

Zoonotic pathogens in the ectoparasites of European bats: a review

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Bats are an important group of mammals that perform significant ecological functions, such as regulating insect populations, pollinating plants, and dispersing seeds. However, these animals also host a wide range of ectoparasites, which may harbour microorganisms of public health importance. This review summarises data on potentially zoonotic and vector-borne microorganisms detected in the ectoparasites of European bats between 2010 and 2025. The review is based on 17 scientific publications investigating bat-associated ectoparasites, including ticks, bat flies, fleas, mites and bat bugs, from twelve European countries. The reviewed studies reported microorganisms belonging to the genera *Bartonella*, *Rickettsia*, *Borrelia*, *Anaplasma*, *Ehrlichia*, *Babesia*, *Mycoplasma* and *Neoehrlichia*. *Bartonella* spp. were the most frequently detected microorganisms and were reported in several ectoparasite groups, particularly bat flies, fleas, and mites. In contrast, *Rickettsia*, *Borrelia*, *Ehrlichia*, and *Babesia* were most commonly associated with bat ticks. Most studies were conducted in Central and Eastern Europe, whereas some European regions remain poorly investigated. The detection of microbial DNA in bat ectoparasites suggests that these ectoparasites may be involved in pathogen circulation; however, molecular evidence alone does not prove their ability to transmit pathogens to humans. Further studies are needed to better understand the role of bat ectoparasites in the circulation of microorganisms within bat populations.

Keywords: Chiroptera, ectoparasites, vector-borne pathogens, zoonotic microorganisms, bat flies, bat fleas, bat ticks, bat mites, bat bugs

INTRODUCTION

Bats are widely distributed throughout the world, with more than 1,400 species belonging to over 220 genera inhabiting all continents except Ant-

arctica. Numerous bat species serve as keystone components of ecosystems, playing important roles in pollination, seed dispersal, and pest control (Kunz et al., 2011). Bats are the only mammals capable of sustained flight allowing them to migrate over long distances and potentially act as hosts or reservoirs for a variety of pathogens (Kohl et al., 2021). As urbanisation continues to

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alter natural habitats, bats may increasingly occur in human-modified environments, which can create more opportunities for contact between bats, their ectoparasites, and humans.

Bats harbour various ectoparasitic organisms, including bugs (*Hemiptera*: *Cimicidae* and *Polychtenidae*), fleas (*Siphonaptera*: *Ischnopsyllidae*), bat flies (*Diptera*: *Nycteribiidae* and *Streblidae*), mites (*Mesostigmata*: *Spinturnicidae* and *Macronyssidae*), and ticks (*Argas* spp., *Carios* spp., *Ixodes* spp.) (Szentiványi et al., 2019; Tendu et al., 2022). Bat ectoparasites belong to the phylum Arthropoda and are generally classified into two classes: insects and arachnids. Insects include ectoparasitic bugs, fleas, and bat flies, whereas arachnids include ticks and mites.

Although the condition of the host bat can partially limit parasite load, the development of diverse parasite communities is influenced by competition for resources and the host immune response (Haelewaters et al., 2018). In parasite communities, morphological adaptations often lead to resource partitioning, allowing different parasite species to coexist on a single host (Mouillot et al., 2003). While endoparasites are often strictly associated with a single host, ectoparasites are mobile and can colonise host populations while occupying specific microhabitats on the host or occasionally moving between different hosts (Haelewaters et al., 2018).

Vector-borne diseases represent a significant global public health challenge in the twenty-first century, with their prevalence increasing worldwide. Bat ectoparasites may be of considerable ecological and public health importance (Burazerović et al., 2018), as they can act as potential vectors of infectious agents such as *Bartonella*, *Borrelia*, *Ehrlichia*, *Anaplasma*, *Babesia* and *Rickettsia* (Han et al., 2022; Socolovschi et al., 2012). Bat ectoparasites can harbour multiple pathogens simultaneously, and although the transmission route of *Bartonella* spp. has not been experimentally confirmed, this bacterium has been detected in various bat ectoparasites, suggesting a possible association between bats and their ectoparasites in the circulation of *Bartonella* spp. Moreover, a positive correlation has been observed between ectoparasite and

virus species richness, suggesting a possible vectorial role of ectoparasites in virus transmission (Gay et al., 2014). This review discusses the most common bat ectoparasites, including bat flies, fleas, mites, ticks, and bugs, as well as the pathogens they may carry, and summarises current knowledge on bat ectoparasite-associated pathogens reported across Europe.

This review aims to summarise data published between 2010 and 2025 on potentially zoonotic and vector-borne microorganisms detected in European bat ectoparasites, with emphasis on ectoparasite groups, host associations, geographical distribution, and current knowledge gaps.

MATERIALS AND METHODS

This review summarises the available literature on bacterial and other potentially zoonotic microorganisms detected in ectoparasites associated with bats in Europe. A total of 17 scientific publications were analysed, focusing on bat flies, fleas, mites, ticks and bugs. The principal microorganisms investigated included *Bartonella* spp., *Rickettsia* spp., *Borrelia* spp., *Anaplasma* spp., *Ehrlichia* spp., *Coxiella* spp., *Mycoplasma* spp., *Babesia* spp., *Theileria* spp., and other bacterial and protozoan agents of potential veterinary or public health relevance.

The reviewed studies were conducted in several European countries, including France, Hungary, Poland, Lithuania, Portugal, Romania, Slovenia, Sweden, Finland, Ukraine, the Czech Republic, and the United Kingdom. Some publications included samples from more than one European country or combined European and non-European sampling locations.

Literature was searched using Google Scholar, PubMed, Web of Science, and Scopus, applying combinations of keywords such as 'bat ectoparasites', 'bat flies', 'bat fleas', 'bat ticks', 'bat mites', 'bat bugs', 'Bartonella', 'Rickettsia', 'Borrelia', 'Anaplasma', 'Babesia', and 'Europe'. For each study, the following information was recorded: author(s) and year of publication, country of investigation, bat host species, ectoparasite species, pathogen detected, number

of ectoparasites examined, number of positive samples, and prevalence (%). The articles included in this review were published between 2010 and 2025.

RESULTS AND DISCUSSION

The studies included in this review covered twelve European countries and five main groups of bat ectoparasites: ticks (Ixodidae and

Argasidae), bat flies (Nycteribiidae), bat fleas (Ischnopsyllidae), bat bugs (Cimicidae), and bat-associated mites, including Spinturnicidae and Macronyssidae. A summary of microorganisms detected in bat ectoparasites in Europe between 2010 and 2025 is presented in the Table.

The reviewed studies reported DNA of several potentially zoonotic or vector-borne microorganisms, including members of the genera

Table. Pathogens detected in bat ectoparasites in Europe (2010–2025)

Bat species	Ectoparasite species	Pathogen genus	Prevalence (%); positive/tested	Country	Source
Unspecified bats from infested attic	<i>Argas vespertilionis</i>	<i>Rickettsia</i> spp.	60 (3/5)	France	(Socolovschi et al., 2012)
		<i>Borrelia</i> spp.	80 (4/5)		
		<i>Ehrlichia</i> spp.	60 (3/5)		
<i>Pipistrellus pipistrellus</i> , <i>Plecotus auritus</i> , <i>Myotis daubentonii</i>	<i>Argas vespertilionis</i>	<i>Babesia</i> spp.	2.5 (3/120)	United Kingdom	(Lv et al., 2018)
		<i>Rickettsia</i> spp.	13.3 (16/120)		
		<i>Ehrlichia</i> spp.	4.2 (5/120)		
<i>Rhinolophus hipposideros</i> , <i>Myotis myotis</i> , <i>Myotis bechsteinii</i> , <i>Myotis daubentonii</i>	<i>Ixodes ricinus</i>	<i>Rickettsia</i> spp.	37.5 (3/8)	Poland	(Piksa et al., 2016)
		<i>Borrelia</i> spp.	12.5 (1/8)		
<i>Pipistrellus pygmaeus</i>	<i>Carios vespertilionis</i>	<i>Borrelia</i> spp.	23.9 (22/92)	Sweden	(Jaenson & Wilhelmsson, 2021)
<i>Pipistrellus pygmaeus</i>	<i>Argas vespertilionis</i>	<i>Bartonella</i> spp.	1 (2/205)	Hungary	(Hornok et al., 2019)
<i>Myotis daubentonii</i> , <i>Myotis capaccinii</i> , <i>Eptesicus serotinus</i> , <i>Rhinolophus ferrum-equinum</i>	<i>Ixodes vespertilionis</i>	<i>Bartonella</i> spp.	4 (5/124)	Romania	
<i>Myotis alcathoe</i> , <i>Myotis bechsteinii</i> , <i>Myotis daubentonii</i>	<i>Ixodes ariadnae</i>	<i>Bartonella</i> spp.	11.1 (5/45)	Hungary	
<i>Miniopterus schreibersii</i>	<i>Ixodes simplex</i>	<i>Bartonella</i> spp.	4.3 (6/138)	Romania	
		<i>Anaplasma</i> spp.	1.4 (2/138)	Hungary, Romania	
		<i>Mycoplasma</i> spp.	0.7 (1/138)	Hungary	
<i>Myotis daubentonii</i>	<i>Nycteribia ko-lenatii</i> , <i>Penicillidia monoceros</i>	<i>Bartonella</i> spp.	25 (3/12)	Finland	(Veikkolainen et al., 2014)
<i>Myotis nattereri</i>	<i>Basilia nattereri</i>	<i>Bartonella</i> spp.	100 (1/1)	Slovenia	(Morse et al., 2012a)

Table. (Continued)

Bat species	Ectoparasite species	Pathogen genus	Prevalence (%); positive/tested	Country	Source
<i>Miniopterus schreibersii</i> , <i>Myotis bechsteini</i> , <i>Myotis blythii</i> , <i>Myotis capaccinii</i> , <i>Myotis daubentonii</i> , <i>Myotis myotis</i> , <i>Myotis nattereri</i> , <i>Rhinolophus blasii</i> , <i>Rhinolophus euryale</i> , <i>Rhinolophus ferrumequinum</i> , and <i>Rhinolophus mehelyi</i>	<i>Nycteribiidae</i> spp.	<i>Bartonella</i> spp.	29.1 (158/544)	Hungary, Romania	(Sándor et al., 2018)
<i>Myotis dasycneme</i> , <i>Myotis daubentonii</i> , <i>Pipistrellus kuhlii</i> , <i>Pipistrellus pygmaeus</i> , <i>Plecotus auritus</i>	<i>Carios vespertilionis</i>	<i>Anaplasma/Ehrlichia</i> spp.	4.7 (2/43)	Ukraine	(Vlaschenko et al., 2022)
<i>Pipistrellus pygmaeus</i> , <i>Pipistrellus kuhlii</i>		<i>Rickettsia</i> spp.	16.3 (7/43)		
<i>Myotis daubentonii</i>	<i>Nycteribia kolenatii</i>	<i>Bartonella</i> spp.	21.8 (17/78)		
	<i>Nycteribia pedicularia</i>	<i>Bartonella</i> spp.	27.8 (5/18)		
	<i>Nycteribia kolenatii</i>	<i>Anaplasma/Ehrlichia</i> spp.	69.2 (54/78)		
	<i>Nycteribia pedicularia</i>	<i>Anaplasma/Ehrlichia</i> spp.	55.6 (10/18)		
<i>Nyctalus noctula</i>	<i>Nycteridopsylla eusarca</i>	<i>Anaplasma/Ehrlichia</i> spp.	56 (56/100)	Czech Republic	(Kejřiková et al., 2022)
		<i>Bartonella</i> spp.	7 (7/100)		
<i>Myotis myotis</i>	<i>Cimex pipistrelli</i>	<i>Bartonella</i> spp.	1.79 (2/112)		
<i>Rhinolophus hipposideros</i> , <i>Rhinolophus ferrumequinum</i> , <i>Myotis myotis</i>	<i>Ixodes vespertilionis</i>	<i>Bartonella</i> spp.	14.3 (1/7)	Hungary	(Hornok et al., 2012)
<i>Nyctalus noctula</i>	<i>Nycteridopsylla eusarca</i>	<i>Rickettsia</i> spp.	50 (1/2)		
<i>Myotis myotis</i>	<i>Steatonyssus occidentalis</i>	<i>Bartonella</i> spp.	25 (1/4)		
	<i>Spinturnix myoti</i>	<i>Bartonella</i> spp.	100 (2/2)		
	<i>Nycteribia</i> sp.	<i>Bartonella</i> spp.	100 (3/3)		

Table. (Continued)

Bat species	Ectoparasite species	Pathogen genus	Prevalence (%); positive/tested	Country	Source
<i>Myotis myotis</i>	<i>Spinturnix myoti</i>	<i>Bartonella</i> spp.	28.4 (38/134)	Poland	(Szubert-Kruszyńska et al., 2019)
		<i>Rickettsia</i> spp.	1.5 (2/134)		
<i>Miniopterus schreibersii</i> , <i>Myotis capaccinii</i>	<i>Nycteribia schmidlii</i> , <i>Nycteribia pedicularia</i>	<i>Bartonella</i> spp.	15 (12/80)	Romania	(Corduneanu et al., 2023)
	<i>Ixodes simplex</i>	<i>Mycoplasma</i> spp.	1.25 (1/80)		
<i>Pipistrellus nathusii</i> , <i>P. pygmaeus</i> , <i>Nyctalus noctula</i> , <i>Eptesicus nilssonii</i> , <i>Myotis daubentonii</i> , <i>Barbastella barbastellus</i>	<i>Ischnopsyllus variabilis</i> , <i>Ischnopsyllus octactenus</i> , <i>Ischnopsyllus simplex</i> , <i>Ischnopsyllus elongatus</i> , <i>Ischnopsyllus hexactenus</i> , <i>Nycteridopsylla pentactena</i> , <i>Nycteridopsylla eusarca</i>	<i>Bartonella</i> spp.	41.4 (24/58)	Lithuania	(Sakalauskas et al., 2024)
<i>Rhinolophus ferrumequinum</i>	<i>Ixodes vespertilionis</i>	<i>Bartonella</i> spp.	0.7 (1/141)	Hungary	(Szentiványi et al., 2024a)
<i>Miniopterus schreibersii</i>	<i>Ixodes simplex</i>	<i>Neoehrlichia</i> spp.	11.1 (1/9)	Romania	
<i>Miniopterus schreibersii</i> , <i>Myotis myotis</i>	<i>Ixodes vespertilionis</i>	<i>Neoehrlichia</i> spp.	2.1 (3/141)	Hungary, Romania	
<i>Miniopterus schreibersii</i>	<i>Spinturnix myoti</i>	<i>Bartonella</i> spp.	39.9 (77/193)	Portugal	(Sanches et al., 2025)
	<i>Nycteribia schmidlii</i>	<i>Bartonella</i> spp.	28.6 (2/7)		
	<i>Penicillidia conspiciua</i>	<i>Bartonella</i> spp.	42.9 (21/49)		
	<i>Ixodes simplex</i>	<i>Bartonella</i> spp.	7.3 (3/41)		

Bartonella, *Rickettsia*, *Borrelia*, *Anaplasma*, *Ehrlichia*, *Babesia*, *Mycoplasma*, and *Neoehrlichia*. *Bartonella* spp. were the most frequently reported microorganisms and were detected in several ectoparasite groups, particularly bat flies, fleas, and mites, as well as in some bat-associated ticks and cimicid bugs (Hornok et al., 2012; Veikkolainen et al., 2014; Sándor et al., 2018; Hornok et al., 2019; Szubert-Kruszyńska et al., 2019; Kejíková et al., 2022; Vlaschenko et al., 2022; Corduneanu et al., 2023; Sakalauskas et al., 2024; Sanches et al., 2025). In contrast, *Borrelia* spp., *Rickettsia* spp., *Ehrlichia* spp., *Ana-*

plasma spp., *Babesia* spp., and *Neoehrlichia* spp. were mainly reported from bat-associated ticks, although some of these microorganisms were also detected in bat flies or fleas (Socolovschi et al., 2012; Piksa et al., 2016; Lv et al., 2018; Jaenson, Wilhelmsson, 2021; Vlaschenko et al., 2022; Szentiványi et al., 2024a).

The geographical distribution of the reviewed studies is shown in Fig. 1. Research activity was not evenly distributed across Europe. The highest number of studies was recorded in Hungary and Romania (four studies each), followed by Poland (two studies) (Hornok et

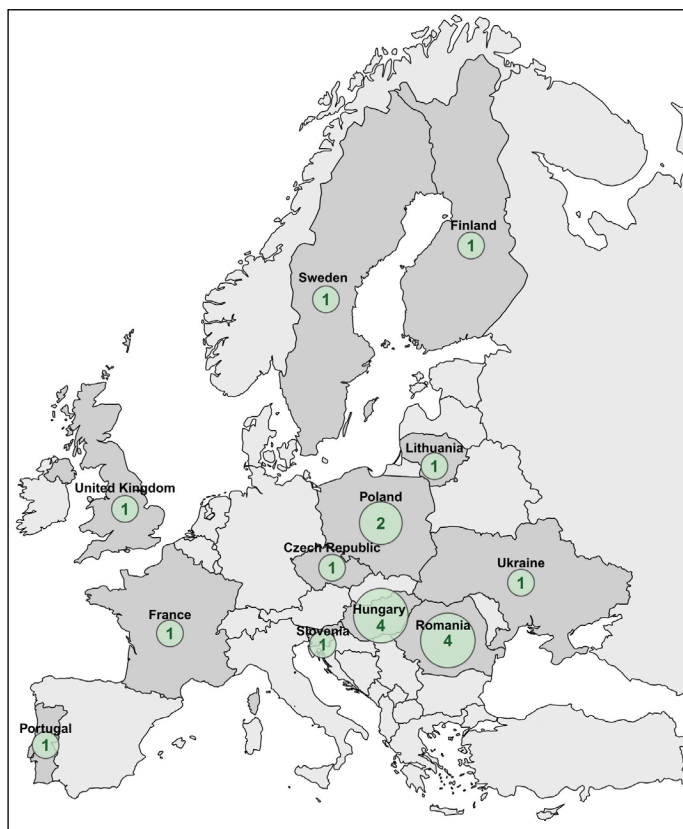


Fig. 1. Geographic distribution of studies reporting microorganisms in bat ectoparasites in Europe between 2010 and 2025. Each circle represents a country in which at least one study was identified. Circle size and number indicate the number of studies conducted in each country. The map was prepared in R using the ggplot2, sf, rnatualearth and rnatualearth-data packages

al., 2012; Piksa et al., 2016; Sándor et al., 2018; Hornok et al., 2019; Szubert-Kruszyńska et al., 2019; Corduneanu et al., 2023; Szentiványi et al., 2024a). The remaining countries, including France, the United Kingdom, Sweden, Finland, Ukraine, the Czech Republic, Lithuania, Slovenia and Portugal, were represented by a single study (Socolovschi et al., 2012; Morse et al., 2012a; Veikkolainen et al., 2014; Lv et al., 2018; Jaenson, Wilhelmsson, 2021; Kejíková et al., 2022; Vlaschenko et al., 2022; Sakalauskas et al., 2024; Sanches et al., 2025). Overall, the available literature indicates a stronger research focus on Central and Eastern Europe, whereas several regions of Europe remain poorly investigated.

The data summarised in Table 1 also show that some studies reported high prevalence values, particularly for *Bartonella* spp. in bat flies, fleas and mites, and for *Anaplasma/Ehrlichia* spp. in some bat-associated ectoparasites (Hornok et al., 2012; Sándor et al., 2018; Szubert-Kruszyńska et al., 2019; Vlaschenko et al., 2022; Sakalauskas et al., 2024; Sanches et al., 2025). However, these values should be interpreted

cautiously, especially when based on small sample sizes. For example, some prevalence estimates were derived from only one to a few examined specimens, which limits broader epidemiological interpretation (Morse et al., 2012a; Hornok et al., 2012).

Although the detection of microbial DNA in bat ectoparasites suggests possible involvement in the circulation of microorganisms within bat populations, molecular detection alone does not confirm active infection, pathogen maintenance, or vector competence. Detected DNA may originate from an infected blood meal, transient microbial presence in the ectoparasite gut, or possible colonisation of ectoparasite tissues. Therefore, further studies combining molecular screening, host–ectoparasite paired sampling, and experimental approaches are needed to clarify the role of bat ectoparasites in pathogen transmission.

The relationships between study countries, ectoparasite types, and detected pathogen genera are summarised in Fig. 2. *Bartonella* spp. emerged as the most broadly distributed

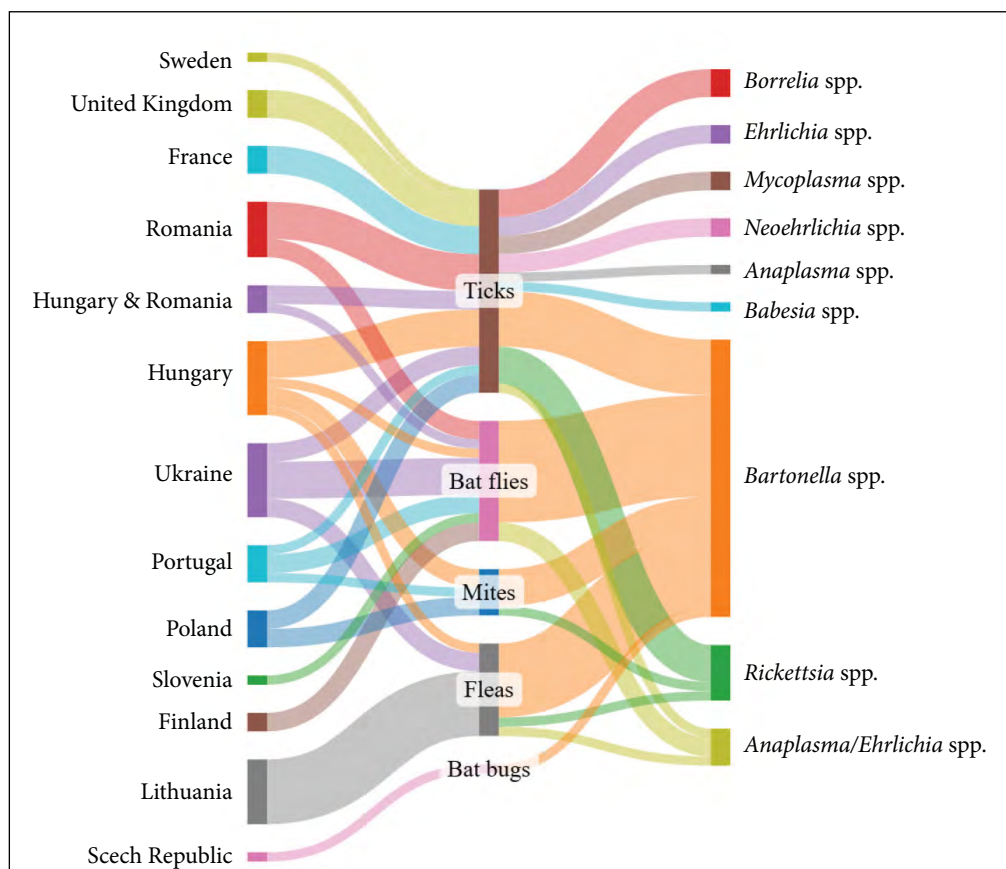


Fig. 2. Sankey diagram illustrating the relationships between European countries where studies were conducted (left), ectoparasite groups examined (centre), and pathogen genera detected (right). The width of each flow is proportional to the number of recorded associations between a given country, ectoparasite type, and pathogen genus. Created with Sankey-MATIC

pathogen genus, detected across all ectoparasite groups and in the majority of countries, whereas *Rickettsia* spp., *Borrelia* spp., and *Ehrlichia* spp. were more consistently associated with bat ticks than with other ectoparasite groups. The following sections discuss the available evidence separately for each ectoparasite group.

Bat ticks

Ticks, belonging to the Acari subclass families *Ixodidae* and *Argasidae*, are external parasites of terrestrial vertebrates (Anderson, Magnarelli, 2008). Their specialisation to hosts can vary, extending from generalists to highly exclusive, species-specific parasites. While many ticks have diverse groups of vertebrates as hosts

during different life stages, certain species, particularly those found in nests or burrows, exhibit greater specificity by utilizing a few related species or, in extreme instances, relying on just one species as their host (Nava, Guglielmo, 2013). Bat-associated ticks are often highly host-specific and exhibit adaptations to the ecology and behaviour of bats, including their roosting habits, mobility, and close associations with specific host species (Szentiványi et al., 2024a).

Several bat-associated tick species, including *Carios vespertilionis*, *Ixodes simplex*, and *Ixodes vespertilionis*, occasionally feed on humans. In addition, some bat-associated ticks have been reported feeding on other non-chiropteran hosts. This behaviour increases their epidemiological

importance and highlights their potential role as bridge vectors between bats, humans, and other vertebrate hosts. However, the frequency of such interactions and their contribution to pathogen transmission remain poorly understood (Szentiványi et al., 2024b).

In Europe, bats exhibit specialisation with two species of soft ticks (family *Argasidae*: *Argas transgarepinus* and *A. vespertilionis*) and three species of hard ticks (family *Ixodidae*: *Ixodes ariadnae*, *I. simplex*, and *I. vespertilionis*) (Sándor et al., 2019). The usual locations of ticks on bats are around the mouth, eyes, and ears, as well as on the dorsal and ventral surfaces of the body (Burazerović et al., 2018). The widely distributed parasite *Ixodes vespertilionis* commonly infests numerous bat species from the families Rhinolophidae and Vespertilionidae, with a prevalent presence in Europe, North Africa, and the Middle East (Sándor et al., 2019). *Ixodes ariadnae*, a recently described species, has sporadic occurrences in central and western Europe and primarily parasitises bats of the family Vespertilionidae. Conversely, *Ixodes simplex* exhibits host specialisation, primarily affecting members of the Miniopteriidae family, especially *Miniopterus schreibersii*, across Europe, North Africa, and Asia. These tick species are mainly associated with bats using subterranean roosts, such as caves and mines (Sándor et al., 2019). Soft ticks associated with bats are commonly found in sheltered roosting sites, including crevices, hollows, caves, and buildings (Hoogstraal, 1985). Both species exhibit extensive distribution ranges, with *A. transgarepinus* being found in Africa and southern Europe, and *A. vespertilionis* occurring in Africa, Asia, and Europe (Hoogstraal, 1985). *Argas vespertilionis*, a tick species associated with bats and bat habitats in Europe, Africa and Asia, feeds not only on bats but also on humans (Sándor et al., 2019).

The presence of bacterial DNA in bat-associated ticks has been studied more extensively than in other bat ectoparasites in Europe. However, knowledge of bat tick-associated pathogens remains limited. In Western Europe, five adult *Argas vespertilionis* ticks collected from

a bat-infested attic in south-western France were examined for bacterial microorganisms (Socolovschi et al., 2012). *Rickettsia* sp. AvBat DNA, representing a previously uncharacterised genotype within the spotted fever group, was detected in three ticks. Viable rickettsiae were successfully isolated from two of these ticks using L929 and XTC-2 cell cultures (Socolovschi et al., 2012). An *Ehrlichia canis*-group genotype, designated *Ehrlichia* sp. AvBat, was also detected in three ticks (Socolovschi et al., 2012). Furthermore, four ticks contained DNA of *Borrelia* sp. CPB1, a relapsing-fever-group spirochete. Its 16S rRNA and *flaB* sequences were identical to those previously obtained from the liver of a pipistrelle bat that died from fatal borreliosis in the United Kingdom (Evans et al., 2009; Socolovschi et al., 2012). Although an *A. vespertilionis* larva was found attached to the affected bat, the tick was not tested for *Borrelia*. Therefore, tick-mediated transmission was suspected but not proved (Evans et al., 2009).

In a study conducted in England, 296 *Argas vespertilionis* ticks were collected from British bat carcasses over a seven-year period, and zoonotic pathogens including *Babesia* spp., *Rickettsia* spp., and *Ehrlichia* spp. were detected (Lv et al., 2018). Similarly, studies conducted in Poland revealed that ixodid ticks (*I. ricinus*) collected from bats were infected with two pathogenic bacterial species, *Borrelia* (*B. garinii*) and *Rickettsia* (*R. helvetica*) (Piksa et al., 2016). In south-central Sweden, where the bat tick *C. vespertilionis* is known to occasionally feed on humans and has been associated with disease symptoms, 24% (22/92) of the analysed ticks tested positive for *Borrelia* spp. (Jaenson, Wilhelmsson, 2021). Furthermore, *Anaplasma phagocytophilum* DNA was detected in the hard tick species *I. simplex* in Hungary and Romania (Hornok et al., 2019). Additionally, *Rickettsia* spp. and *Anaplasma/Ehrlichia* spp. were detected in bat ticks collected in Ukraine (Vlaschenko et al., 2022).

In Romania, *Mycoplasma* spp. was detected in larvae of the bat-specific tick *Ixodes simplex*. The pathogen was identified both in the

tick and in its host (*Miniopterus schreibersii*), suggesting a possible role of bat ticks in pathogen circulation. These findings expand the diversity of microorganisms known to be associated with bat ticks and highlight the potential involvement of bat-associated ticks in the maintenance and transmission of bacterial pathogens within bat populations (Corduneanu et al., 2023).

Molecular blood-meal analysis of 161 bat-associated ticks collected from cave and mine walls in Hungary and Romania detected vertebrate DNA in 70 ticks (43.5%). Although most identified blood meals originated from bats, DNA from non-chiropteran hosts, including domestic dogs, horses, and wild boars, was also detected, indicating that *Ixodes ariadnae*, *I. simplex*, and *I. vespertilionis* may occasionally feed on non-bat hosts. In the same study, the zoonotic bacterium *Neohrlichia mikurensis* was detected for the first time in bat-associated ticks, including one *I. simplex* and three *I. vespertilionis*. Furthermore, *Bartonella* sp. DNA was detected in one *I. vespertilionis* nymph, whereas *Wolbachia* sp. DNA was identified in nine *I. ariadnae*. These findings suggest that bat-associated ticks may have a broader host range than previously recognised and could represent potential ecological links between bats and other vertebrates. However, the detection of vertebrate and bacterial DNA does not demonstrate pathogen transmission or vector competence, and the epidemiological significance of these findings remains uncertain (Szentiványi et al., 2024a).

Bat flies

Bat flies are obligate hematophagous ectoparasites of bats that mainly inhabit bat fur and wing membranes. Bat flies are divided into two families: the winged Streblidae and the wingless, spider-like Nycteribiidae (Han et al., 2022). These families belong to the superfamily Hippoboscoidea, along with Glossinidae (tsetse flies) and Hippoboscidae (louse and ked flies) (Szentiványi et al., 2019). Currently, the family Nycteribiidae includes 275 species, whereas the family Streblidae comprises 227

species. Nycteribiidae have a higher diversity in the Eastern Hemisphere, whereas Streblidae are found predominantly in the Western Hemisphere (Szentiványi et al., 2019).

The superfamily Hippoboscoidea exhibits a distinctive reproductive strategy known as adenotrophic viviparity, in which a single larva develops within the female and is nourished by secretions from specialised milk glands. Third-instar larvae are deposited by female bat flies onto substrates within the bat roost, such as cave walls, where they rapidly pupate (Morse et al., 2013). Endosymbiotic bacteria have been detected in the milk glands of bat flies, suggesting vertical transmission from mother to offspring through gland secretions (Hosokawa et al., 2012; Morse et al., 2013). Several bacterial taxa, including *Arse-nophonus*, *Wolbachia*, and *Bartonella*, have been reported in bat flies and related hippoboscoid flies, indicating long-term associations between these insects and their bacterial symbionts (de Bruin et al., 2015; Duron et al., 2014; Morse et al., 2012b). Shortly after deposition, the larvae pupate and remain in the roost environment until adult emergence. Newly emerged flies actively search for a suitable bat host. Environmental conditions, particularly temperature, influence the duration of pupal development and the survival of newly emerged flies (Szentiványi et al., 2019).

Bat flies harbour a variety of microorganisms, including *Bartonella* spp. and fungal microparasites. The distribution of these microorganisms appears to be influenced by long-term host–parasite associations, although observed patterns may also reflect sampling biases (Szentiványi et al., 2019). A study of 10 bat fly species collected from 14 European bat species revealed a high prevalence of *Bartonella* spp., particularly in bats forming large cave-dwelling colonies in Hungary and Romania (Sándor et al., 2018). *Bartonella* spp. was also detected in bat flies in Finland (Veikkolainen et al., 2014). Similar findings were reported in Slovenia, where *Bartonella* spp. was detected in a nycteribiid bat fly collected from *Myotis nattereri* (Morse et al., 2012a). In addition,

Bartonella spp. was detected in *Nycteribia kolenatii* and *N. pedicularia* collected in Ukraine (Vlaschenko et al., 2022).

More recently, *Bartonella* spp. was detected in the bat flies *Nycteribia schmidlii* and *Nycteribia pedicularia* collected from *Miniopterus schreibersii* and *Myotis capaccinii* in Romania. Identical *Bartonella* strains were identified in both bat flies and their respective bat hosts, and positive bat–ectoparasite pairs were recorded. These findings provide further evidence that bat flies may contribute to the maintenance and circulation of *Bartonella* spp. within bat populations (Corduneanu et al., 2023). Evidence from previous studies suggests that certain bat-associated *Bartonella* strains may infect humans, indicating their potential public health relevance (Bai et al., 2018; Frank et al., 2018).

In contrast to bat ticks, bat flies appear to be highly host-specific and there is currently no evidence that they regularly feed on humans or other vertebrates. Therefore, although they frequently harbour bacterial pathogens such as *Bartonella* spp., their direct role in zoonotic spillover remains unclear (Szentiványi et al., 2024b).

Bat fleas

Bat fleas (Ischnopsyllidae) are ectoparasites associated with bats. Adult fleas occur on the host, whereas immature stages develop within roost debris and guano accumulated beneath bat colonies. Flea abundance may be influenced by roost characteristics, host behaviour, and the proximity between bats and larval development sites. Consequently, the occurrence and abundance of bat fleas can vary among bat species with different roosting ecologies and colony structures (Zahn, Rupp, 2004).

Few studies have investigated bat fleas during the past decade. An unusual ecological interaction was described for the ischnopsyllid fleas *Lagaropsylla signata* and *L. turba*, which exhibit phoretic behaviour involving the earwig *Arixenia esau* and the bat *Cheiromeles torquatus*. In this association, the earwig serves as a transport host, facilitating flea contact with its bat host. These observations provide an exam-

ple of the complex ecological relationships that may occur between bat fleas, their hosts, and other arthropods (Hastriter et al., 2017).

In a study conducted in Ukraine, *Bartonella* spp. was detected in the bat flea *Nycteridopsylla eusarca* (Vlaschenko et al., 2022). Similar findings were reported in Hungary, where *Bartonella* DNA was identified in *Nycteridopsylla eusarca* collected from *Nyctalus noctula* bats (Hornok et al., 2012). In the same study, the eight-combed bat flea (*Ischnopsyllus octactenus*) and the five-combed bat flea (*Nycteridopsylla eusarca*) were screened for the presence of *Rickettsia helvetica*. The pathogen was detected in *N. eusarca*, representing the first report of *R. helvetica* in bat fleas (Hornok et al., 2012).

A recent comprehensive study by Sakalauskas et al. (2024) provides the first assessment of ischnopsyllid flea diversity and pathogen prevalence in Lithuanian bats. Analysing 58 specimens, the researchers identified seven flea species: *Ischnopsyllus variabilis*, *I. octactenus*, *I. simplex*, *I. elongatus*, *I. hexactenus*, *Nycteridopsylla pentactena*, and *N. eusarca*. Screening for various vector-borne pathogens revealed that *Bartonella* DNA was present in 41.4% of the fleas, which is a significantly higher prevalence than reported in Ukraine or Hungary, while other targeted pathogens were absent. Phylogenetic analysis confirmed that these *Bartonella* sequences are specific to bats or their ectoparasites. Additionally, *Wolbachia* sp. was identified in *I. elongatus*, and the study documented several new host and flea associations within the region.

Bat bugs

Bat bugs, mainly species of the genus *Cimex* (Hemiptera: Cimicidae), represent a relatively understudied group of bat ectoparasites in Europe compared with bat flies, ticks and mites. Unlike many other ectoparasites, cimicids are not permanently attached to the host (Balvín, Bartonička, 2014). Both immature stages and adults usually remain hidden in roost refugia and visit bats only for blood feeding, which may contribute to their underrepresentation in ectoparasite surveys. European bat-associated

Cimex fauna includes *Cimex lectularius*, *Cimex pipistrelli* and *Cimex emarginatus*, with host associations varying by bat species, roost type and geographical region. *C. pipistrelli* is particularly associated with crevice-dwelling bats in Central Europe, whereas bat-associated lineages of *C. lectularius* are mainly linked to synanthropic bat roosts, especially those of *Myotis myotis* and *M. emarginatus* (Hamlili et al., 2023; Balvín, Bartonička, 2014).

In the reviewed European literature, pathogen screening in bat bugs was very limited. The most relevant finding was the molecular detection of *Bartonella* spp. DNA in *Cimex pipistrelli* from Central Europe. In that study, *Bartonella* was screened using partial sequences of the *gltA*, *ssrA* and 16S-23S rDNA ITS regions, and *Bartonella* DNA was detected in two of 112 bat bug samples, corresponding to a prevalence of 1.79%. This represents the first reported detection of *Bartonella* spp. in European bat bugs and indicates that cimicids may participate in the ecology of bat-associated *Bartonella* genotypes, although available evidence remains too limited to infer their vector competence (Kejíková et al., 2022).

The low number of positive samples suggests that *Bartonella* occurrence in bat bugs may be sporadic or strongly dependent on local ecological conditions, bat host species, roost structure and ectoparasite population dynamics. However, detection of bacterial DNA alone does not demonstrate active transmission. It may reflect an infected blood meal, transient bacterial presence in the gut. Therefore, the role of bat bugs as biological vectors remains unresolved. This is particularly important because bat bugs can occasionally bite humans when they occur in buildings inhabited by bat colonies. Such behaviour creates a potential, although currently unquantified, interface between bats, their ectoparasites, and humans (Kejíková et al., 2022).

Compared with other bat ectoparasites in Europe, bat bugs remain poorly investigated for zoonotic and vector-borne pathogens. Recent European studies on bat-associated ectoparasites have more frequently focused on mites, ticks and bat flies, in which *Bartonella* spp.,

Rickettsia spp., *Anaplasma* spp., *Ehrlichia* spp., and piroplasmids have been reported. In contrast, records from bat bugs are scarce and, to date, mainly limited to *Bartonella* detection. This gap is notable because *Bartonella* spp. are among the most frequently detected bacteria in bat ectoparasites, and several bat-associated genotypes have been reported from different ectoparasite groups across Europe (Sanches et al., 2025).

Bat mites

Mites of the family Spinturnicidae (Acari: Mesostigmata) are permanent ectoparasites found on bat wing membranes, the uropatagium and, in some cases, around the anal region (Orlova et al., 2021). Unlike bat flies, spinturnicid mites complete their entire life cycle on the host and do not leave it during development. The highest infestation levels are typically observed in pregnant and lactating females and particularly in their offspring, which are nursed in maternity colonies during the summer months in Europe. Eggs and larval stages develop inside the gravid female mite, whereas each active developmental stage (protonymph, deutonymph and adult) feeds repeatedly on host blood and lymph. Because reproduction is viviparous and immature stages develop within the female, spinturnicid mites do not require a free-living stage away from the host (Giorgi et al., 2004; Szubert-Kruszyńska et al., 2019).

Mites belonging to the family Spinturnicidae exhibit a high degree of specialisation as bat ectoparasites. Currently, the family comprises approximately 110 species assigned to 11 genera worldwide. Six genera – *Paraperiglischrus*, *Oncoscelus*, *Parameristaspis*, *Meristaspis*, *Eyndhovenia* and *Ancystropus* – parasitise horseshoe bats (*Rhinolophidae*) and fruit bats (*Pteropodidae*) in the Old World, including Africa, Southern Europe, Central Asia, and South and Southeast Asia. Four genera – *Periglischrus*, *Mesoperiglischrus*, *Cameronieta* and *Emballonuria* – occur on bats of the families Phyllostomidae, Natalidae, Mormoopidae and Emballonuridae in the New World. The genus *Spinturnix* is the most diverse and widespread

genus within the family, comprising more than 50 species that primarily parasitize vesper bats (Vespertilionidae) in both the Old and New World (Orlova et al., 2021).

Bacterial pathogens have also been detected in bat-associated mites of the family Spinturnicidae. In Hungary, *Bartonella* spp. DNA was identified in *Spinturnix myoti* mites collected from *Myotis myotis* bats, representing one of the first reports of *Bartonella* in European bat mites (Hornok et al., 2012). Similar findings were later reported in Poland, where *Bartonella* spp. DNA was detected in 28% of *Spinturnix myoti* mite pools and in 25% of their bat hosts, *Myotis myotis*. Identical *Bartonella* genotypes were identified in mites and bats, suggesting that *Bartonella* may be shared between wing mites and their hosts (Szubert-Kruszyńska et al., 2019). The same study also detected *Rickettsia* spp. DNA in *S. myoti* mites, providing the first evidence of rickettsial bacteria in bat-associated wing mites (Szubert-Kruszyńska et al., 2019). More recently, a study from China reported diverse *Bartonella* genotypes in bat mites (*Spinturnicidae*), including genotypes shared between bats and their ectoparasites, indicating a close association between *Bartonella* genotypes detected in bats and their ectoparasites (Han et al., 2022).

A recent study from Portugal detected *Bartonella* spp. in *Spinturnix myoti* mites collected from cave-dwelling bats. Phylogenetic analyses showed that the detected genotypes clustered with *Bartonella* strains previously reported in bats and bat flies from Europe, Asia, and Africa, indicating close genetic relationships among *Bartonella* lineages circulating in bat-associated hosts and ectoparasites. The authors noted that the epidemiological role of Spinturnicidae mites remains poorly understood and requires further investigation (Sanches et al., 2025).

CONCLUSIONS

European bats host a diverse assemblage of ectoparasites, including ticks, bat flies, mites, fleas and cimicid bugs. Studies conducted across Europe have detected DNA of various potentially

zoonotic and vector-borne microorganisms in these ectoparasites, including *Bartonella*, *Borrelia*, *Anaplasma*, *Ehrlichia*, *Rickettsia*, *Babesia*, and *Mycoplasma* spp. These findings suggest that bat ectoparasites may be involved in the circulation of microorganisms within bat populations. Ticks and bat flies are the most extensively studied bat ectoparasites and have been associated with the greatest diversity of detected microorganisms. *Bartonella* spp. and *Rickettsia* spp. have also been reported in bat fleas and mites, whereas data on bat-associated cimicid bugs in Europe remain scarce. Recent molecular studies have shown close genetic relationships between microorganisms detected in bats and their ectoparasites, indicating strong ecological links within bat–ectoparasite systems. However, the detection of microbial DNA alone does not confirm pathogen transmission or vector competence. Further studies are needed to determine whether bat ectoparasites can actively maintain and transmit these microorganisms.

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ZOONOTINIAI PATOGENAI EUROPOS ŠIKŠNOSPARNIŲ EKTOPARAZITUOSE: APŽVALGA

Santrauka

Šikšnosparniai yra svarbi žinduolių grupė, atliekanti reikšmingas ekologines funkcijas, tokias kaip vabzdžių populiacijų reguliavimas, augalų apdulkinimas ir sėklų platinimas. Tačiau šie gyvūnai yra ir įvairių ektoparazitų šeimininkai, o jų ektoparazituose gali būti aptinkami visuomenės sveikatai svarbūs mikroorganizmai. Šioje apžvalgoje apibendrinami duomenys apie potencialiai zoonotinius ir vektorių platinamus mikroorganizmus, aptiktus Europos šikšnosparnių ektoparazituose 2010–2025 metais. Apžvalga parengta remiantis 17 mokslinių publikacijų, kuriose tirti šikšnosparnių ektoparazitai – erkės, kraujasiurbės musės, blusos, erkutės ir blakės – iš dvylikos Europos šalių. Apžvelgtuose tyrimuose nustatyti *Bartonella*, *Rickettsia*, *Borrelia*, *Anaplasma*, *Ehrlichia*, *Babesia*, *Mycoplasma* ir *Neoehrlichia* genčių mikroorganizmai. Dažniausiai aptinkamos *Bartonella* spp. buvo nustatytos keliose ektoparazitų grupėse, ypač kraujasiurbėse musėse,

blusose ir erkutėse. *Rickettsia*, *Borrelia*, *Ehrlichia* ir *Babesia* gentys dažniausiai buvo siejamos su šikšnosparnių erkėmis. Tokių tyrimų daugiausia atlikta Vidurio ir Rytų Europoje, o kai kurie Europos regionai lieka menkai ištirti. Mikroorganizmų DNR aptikimas šikšnosparnių ektoparazituose leidžia manyti, kad pastarieji gali būti susiję su patogenų cirkuliacija, tačiau vien molekuliniai duomenys neįrodo jų gebėjimo perduoti patogenus žmonėms. Ateityje reikėtų daugiau tyrimų, kurie padėtų geriau suprasti šikšnosparnių ektoparazitų vaidmenį mikroorganizmams šikšnosparnių populiacijose.

Reikšminiai žodžiai: šikšnosparniai, ektoparazitai, vektorių platinami patogenai, zoonotiniai mikroorganizmai, šikšnosparnių musės, šikšnosparnių blusos, šikšnosparnių erkės, šikšnosparnių erkutės, šikšnosparnių blakės