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The role of canines (Canidae) in the spread of vector-borne pathogens

Ugnė Medikaitė,

Indrė Lipatova*,

Algimantas Paulauskas

Vytautas Magnus University,
K. Donelaičio St. 58,
44248 Kaunas, Lithuania

This review aimed to summarise the available literature on the prevalence and distribution of *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., *Anaplasma* spp., *Borrelia* spp., and *Rickettsia* spp. in wild canids (foxes, wolves, jackals, and raccoon dogs) across Europe from 2010 to 2024. A total of 25 published studies were analysed. For each study, data on host species, country, sample size, detection methods, and pathogen prevalence were extracted and compared. All six pathogens were detected in foxes, which showed the highest prevalence rates compared to other canids. *Hepatozoon* spp., *Babesia* spp., and *Anaplasma* spp. were the most frequently studied pathogens. Pathogen prevalence varied by host species and geographical location, with higher rates generally observed in Central and Southern Europe. Foxes appear to play a key role as potential reservoirs for multiple vector-borne pathogens. Climatic conditions, host behaviour, and vector distribution are likely contributing factors. Further research is needed, particularly on jackals and raccoon dogs, which remain understudied.

Keywords: *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., *Anaplasma* spp., *Borrelia* spp., *Rickettsia* spp.

INTRODUCTION

In recent decades, vector-borne diseases (VBDs) have played a significant role in increasing incidence of infectious diseases worldwide. These infections are transmitted by vectors such as ticks, fleas, mosquitoes, and lice (Bitam et al., 2010; Madison-Antenucci et al., 2020; Kolimenakis et al., 2021). The global spread of VBDs is related to multiple factors, including climate change, which is changing the distribution and seasonality of vectors; increased movement of animals between countries; and the spread of wildlife in suburban and urban environments (Ebani et al., 2023). This increases the movement of vectors into previously non-endemic areas and increases the risk of pathogen transmission to domestic animals and humans.

Members of the Canidae family, including red foxes (*Vulpes vulpes*), wolves (*Canis lupus*), golden jackals (*Canis aureus*), and raccoon dogs (*Nyctereutes procyonoides*), play an important role in the transmission of vector-borne pathogens (Duscher et al., 2015). Wild carnivores are increasingly found in urban and peri-urban areas. Animals such as the red fox have well adapted to living in urbanised landscapes and becoming more frequent across Europe (Battisti et al., 2020). Understanding the ecology and distribution of

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* Corresponding author. Email: indre.lipatova@vdu.lt

vector-borne pathogens in these wild canids is therefore essential for the development effective prevention and control strategies targeting both animal and human health.

The aim of this article was to synthesise available data on vector-borne pathogens in wild canids in Europe and to identify current knowledge gaps relevant for future research and surveillance.

MATERIAL AND METHODS

This review article summarises the available literature on vector-borne pathogens in wild canids. A total of 25 scientific publications were analysed, focusing on infections caused by *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., *Anaplasma* spp., *Borrelia* spp. and *Rickettsia* spp. in foxes, wolves, jackals and raccoon dogs in Europe.

The studies reviewed were conducted in various countries: four in Germany, two in Italy, Poland, Hungary and Spain each, and one in France, Bosnia and Herzegovina, Croatia, Austria, Romania, Iraq, Israel, Serbia, Portugal, Great Britain, Slovakia, Lithuania, and Norway each.

For each study, the following information was recorded: the author(s) and the year of publication, the Canidae species studied, the number and percentage of positive samples, the year(s) during which the samples were collected, and the country in wich the reaserch was conducted. The articles included in this review were published between 2010 and 2024.

RESULTS AND DISCUSSION

All 25 studies reviewed used polymerase chain reaction (PCR) for pathogen detection. The most frequently studied host species was the red fox, which was investigated in 18 out of 25 articles (Table 1). Wolves and jackals were each included in four studies, while racoon dogs were

Table 1. **Scientific articles on phatogens in different animals**

Host species	Pathogens	Prevalence	Year	Country	Author, year of publication
V. vulpes	*Hepatozoon* spp.	24.1% (46/191)	2007–2008	Croatia	Dežđek et al., 2010
V. vulpes	*B. microti*	69.2% (63/91)	2008–2010	Portugal	Cardoso et al., 2013
V. vulpes	*Anaplasma* spp.	7.7% (1/13)	2011–2012	Italy	Torina et al., 2013
	E. canis	30.7% (4/13)			
	Rickettsia spp.	0% (0/13)			
	B. microti	0% (0/13)			
V. vulpes	*B. microti*	50% (18/36)	2014	Austria	Duscher et al., 2014
	H. canis	58.3% (21/36)			
V. vulpes	*A. phagocytophilum*	8.2% (10/122)	2009	Germany	Härtwig et al., 2014
N. procyonoides	*A. phagocytophilum*	23.1% (3/13)			
V. vulpes	*Babesia* spp.	46.4% (121/261)	2009	Germany	Najm et al., 2014
V. vulpes	*B. cf. microti*	20.1% (81/404)	2011	Hungary	Farkas et al., 2015
V. vulpes	*Hepatozoon* spp.	38.6% (46/119)	2013–2014	Bosnia and Herzegovina	Hodžić et al., 2015
	Babesia spp.	32.7% (39/119)			
V. vulpes	*H. canis*	22.2% (92/415)	2013–2014	Hungary	Tolnai et al., 2015
	A. phagocytophilum	12.5% (52/415)			
V. vulpes	*B. annae*	14.6% (46/316)	No information	Great Britain	Bartley et al., 2016

Table 1. **(Continued)**

Host species	Pathogens	Prevalence	Year	Country	Author, year of publication
N. procyonoides	*Borrelia* spp.	25% (7/28)	2009–2011	Poland	Wodecka et al., 2016
V. vulpes	*Babesia* spp.	9.7% (29/300)	No information	Slovakia	Koneval et al., 2017
C. aureus	*Hepatozoon* spp.	69.6% (39/56)	2013–2015	Romania	Mitková et al., 2017
	Leishmania spp.	1.8% (1/56)			
C. lupus	*Leishmania* spp.	33.3% (34/102)	2008–2014	Spain	Oleaga et al., 2018
C. aureus	*Hepatozoon canis*	45.9% (50/109)	No information	Israel	Margalit Levi et al., 2018
	Babesia spp.	0% (0/109)			
V. vulpes	*Hepatozoon canis*	42.9% (9/21)			
	Babesia spp.	19.1% (4/21)			
C. aureus	*Babesia* spp.	4.2% (9/216)	2010–2013	Serbia	Sukara et al., 2018
	A. phagocytophilum	0.9% (2/216)			
V. vulpes	*Borrelia* spp.	16.7% (1/6)	2013–2016	Norway	Mysterud et al., 2019
C. aureus	*Hepatozoon* spp.	49.1% (27/55)	2008	Iraq	Otranto et al., 2019
	Babesia spp.	1.8% (1/55)			
V. vulpes	*Hepatozoon* spp.	47.3% (18/38)			
	Babesia spp.	21.1% (8/38)			
V. vulpes	*Anaplasma* spp.	48.4% (15/31)	2016–2018	Lithuania	Sakalauskas et al., 2019
	Rickettsia spp.	9.7% (3/31)			
	Borrelia spp.	25.8% (8/31)			
	Babesia spp.	64.5% (20/31)			
V. vulpes	*Babesia* spp.	82.8% (130/157)	2009–2017	Italy	Battisti et al., 2020
	Hepatozoon spp.	5.1% (8/157)			
C. lupus	*Babesia* spp.	39.4% (13/33)			
	Hepatozoon spp.	75.8% (25/33)			
C. lupus	*H. canis*	46% (127/276)	2006–2019	Germany	Hodžić et al., 2020
	A. phagocytophilum	0.7% (2/276)			
V. vulpes	*Hepatozoon* spp.	92.5% (86/93)	2008–2018	France	Medkour et al., 2020
	Leishmania spp.	15.1% (14/93)			
	Babesia spp.	3.2% (3/93)			
	Anaplasma spp.	2.2% (2/93)			
	Borrelia spp.	0% (0/93)			
	Rickettsia spp.	0% (0/93)			
V. vulpes	*Babesia* spp.	64% (57/89)	2011–2018	Spain	Ortuño et al., 2022
	Hepatozoon spp.	91% (81/89)			
	L. infantum	97.8% (87/89)			
N. procyonoides	*Borrelia* spp.	0.93% (1/107)	2021–2022	Germany	Klink et al., 2024
	Rickettsia spp.	0% (0/107)			
C. lupus	*B. canis*	18% (9/50)	2001–2020	Poland	Wymazał et al., 2024
	Anaplasma spp.	2% (1/50)			

examined in three studies. Four articles analysed more than one canid species: two studies investigated both foxes and jackals, one study included foxes and wolves, and one examined foxes and racoon dogs. Regarding pathogen diversity, 15 articles tested for more than one pathogen, whereas ten focused on a single phatogen. The largest number of the studies ($n = 4$) were conducted in Germany (Figure A). Italy, Hungary and Poland each contributed two studies, while Croatia, Austria, Bosnia and Herzegovina, Romania, Spain, Israel, Serbia, Iraq, France, Portugal, Great Britain, Slovakia, Lithuania and Norway were each represented by one study.

The largest study group was examined by Tolnai et al. (2015) in Hungary, in which 415 foxes were tested for *Hepatozoon canis* and *Anaplasma phagocytophilum.* The second largest group was analysed by Farkas et al. (2015) also in Hungary; 404 red foxes were tested for *Babesia cf. microti.* Another large study was done by Bartley et al. (2016) in Great Britain, in which 316 red foxes were tested for *Babesia annae.* In Slovakia, Koneval et al. (2017) tested 300 red foxes for *Babesia* spp. In addition, ten studies involved large sample sizes, ranging from 100 to 300 animals. These included five groups of red foxes, two groups of wolves, two groups of jackals, and one group of racoon dogs.

The smallest study group was reported by Mysterud et al. (2019) in Norwa, where only six red foxes were tested for *Borrelia* spp. The second smallest group was analysed by Torina et al. (2013) in Italy, who tested 13 red foxes for a broad range of pathogens, including *Anaplasma* spp., *Ehrlichia canis*, *Rickettsia* spp. and *Babesia microti.* Similarly, Härtwig et al. (2014) in Germany tested 13 racoon dogs for *A. phagocytophilum.* Another small group was conducted by Margalit Levi et al. (2018) in Israel, in which 21 foxes and larger group of golden jackals ($n = 109$) were tested for *Babesia* spp. and *H. canis. A* further study by Wodecka et al. (2016) in Pland analysed 28 racoon dags for *Borrelia* spp. In addition, nine other studies analysed sample sizes ranging from 30 to 100 animals, including five groups of red foxes and two groups of wolves and jackals each.

The most commonly studied pathogen was *Babesia* spp. (Table 1), which was tested in 16 out of 25 articles. In three of these studies, *Babesia* spp. was tested in two different host species. The second most frequently studied phatogen was *Hepatozoon* spp. It was tested in 11 articles, three of which also includes two different host species. *Anaplasma* spp. was investigated in eight articles, *Borrelia* spp. in five, *Leishmania* spp. and *Rickettsia* spp. in four, and *E. canis* in one article.

Babesia spp. is frequently detected, likely due to its strongly dependance on tick vectors, whose populations and infection rates have significantly increased in recent years (Jaenson et al., 2024). Canid species inhabit different habitats and therefore have different contact with vectors. For example, foxes have more frequent contact with small rodents, the main reservoirs of several tick-borne pathogens (Solano-Gallego et al., 2016). *Hepatozoon* spp. is widespread due to its atypical transmission rout. Unlike most tick-borne pathogens, *Hepatozoon* spp. is not transmitted by tick bite but rather through ingestion of infected ticks (Baneth, Allen, 2022). Canids often feed on prey such as rodents, which may themselves be infected or carry ticks, making these carnivores effective reservoir for *Hepatozoon* spp. (Thomas et al., 2024). *Leishmania* spp. is transmitted by sand flies (*Phlebotomus* spp.), which are very effective vectors. These insects are active in warm climates, which explains the high prevalence of *Leishmania* spp. in southern Europe (Sadlova et al., 2024). With climate warming and the expansion of sand fly, *Leishmania* spp. is now spreading further north into previously non-endemic areas (Ratzlaff et al., 2023).

Among canid species, the highest prevalence of *Hepatozoon* spp. was observed in red foxes, reaching 92.5% (86/93), followed by wolves at 75.8% (25/33) and jackals at 69.6% (39/56). The prevalence of *Babesia* spp. was also highest in foxes, at 82.8% (130/157), while lower rates were recorded in wolves at 39.4% (13/33) and jackals at 4.2% (9/216). For *Anaplasma* spp., the highest prevalence was detected in foxes at 48.4% (15/31), followed by racoon dogs at 23.1% (3/13), jackals at 0.9% (2/216), and wolves at 0.7% (2/276). *Leishmania* spp. was found in foxes with a prevalence of 97.8% (87/89). *Borrelia* spp. was detected in foxes at 25.8% (8/31) and in racoon dogs at 25.0% (7/28). *Rickettsia* spp. was found only in foxes, with a prevalence of 9.7% (3/31); in three other studies, it was not detected. *E. canis* was tested in a single study and was detected in foxes at 30.7% (4/13).

In 15 studies, two or more pathogens were tested. Among them, 11 research groups analysed two pathogens, while four groups investigated 3–6 pathogens per animal. Medkour et al. (2020) in France tested red foxes for *Hepatozoon* spp., *Leishmania* spp., *Babesia* spp., *Anaplasma* spp., *Borrelia* spp. and *Rickettsia* spp. (Table 1). The results showed that 92.5% (86/93) of foxes were positive for *Hepatozoon* spp., 15.1% (14/93) for *Leishmania* spp., 3.2% (3/93) for *Babesia* spp. and 2.2% (2/93) for *Anaplasma* spp. *Borrelia* spp. and *Rickettsia* spp. were not detected in this study. In Lithuania, Sakalauskas et al. (2019) tested red foxes for *Anaplasma* spp., *Rickettsia* spp., *Borrelia* spp. and *Babesia* spp. he prevalence was as follows: *Anaplasma* spp. – 48.4% (15/31), *Rickettsia* spp. – 9.7% (3/31), *Borrelia* spp. – 25.8% (8/31), and *Babesia* spp. – 64.5% (20/31). Torina et al. (2013) in Italy tested red foxes for *Anaplasma* spp.*,* *E. canis*, *Rickettsia* spp. and *B. microti.* They found *E. canis* in 30.7% (4/13) and *Anaplasma* spp. in 7.7% (1/13) of foxes. *Rickettsia* spp. and *B. microti* were not detected. Ortuna et al. (2022) in Spain tested foxes for *Babesia* spp., *Hepatozoon* spp. and *Leishmania infantum.* All three phatogens showed high infection rates: *Babesia* spp. – 64% (57/89), *Hepatozoon* spp. – 91% (81/89) and *L. infantum* – 97.8% (87/89).

Among the 11 studies that tested two pathogens per animal, five tested for *Babesia* spp. and *Hepatozoon* spp. In Austria, for example, Dusher et al. (2014) found *B. microti* in 50% (18/36) and *H. canis* in 58.3% (21/36) of foxes. Similarly, Hodžić et al. (2015) in Bosnia and Herzegovina found *Babesia* spp. in 32.7% (39/119) and *Hepatozoon* spp. in 38.6% (46/119) of foxes. A different pattern was observed by Margalit Levi et al. (2018) in Israel, where *Hepatozoon* spp. was detected in 42.9% (9/21) of foxes and 45.9% (50/109) of jackals, whereas *Babesia* spp. was not found in jackals and was present in 19.1% (4/21) of foxes. Battist et al. (2020) in Italy reported contrasting results between species: in foxes, the prevalence of *Babesia* spp. was 82.8% (130/157), much higher than *Hepatozoon* spp. at 5.1% (8/157). In contrast, in wolves, *Babesia* spp. was 39.4% (13/33), while *Hepatozoon* spp. was 75.8% (25/33).

Two out of 11 studies tested *Babesia* spp. and *Anaplasma* spp. In both cases, *Babesia* spp. prevalence was higher than that of *Anaplasma* spp. For example, Sukara et al. (2018) reported *A. phagocytophilum* in 0.9% (2/216) and *Babesia* spp. in 4.2% (9/216) of jackals. Similarly, Wymazał et al. (2024) found *Anaplasma* spp. in 2% (1/50) and *Babesia* spp. in 18% (9/50) of wolves.

Two additional studies tested *Hepatozoon* spp. and *Anaplasma* spp. *Hepatozoon* spp. showed higher prevalence in foxes and wolves (22.2% and 46%, respectively) than *Anaplasma* spp. (12.5% and 0.7%, respectively) (Tolnai et al., 2015; Hodžić et al., 2020). *Hepatozoon* spp. and *Leishmania* spp. were tested together in one study, where Mitková et al. (2017) found *Hepatozoon* spp. in 69.6% (39/56) and *Leishmania* spp. in 1.8% (1/56) of jackals. Finally, Klink et al. (2024) tested racoon dogs for *Borrelia* spp. and *Rickettsia* spp.; *Borrelia* spp. was detected at 0.9% (1/107) prevalence, while *Rickettsia* spp. was not detected.

The broadest diversity of pathogen species was detected in red foxes, including *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., *Anaplasma* spp., *Borrelia* spp., and *Rickettsia* spp. (Table 2). *Leishmania* spp. was detected in foxes at rates ranging from 15% up to 98%. *Hepatozoon* spp. prevalence ranged from 5.1% to 92%, while *Babesia* spp. was found in up to 82.8% of foxes. *Anaplasma* spp. was detected in up to 48.4%, *Borrelia* spp. in up to 25.8%, and *Rickettsia* spp. was identified in a single study at 9.7%. Foxes inhabit and move through environments where ticks are commonly found, such as dense

Table 2. **Prevalence of vector-borne pathogens across different wild carnivore species**

Species	*Babesia* spp.	*Hepatozoon* spp.	*Leishmania* spp.	*Anaplasma* spp.	*Borrelia* spp.	*Rickettsia* spp.
Vulpes vulpes	0–82.8%	5.1–92.5%	15–98%	0–48.4%	0–25.8%	0–9.7%
Canis lupus	20–39.4%	5.1–46%	33.3%	0–0.7%	–	–
Canis aureus	0–4.2%	0.9–70%	1.8%	0.9%	–	–
Nyctereutes procyonoides	–	–	–	23%	0.93–25%	0%

grasslands, forests, and scrubland. They are widespread and highly adaptable, occupying a range of habitats from natural forests to urban and peri-urban areas (Gil-Fernández et al., 2020). In addition, foxes frequently interact with small rodents, which serve as important reservoir hosts for various tick-borne pathogens (Krawczyk et al., 2020). These ecological and behavioural traits significantly increase the likelihood of foxes becoming carriers and potential reservoirs of tick-borne infections (Millán et al., 2016; Lesiczka et al., 2023). Although data on the prevalence of pathogens transmitted by ticks and other ectoparasites in canids are still limited, the knowledge gap is particularly evident for species other than red foxes, especially jackals and raccoon dogs.

In wolves, four pathogen species were found: *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., and *Anaplasma* spp. The highest prevalence was observed for *Hepatozoon* spp. (5.1–46%), followed by *Babesia* spp. (20–39.4%) and *Leishmania* spp. (33%). *Anaplasma* spp. was detected in only 0.7% of wolves. In golden jackals, the same four pathogens were detected. The highest prevalence was observed for *Hepatozoon* spp. (0.9–70%), while *Babesia* spp. reached up to 4.2%, *Leishmania* spp. up to 1.8%, and *Anaplasma* spp. up to 0.9%. In racoon dogs, only two pathogens were identified: *Anaplasma* spp. and *Borrelia* spp. *Borrelia* spp. prevalence ranged from 0.93% to 25%, and *Anaplasma* spp. was detected in up to 23% of individuals. *Rickettsia* spp. was not detected in racoon dogs.

To compare the prevalence of pathogens between countries, we selected three most commonly studied pathogens: *Babesia* spp., *Hepatozoon* spp., and *Anaplasma* spp. The highest prevalence of *Babesia* spp. was observed in Italy (82.8%), Portugal (69.2%), and Lithuania (64.5%), while the lowest prevalence was reported in France (3.2%) and Iraq (1.8%). Overall, *Babesia* spp. appeared to be more prevalent in Southern and Central Europe (Figure B). The highest prevalence of *Hepatozoon* spp. was found in France (92.5%) and Spain (91%), wheres lower rates were recorded in Croatia (24.1%) and Hungary (22.2%). This suggest that *Hepatozoon* spp. is more prevalent in Western Europe (Figure C). *Anaplasma* spp. showed the highest prevalence in Lithuania (48.4%) and Germany (46.4%), while the lowest prevalence was recorded in Serbia (0.9%) and France (2.2%). Overall, *Anaplasma* spp. appears to be more prevalent in Central Europe (Figure D). All three phatogens were reported in four countries: Germany, Italy, Hungary, and France. In Germany and Hungary, the prevalence were relatively similar: 0.7% to 46.4% in Germany and 12.5% to 22.2% in Hungary. In Italy, both *Babesia* spp. and *Hepatozoon* spp. showed high prevalence rates (89.7% and 75.8%, respectively), while *Anaplasma* spp. was comparatively low (7.7%). In France, *Hepatozoon* spp. had the highest prevalence (92.5%), whereas both *Babesia* spp. (3.2%) and *Anaplasma* spp. (2.2%) were detected at low levels.

The distribution of vector-borne pathogens varies between countries and is influenced by several ecological and climatic factors. Warmer regions facilitate the spread and reproduction of vectors such as sand flies and ticks, contributing to higher pathogen prevalence in these areas (Adepoju et al., 2023). In contrast, tick-borne pathogens such as *Babesia* spp., *Anaplasma* spp.,

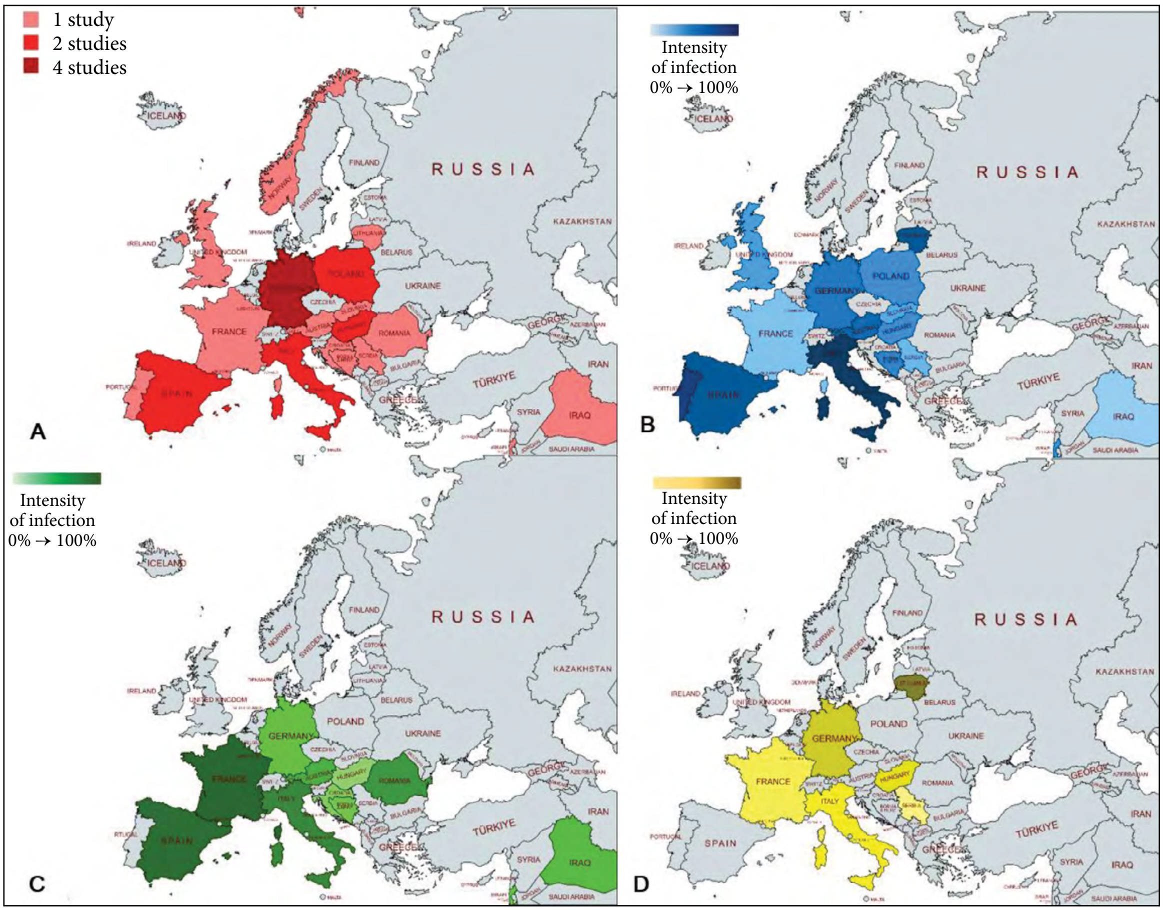

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Figure. Prevalence of three pathogens between the countries. A – a map showing studied countries and the number of articles from each country viewed in this study; B – a map showing *Babesia* spp. prevalence; C – a map showing *Hepatozoon* spp. prevalence; D – a map showing *Anaplasma* spp. prevalence

and *Borrelia* spp. are more prevalent in temperate climate zones (Duscher et al., 2014; Wodecka et al., 2016; Sakalauskas et al., 2019; Wymazał et al., 2024). In addition to climate, landscape composition – including the proportion of forests, grasslands, agricultural land, and urbanised areas – also affects vector and host distribution (Wilke et al., 2019). Furthermore, the abundance and distribution of wild canids vary across countries, influencing local pathogen dynamics (Leschnik et al., 2020).

CONCLUSIONS

This review summarises the prevalence of *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., *Anaplasma* spp., *Borrelia* spp., and *Rickettsia* spp. in wild canids (foxes, wolves, jackals, and raccoon dogs) in European countries between 2010 and 2024. The prevalence of these phatogens varies by host species and geographical region. Foxes were found to be infected with all six pathogens and have the highest infections rates compared to other canids.

Climate change contributes not only to the expansion of tick populations, but also to the increasing distribution of foxes. In parallel, urban expansion and growing human presence in natural environments have led to more frequent encounters between foxes and humans. If foxes serve as significant reservoir hosts, pathogen transmission may increase among wildlife, domestic animals, and potentially humans.

Geographically, these phatogens were detected in many European countries, with the highest reported prevalence observed in

Central and Southern Europe. However, these results may not fully reflect the actual situation, as further research is needed, particular in understudied canid species and regions lacking surveillance data on vector-borne pathogens in canines.

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Ugnė Medikaitė, Indrė Lipatova,
Algimantas Paulauskas

ŠUNINIŲ GYVŪNŲ (CANIDAE) VAIDMUO PLATINANT VEKTORIŲ PERNEŠAMUS PATOGENUS

Santrauka

Šios apžvalgos tikslas buvo apibendrinti turimą literatūrą apie *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., *Anaplasma* spp., *Borrelia* spp. ir *Rickettsia* spp. paplitimą ir pasiskirstymą tarp laukinių šuninių gyvūnų (lapių, vilkų, šakalų ir usūrinių šunų) visoje Europoje 2010–2024 metais. Iš viso išanalizuoti 25 publikuoti tyrimai. Buvo lyginami duomenys apie šeimininko rūšis, šalį, imties dydį, aptikimo metodus ir patogenų paplitimą. Visi šeši patogenai buvo aptikti lapėse, kurios, palyginti su kitais šuniniais gyvūnais, buvo labiausiai paplitusios. Dažniausiai buvo randami *Hepatozoon* spp., *Babesia* spp. ir *Anaplasma* spp. patogenai. Patogenų paplitimas priklausė nuo šeimininko rūšies ir geografinės vietos, didesnis buvo nustatytas Vidurio ir Pietų Europoje. Paaiškėjo, kad lapės yra potencialūs pagrindiniai daugelio vektorių platinamų patogenų šaltiniai. Reikšmingi veiksniai yra klimato sąlygos, šeimininko elgesys ir vektorių pasiskirstymas. Šakalai ir usūriniai šunys vis dar nepakankamai ištirti, todėl būtina atlikti daugiau tyrimų.

Raktažodžiai: *Babesia* spp., *Hepatozoon* spp., *Leishmania* spp., *Anaplasma* spp., *Borrelia* spp., *Rickettsia* spp.