome with three rows of teeth on the distal end. The 16 S rDNA gene sequences showed a similarity of 95.3–95.6% with other sequences belonging to O. hasei. Nymphs were only confirmed molecularly as O. cf. hasei comparing the sequences with the larvae (100% similarity). ML analysis placed this species with other O. hasei specimens from Brazil and Argentina (Fig. 1).

In total 3,427924 sequencing reads were obtained from the total samples; 1,613538 reads from tick samples and 1,814386 reads from mammalian blood samples. The average number of reads for each sample was 107123 (57288–154859) and with an average length of 297 bp. The Shannon index and the species accumulation curves showed that all samples except for 8SAN-pool manage to achieve a correct species richness upon sampling (Fig. 2). Argasid pools presented a higher diversity (higher number of taxa described) of bacteria found, as well as a higher average number of reads (115252) compared to host blood (100799) (Table S2). Based on the analysis of bacterial abundances and identification, bacterial groups belonging to Proteobacteria (38.8%), Enterobacteriaceae (25%), Firmicutes (12.3%) and Actinobacteria (10.9%) were found in mammalian blood. For ticks, higher abundances were found for Rickettsiaceae (39%), Firmicutes (25%), Actinobacteria (13.1%) and Proteobacteria (9%) and between 0.8 and 1.41% was not taxonomically assigned (Fig. 3).

The readings confirmed the presence of tick-associated pathogenic bacteria, which were found on the families Anaplasmacetaceae, Bartonellaceae, Borrelliaceae, Francisellaceae and Rickettsiaceae (Table 2). Rickettsiaceae presented the highest abundance (up to 85%), represented mainly by Rickettsia-like endosymbionts. The identification of the deepest taxonomic level for the pathogenic species resulted as Borrelia sp., Bartonella tamiae, Ehrlichia sp., Francisella cantonensis, and Rickettsia-like endosimbiont. Bartonella tamiae and Francisella cantonensis species were not found to be present in both tick and host blood samples. Francisella cantonensis was only detected in O. cf. hasei. Analysis of shared OTUs (genera and species) between ticks and host blood showed that about 41–48.6% is shared (Fig. 4).

**Discussion**

Our results demonstrate the high diversity of bacteria found in both the blood of small wild mammals and ticks. The results agree with previous studies where Actinobacteria, Proteobacteria and Firmicutes, are the most common bacteria in the tick-related microbiome (Narasimhan and Fikrig 2015), such as O. turicata (Barraza-Guerrero et al. 2020), A. americanum (Maldonado-Ruiz et al. 2021) and A. tuberculatum (Budachetri et al. 2016). Moreover, Proteobacteria has been related as one of the most common and dominant bacterial types in the tick microbiome in general, and it has been reported as the main abundant taxon in species such as A. japonicus (Yan et al. 2019), Dermacentor marginatus, I. ricinus, and Rhipicephalus sanguineus (Portillo et al. 2019). On the other hand, although Proteobacteria is abundant in the blood of mammals, in ticks it was the most prominent in only half of the pools, Rickettsiaceae dominating the other half. The dominance of Rickettsiaceae is comprised on two taxa: Rickettsia-like endosymbionts and Wolbachia-like endosymbionts (Table 2). These two taxa have been considered as parasites of ticks and in the case of Rickettsia as disease-causing in vertebrates (Miranda et al. 2012; Plantard...
et al. 2012; Rivera-Páez et al. 2018a, b; López-Pérez et al. 2019; Muñoz-Leal et al. 2019; Bobo 2020), and specifically related to soft ticks (Duh et al. 2010; Sánchez-Montes et al. 2016; Muñoz-Leal et al. 2019; Han et al. 2021; Peixoto et al. 2021). In addition, both have been related to the transmission or interference to other pathogens or bacterial communities (Haine 2008; Walker et al. 2011).

Other tick-related pathogenic bacteria include the families Anaplasmacetaceae, Bartonellaceae, Borreliaeae and Francisellaeae (Table 1). In the case of Anaplasmacetaceae,
Ehrlichia has been reported widely for ticks of the genus Amblyomma and Rhipicephalus (Bekker et al. 2002; Loftis et al. 2006; Stich et al. 2008; Doudier et al. 2010). Although Ehrlichia is not related with soft ticks, it has been listed as an effective pathogen in

Fig. 2 Shannon index and species accumulation curves (Observed) for each pool sequenced

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Fig. 3  Relative abundance of bacterial taxa in *Ornithodoros* cf. *hasei* from the blood of their mammalian hosts. Bacterial taxa are grouped at the phyla (top panel) and family (bottom panel) level. Every bar represents a pooled sample for *O. cf. hasei* and the corresponding mammalian host blood (Table 1). The order of taxa and their respective color is consistent from top to bottom.
Table 2 Description of taxa detected in the study related to ticks, abundance, and their relationship with hosts (direct: present in ticks and host and not direct: present in only one organism)

| Host                                      | Relation                  | Family             | Genus                 | Abundance (%) |
|-------------------------------------------|---------------------------|--------------------|-----------------------|---------------|
| O. cf. hasei – M. pretiosus              | Direct (M. pretiosus – O. cf. hasei) | Anaplasmacetaceae  | Ehrlichia sp.         | 0.005–0.091   |
| O. cf. hasei, N. albiventeris and C. planirostris | Direct (N. albiventeris – O. cf. hasei) | Borreliaceae       | Borrelia sp.          | 0.007–2.61    |
| O. cf. hasei – N. albiventeris            | Not direct                | Bartonellaceae     | Bartonella taniae     | 0.008–5.26    |
| O. cf. hasei                              | Not direct                | Francisellaceae    | Francisella cantonensis | 0.01         |
| O. cf. hasei, N. albiventeris, C. planirostris and M. pretiosus | Direct (N. albiventeris/M. pretiosus/C. planirostris – O. cf. hasei) | Rickettsiaceae     | Rickettsia-like endosimbiont | 0.08–85      |
circulation among mammals, such as *E. canis* (Stich et al. 2008). Therefore, central studies in mammals could reveal much more information about its cycle and related vectors. *Ehrlichia* sp. was detected only in ticks and in the blood one bat host (*Molossus pretiosus*) (Table 2). Meanwhile, *Bartonella* and *Francisella* have been most frequently associated with tick-borne transmission, which may contribute to disease in humans (Sun et al. 2000; Chang et al. 2001; Johnson et al. 2003; Scoles 2004; Chomel et al. 2006; Petersen et al. 2009; Gerhart et al. 2016; Wechtaisong et al. 2020). Specifically, *Bartonella tamiae* has been considered a notable pathogen due to reports of blood in humans in Thailand (Kosoy et al. 2008), and ticks of the genus *Ixodes* in Algeria (Leulmi et al. 2016). *Francisella* *cantonensis* is known primarily as an aquatic species (Duodu et al. 2012), though it has been isolated from air systems (Qu et al. 2009). The ability of *F. cantonensis* to act as a pathogen has yet to be determined in humans or other animals, though this requires more research (Qu et al. 2009; Duodu et al. 2012). Given this, the detection of the genus in metagenomic methodologies is critical, as the identification of species-level using a short 16 S segment is highly variable (Poretsky et al. 2014).

*Borrelia* was primarily detected in wild mammal species in the study (*C. planirostris, N. albiventris*). Despite this prevalence, OTUs analysis did not determine a preferred species for *Borrelia* readings, which could suggest the presence of a new species. Reports of *Borrelia* in ticks and wild mammals have been increasing in recent years in South America (Ataliba et al. 2007; Kelly et al. 2014; Muñoz-Leal et al. 2018, 2021b; Morel et al. 2019; Sánchez et al. 2020), but with few records in Colombia (Marinkelle and Grose 1968; Muñoz-Leal et al. 2021b). *Borrelia* and *Rickettsia* have been the only confirmed potential pathogenic bacteria related to *O. hasei* (Tahir et al. 2016; Colombo et al. 2020; Muñoz-Leal et al. 2021a), however, all recorded pathogenic genera were detected in *O. cf. hasei* (Table 2), which relates this tick to the presence of other pathogenic bacteria that have not been studied or classified. The presence of these bacteria could come directly from

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**Fig. 4** Operational taxonomic units (OTUs) shared at the genus and species level for each tick pool and corresponding mammalian host blood. The overall represent all the genus and species OTUs found in the whole pools of tick and mammals.
contamination of blood shared by hosts (Wu-Chuang et al. 2021). Therefore, the role of O. hasei and the maintenance of pathogenic bacteria from hosts has not been fully studied, and the role of O. hasei and its relationship to the presence of Borrelia in South America is still under investigation (Shapiro and Gerber 2011; Wang 2015; Robles et al. 2018; O’Keeffe et al. 2020).

Several studies have been conducted on the shared bacterial assemblages in the microbiome of ticks and blood of their wild hosts (Zhang et al. 2014; Swei and Kwan 2017), as well as in experimental methodologies (Rynkiewicz et al. 2015). These studies have identified a large variety of bacterial species that could be potential pathogens for vertebrates, and a large percentage of bacterial communities that could be transmitted during the feeding process (Zhang et al. 2014; Rynkiewicz et al. 2015; Swei and Kwan 2017). The analysis of OTUs in our study showed that about 41–48.6% are shared between ticks and their hosts (Fig. 4). Previous studies have shown that blood from wild hosts and the suction process during tick feeding is a possible mechanism for sharing of bacterial assemblages (Rynkiewicz et al. 2015; Swei and Kwan 2017). Moreover, there are several factors that may involve host-parasite contamination, such as the presence of non-pathogenic symbiotic communities from the surrounding environment of the sample and errors in sample handling (Wu-Chuang et al. 2021). Thus, the results of this study may suggest that, although a large number of OTUs are shared, only a small proportion may actually be transmissible, and a smaller proportion has pathogenic potential. Other studies have related the shared microbiome to non-pathogenic symbiont species, though this may be confounded by low resolution in species identification analyses (Rynkiewicz et al. 2015; Barraza-Guerrero et al. 2020; Wu-Chuang et al. 2021).

Conclusions

The detection of genera such as Ehrlichia, Bartonella, Borrelia and Rickettsia, allows the involvement of a significant and direct relationship between ticks and wild mammals. However, transmission by other related vectors in the study area must be elucidated. Wild mammals are rarely included in microbiome screening studies or in the search for new bacteria with pathogenic potential. In this sense, the inclusion of these species is emphasized in order to elucidate the dynamics of the disease ecology in which they may be involved.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s10493-022-00724-9.

Acknowledgements We thank to Universidad de Caldas, Universidad Católica de Manizales, Unidad Administrativa Especial de Salud de Arauca, Universidad Nacional Campus Orinoquia, and all the landowners and the general community of the localities. We thank Dr. Sebastian Muñoz Leal for confirming the species of soft ticks related to bats in the study. We also thank to the ELAP (Emerging Leaders in the Americas Program) of the Global Affairs Canada for the travel and research support of Juan David Carvajal Agudelo (JDCA) to Mount Allison University, Sackville, NB, Canada. Ministerio de Ciencia, Tecnología e Innovación de Colombia—Minciencias for funding the PhD in Science-Biology of the student Paula Andrea Ossa López (PAOL) “Convocatoria del Fondo de Ciencia, Tecnología e Innovación del Sistema General de Regalías para la conformación de una lista de proyectos elegibles para ser viabilizados, priorizados y aprobados por el OCAD dentro del Programa de Becas de Excelencia cohorte 1–2019”.

Funding Open Access funding provided by Colombia Consortium. This project was funded by the Ministerio de Ciencia, Tecnología e innovación—Minciencias; Project ‘El papel de las aves y pequeños mamíferos silvestres en la circulación de garrapatas y rickettsias en el departamento de Arauca (Orinoquia
colombiana’ [code: 11277758193, contract 858 of 2017], and by the Vicerrectoria de Investigaciones y Posgrados—’Ticks (Acari: Ixodidae) of small mammals in Arauca (Arauca, Colombia): an approach to the transmission cycle of borreliosis or Lyme disease’ [Code: 0277620].

**Declarations**

**Conflict of interest** The authors declare no conflict of interest.

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