

Pathogen screening in the red fox (*Vulpes vulpes*) from Lithuania

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The aim of this study was to screen free-ranging red foxes from Lithuania for the presence of different vector-borne pathogens. A total of 31 red foxes from three districts of Lithuania were molecularly tested for the presence of pathogens. Five different pathogens were detected in 83.9% of red foxes: *Anaplasma* spp., *Bartonella* spp., *Rickettsia* spp., *Borrellia* spp. and *Babesia* spp. The presence of *Mycoplasma* spp. and *Dirofilaria* spp. was not detected in our study.

Keywords: *Vulpes vulpes*, *Anaplasma* spp., *Bartonella* spp., *Rickettsia* spp., *Borrellia* spp., *Babesia* spp., *Mycoplasma* spp., *Dirofilaria* spp.

INTRODUCTION

The red fox (*Vulpes vulpes*) is the most widely distributed of all wild canids, with a natural range from the deserts to the Arctic tundra (Schipper et al., 2008; Edwards et al., 2012). The red fox is adapted to different environments and can easily survive in urban areas (Teacher et al., 2011; Scott et al., 2014). Living in close proximity to people may pose a risk in the case of the transmission of zoonoses and veterinary diseases (Truyen et al., 1998; Hodžić et al., 2015; Koneval et al., 2017; Víchová et al., 2018). Determining the impact of wildlife for pathogen transmission is important for epidemiological studies.

In the past, red foxes were most commonly associated with the epidemiological cycle of rabies (Chautan et al., 2000; Vos, 2003; Zienius et al., 2007). Also, several studies showed that red foxes are a reservoir for zoonotic parasites, such as *Echinococcus multilocularis*, *Trichinella* spp., and

Toxocara canis (Saeed et al., 2006; Bružinskaitė-Schmidhalter et al., 2012; Franssen et al., 2014; Karamon et al., 2018). Recent studies have revealed that in Europe, red foxes are infected with vector-borne pathogens (Hodžić et al., 2015; Koneval et al., 2017; Hodžić et al., 2018).

A long-term rabies persistence period in the red fox populations was reported in Lithuania (Zienius et al., 2007). Other studies investigated zoonotic helminths of red foxes (Bružinskaitė-Schmidhalter et al., 2012; Janulaitis et al., 2014). However, the real role of the red foxes as a source of different pathogens is unclear. Therefore, the principal aim of this study was to screen free-ranging red foxes from Lithuania for the presence of different vector-borne pathogens.

MATERIALS AND METHODS

Collection of samples

A total of 31 red foxes from three districts of Lithuania were included in the present study (Fig. 1). From 2016 to 2018, carcasses of red foxes

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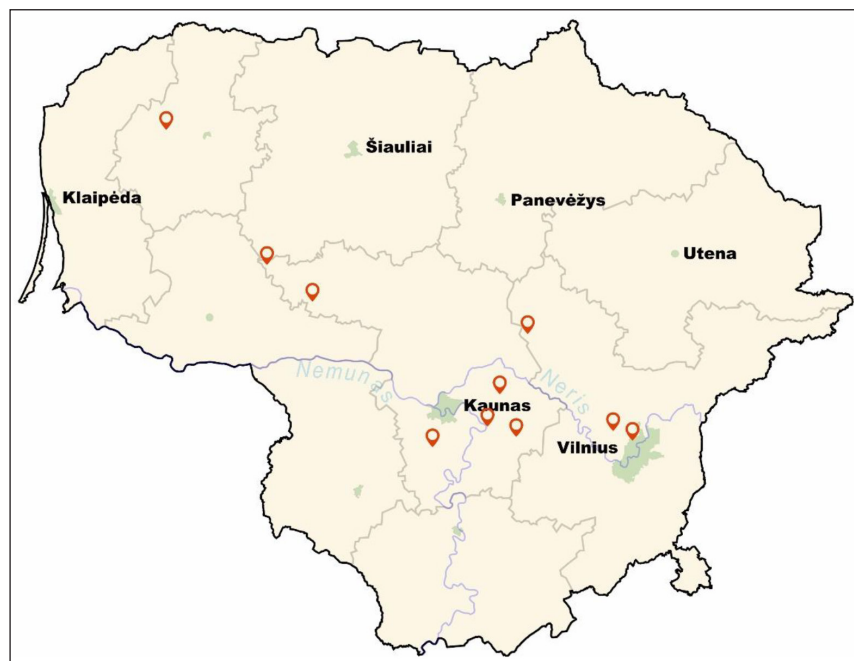


Fig. 1. The map of localities where red foxes were collected

were collected in collaboration with hunters. The data on sex, the area of origin, and the hunting date were recorded for each individual red fox (Table 1). During necropsy, spleen samples were collected and frozen at -20°C until DNA extraction.

DNA extraction, PCR amplification

DNA was isolated using the GeneJET Genomic DNA Purification Kit (Thermo Fisher Scientific, Lithuania) according to the manufacturer's instructions and stored at -20°C for further analyses.

All DNA samples were screened for the presence of *Anaplasma* spp., *Bartonella* spp., *Rickettsia* spp., *Borrelia* spp., and *Babesia* spp. using multiplex real time-PCR assay. Primer sequences and target gene used in this study are presented in Table 2. RT-PCR reactions

were done in total volume of 15 μl consisting of 100 ng of extracted DNA, (1x) SensiMix™ II Probe No-ROX (Bioline), 1 μM of each primer, and 0.5 μM of each probe. Cycling reactions started with an initial activation step of 95°C for 10 min followed by 45 cycles of 95°C for 20 s, 60°C for 60 s (for *Anaplasma*, *Borrelia*, and *Babesia*) and 50°C for 60 s (for *Bartonella* and *Rickettsia*), and 72°C for 20 s. Cycling reactions were carried out using a Rotor Gene 6000 (Corbett Research, Australia).

Mycoplasma spp. and *Dirofilaria* spp. were detected using conventional PCR method. For *Mycoplasma* spp. were amplified 16S RNA region using 322s and 938as primers according Varanat et al. (2011). For filarial screening, pan-filarial primers (DIDR-F1, DIDR-R1) were used that amplify fragments of different length of the internal transcribed spacer region 2 (ITS2) of the ribosomal DNA from six different filarioid species (*Dirofilaria repens*, *D. immitis*, *Acanthocheilonema reconditum*, *A. dracunculoides*, *Brugia pahangi* and *B. malayi*). The PCR were conducted as described by Rishniw et al. (2006). All amplification products were electrophoresed on a 1.5% agarose gel and visualized under UV light after staining with ethidium bromide.

Table 1. Sex of red foxes and their collection areas

	Vilnius	Kaunas	Telšiai	Total
♂	3	12	0	15
♀	3	12	1	16
Total	6	24	1	31

Table 2. Primers used for the amplification of DNA of different pathogens

Pathogen	Primer sequences	Target gene	Length of amplicons (bp) (reference)
<i>Anaplasma</i> spp.	5'-GGACAACATGCTTGTAGCTATGGAA-GG-3' 5'-CCTTGGTCTTGAAGCGCTCGTA-3' 5'-TCTCAAGCTCAACCCTGGCACCAC-CA-3' VIC/BHQ1	<i>msp2</i>	98 (Razanske et al., 2019)
<i>Bartonella</i> spp.	5'-AGTTGCAAATGACAACATATGCGG-3' 5'-AAGGCTTCTGTTGCCAGGYG-3' 5'-ACCCCGCTTAAACCTGCGACGGTT-3' HEX/BHQ1	<i>ssrA</i>	124 (Mardosaitė-Busaitienė et al., 2019)
<i>Rickettsia</i> spp.	5'-TGCMGAYCATGAGCACAATGCTTC-3' 5'-CCCAAAGTGAKGCAATACCCGT-3' 5'-TGCCGGCTCATCYGGAGCTAACCC-3' FAM/BHQ1	<i>gltA</i>	338 (modified from Biernat et al., 2016)
<i>Borrelia</i> spp.	5'-GCTTCAGCCTGGCCATAAATAG-3' 5'-AGCGAGTCTTAAAAGGGCGATT-TAGT-3' 5'-TCACTCGGSTTCGGGTCTACCA-CATCT-3' FAM/BHQ1	<i>23S rRNA</i>	77 (designed in this study)
<i>Babesia</i> spp.	5'-GACTCCTTCAGCACCTTGAGA-3' 5'-GACCCCTTCAGGAGCTTGAGA-3' 5'-CATGCACCACCACCAWAGAATCA-3' 5'-TGACGGAAGGGCACCACCAGGCGT-3' ROX/BHQ2	<i>18S rRNA</i>	214 (Razanske et al., 2019)
<i>Mycoplasma</i> spp.	5'-GCCCATATTCCTACGGGAA-GCAGCAGT-3' 5'-CTCCACCACTTGTTTCAGGTCCC-CGTC-3'	<i>16S rRNA</i>	600 (Varanat et al., 2011)
<i>Dirofilaria</i> sp.	5'-AGTGCGAATTGCAGACGCATTGAG-3' 5'-AGCGGGTAATCACGACTGAGTTGA-3'	<i>5.8S-ITS2-28S</i>	484–542 (Rishniw et al., 2006)

Statistical analysis

The prevalence of different pathogen infection analysis was performed using Microsoft excel software. The InteractiveVenn tool was used to create the Venn diagram and calculate co-infections (Heberle et al., 2015).

RESULTS AND DISCUSSION

In general, vector-borne pathogens were detected in 83.9% (26/31) of red foxes. Five different pathogens were detected: *Anaplasma* spp., *Bartonella* spp., *Rickettsia* spp., *Borrelia* spp., and *Babesia* spp. (Table 3).

The most prevalent pathogen in red foxes from Lithuania was *Babesia* spp. (20/31, 64.5%). This pathogen was detected in all studied areas (Table 3). Females (60.0%; 12/20) were more infected with *Babesia* spp. than males (40.0%; 8/20). A number of studies reported that red foxes were infected with such *Babesia* spp. as *B. canis*, *B. venatorum*, *B. vulpes* (synonyms: *B. microti*, *B. cf. microti*, *B. annae*) (Karbowski et al., 2010; Cardoso et al., 2013; Duscher et al., 2014; Najm et al., 2014; Farkas et al., 2015; Hodžić et al., 2015; Koneval et al., 2017; Hodžić et al., 2018; Baneth et al., 2019). Ticks are the main vector of this blood parasite. Several studies show

Table 3. Infection with different pathogens in red foxes from Lithuania

	<i>Anaplasma</i> spp.		<i>Bartonella</i> spp.		<i>Rickettsia</i> spp.		<i>Borrellia</i> spp.		<i>Babesia</i> spp.	
	♂	♀	♂	♀	♂	♀	♂	♀	♂	♀
Vilnius	2/3	2/3	0/3	3/3	0/3	0/3	0/3	3/3	3/3	3/3
Kaunas	6/12	4/12	2/12	3/12	1/12	1/12	3/12	1/12	5/12	8/12
Telšiai	–	1/1	–	0/1	–	1/1	–	1/1	–	1/1
Total	8/15	7/16	2/15	6/16	1/15	2/16	3/15	5/16	8/15	12/16

Numbers given in the table indicate the number of red foxes infected with pathogens/number of red foxes tested.

the presence of *Babesia* spp. in ticks (*Ixodes hexagonus*, *I. ricinus*) collected from red foxes (Najm et al., 2014; Checa et al., 2018).

Another tick-transmitted bacteria detected in our study was *Anaplasma* spp. A total 48.4% (15/31) of the tested samples showed positive results. This pathogen was also detected in all the studied areas (Table 3). Infection of red foxes with *A. phagocytophilum* was reported from Poland (Karbowiak et al., 2009), Italy (Ebani et al., 2011), Germany (Härtwig et al., 2014), Croatia (Beck et al., 2014), Netherlands (Jahfari et al., 2014), Hungary (Tolnai et al., 2015), Romania (Dumitrache et al., 2015b), Switzerland (Hofmann-Lehmann et al., 2016), and Austria (Hodžić et al., 2018). *A. ovis* was reported in red foxes from Sicily (Italy) (Torina et al., 2013); *A. bovis* in Croatia (Beck et al., 2014); *A. platys* in Portugal (Cardoso et al., 2015). *A. phagocytophilum* has also been detected in *I. ricinus* ticks collected from red foxes (Dumitrache et al., 2015a; Vichová et al., 2018). Moreover, Torina et al. (2013) detected *A. phagocytophilum*, *A. ovis*, and *A. marginale* in fleas (*Xenopsylla cheopis*, *Ctenocephalides canis*) collected from red foxes.

Bartonella spp. are distributed in wild carnivores (Gerrikagoitia et al., 2012; Bai et al., 2016). Red foxes tested in this study were also infected with *Bartonella* spp. (25.8%; 8/31). These results are consistent with findings from other countries. There are some reports that infected red foxes carried *B. rochalimae*, *B. v. berkhoffii*, *B. clarridgeiae* (Henn et al., 2009; Kaewmongkol et al., 2011; Gerrikagoitia et al., 2012; Bai et al., 2016; Hodžić et al., 2018). Ectoparasites, such as fleas and ticks, play a role in the transmission of *Bar-*

tonella species (Chomel et al., 2009). *B. rochalimae* was found in *Pulex irritans* fleas from red foxes in Spain (Márquez et al., 2009); *B. henselae* and *B. clarridgeiae* were detected in *Ctenocephalides felis* fleas from red foxes in Australia (Kaewmongkol et al., 2011). *Bartonella* spp. were found in fleas (*Chaetopsylla globiceps*, *P. irritans*, *Ctenocephalides assimilis*) collected from red foxes in Slovakia (Vichová et al., 2018). The authors performed the obtained sequence analysis that showed identity or similarity to *B. rochalimae* and *B. taylorii* (Vichová et al., 2018).

Infection with Lyme diseases pathogen *Borrellia* spp. was also found in studied red foxes from Lithuania (25.8% (8/31)). Previous studies reported that red foxes were infected with *B. burgdorferi* sensu lato (Isogai et al., 1994; Heidrich et al., 1999; Dumitrache et al., 2015b; Lledó et al., 2016; Mysterud et al., 2019). Data on the diversity of *B. burgdorferi* sl in red foxes present four species *B. burgdorferi* sensu stricto, *B. afzelii*, *B. lusitaniae*, and *B. garinii* (Isogai et al., 1994; Dumitrache et al., 2015b; Sukara et al., 2019). *B. burgdorferi* sl has also been detected in *I. ricinus* and *I. persulcatus* ticks collected from red foxes (Isogai et al., 1994; Dumitrache et al., 2015a).

The prevalence of *Rickettsia* spp. infection detected in the present study is of the lowest level (9.7%; 3/31). Other authors confirmed in serological studies that foxes were exposed to *R. typhi*, *R. slovaca*, *R. conorii* and *R. massiliae/Bar29* (Lledó et al., 2016; Ortuño et al., 2018). *R. helvetica* was detected in foxes from Switzerland (Hofmann-Lehmann et al., 2016). Ortuño et al. (2018) reported that *Rhipicephalus sanguineus complex* ticks collected from red

foxes were infected with *R. massiliae*, *R. aeschlimannii*, and *R. slovaca* (Ortuño et al., 2018). In France, arthropods collected from red foxes showed *Rickettsia*-positive results. Ticks (*Rhipicephalus turanicus*) were found to be infected with *R. massiliae* and fleas (*Archaeopsylla erinacei*) collected in the study contained *R. felis* (Marié et al., 2012). Also, *R. felis* was detected in fleas (*Ctenocephalides felis*) from red foxes in Sicily, Italy (Torina et al., 2013). *R. massiliae* DNA was detected in *Rh. sanguineus* ticks collected from a fox in Sardinia, Italy (Chisu et al., 2017). Moreover, Víchová et al. (2018) reported that fleas (*Archaeopsylla erinacei*) and ticks (*Ixodes ricinus*, *Ixodes hexagonus*, *Haemaphysalis concinna*) removed from red foxes in Slovakia were infected with *Rickettsia* spp. (Víchová et al., 2018).

Mycoplasma is a genus of haemotropic, self-replicating bacteria (Messick 2004). Most of them are responsible for a variety of diseases in humans, animals, insects, and plants (Sumithra et al., 2013). There is a lack of information about mycoplasma in wild animals. Moreover, only a few studies report the occurrence of mycoplasmas in red foxes (Kanamoto et al., 1981; Sasaki et al., 2008; Koneval et al., 2017; Millán et al., 2018). *Mycoplasma* spp. was not detected in any of the tested red fox spleen samples in this study. However, in a study in Slovakia, out of 300 samples of red foxes tested, *Mycoplasma* spp. bacteria was detected in 13 (4.3%) (Koneval et al., 2017). Also, out of 12 red foxes, only one (0.83%) was positive for *M. haemocanis* in Japan (Sasaki et al., 2008). A study in Spain showed 2.4% (1/41) infection of *Mycoplasma* spp. in red foxes (Millán et al., 2018). Considering that studies from other countries have a very low infection rate of *Mycoplasma* spp. in red foxes, future screening of this pathogen is required with a largest sampling site in Lithuania. Also, ectoparasites (ticks, fleas) collected from red foxes in Slovakia were tested for the presence of *Mycoplasma* spp. but the infection was not detected (Víchová et al., 2018).

Dirofilariasis is recognized as a zoonosis spreading across Europe (Genchi et al., 2009;

Genchi et al., 2011; Simón et al., 2012). A previous study showed that *D. repens* is a zoonotic parasite in Lithuania (Sabūnas et al., 2019a). In Lithuania, nine human cases of *D. repens* during the period of 2011–2018 and the prevalence of *D. repens* among shelter dogs have been reported. Furthermore, recently *D. immitis* was found in an imported dog in Lithuania (Sabūnas et al., 2019b). Some researchers consider that free-living carnivores such as red foxes may act as a natural reservoir of zoonotic filariasis (Magi et al., 2008). Seeing that, in this study we analysed the spleen samples of red foxes from Lithuania for filarial infection in order to investigate their role as a potential wildlife reservoir of dirofilariasis. Of all tested foxes, none were positive for filarial parasites. However, *D. repens* infection in red foxes has been recorded in Italy (Marconcini et al., 1996; Magi et al., 2007), Slovakia (Hurníková et al., 2012), Serbia (Ćirović et al., 2014), and Romania (Ionică et al., 2017). Besides, heartworm (*D. immitis*) infection was found in red foxes in Italy (Marconcini et al., 1996; Magi et al., 2007), Spain (Mañas et al., 2005), Serbia (Penezić et al., 2014), Hungary (Tolnai et al., 2014), and Romania (Ionică et al., 2017). Otherwise, there are reports from other researchers that filariasis was not detected in red foxes (Hodžić et al., 2015; Härtwig et al., 2016; Hodžić et al., 2018). Considering that the distribution of filariasis in Europe is continuously spreading (Genchi et al., 2009; Genchi et al., 2011; Simón et al., 2012), future screening for filariasis in wildlife carnivores in Lithuania is required.

Majority of red foxes (77.4%; 24/31) were infected with more than one parasite species. Coinfections with two to four different pathogen species were observed (Fig. 2). Coinfection with two different pathogens were detected in 14 red foxes: one fox was infected with *Babesia* spp. and *Borrelia* spp.; one fox was infected with *Babesia* spp. and *Rickettsia* spp.; three foxes were infected with *Anaplasma* spp. and *Borrelia* spp.; three foxes were infected with *Babesia* spp. and *Bartonella* spp.; six foxes were infected with *Anaplasma* spp. and *Babesia* spp. Coinfection with three different pathogens

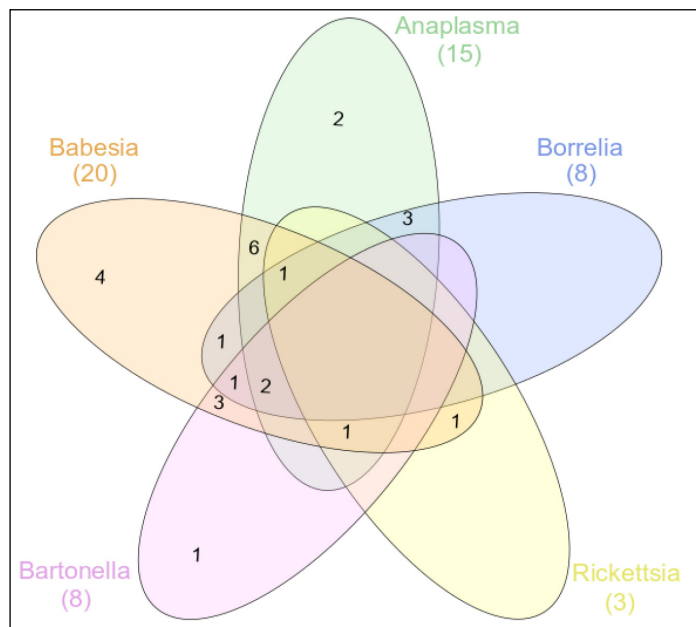


Fig. 2. Venn diagram describing coinfection of red foxes from Lithuania with five different pathogens

(*Babesia* spp., *Borrelia* spp. and *Bartonella* spp.) was detected in one red fox. Coinfection with four different pathogens were detected in four red foxes: one fox was infected with *Babesia* spp., *Anaplasma* spp., *Borrelia* spp. and *Rickettsia* spp.; one fox was infected with *Babe-*

sia spp., *Anaplasma* spp., *Rickettsia* spp. and *Bartonella* spp.; two foxes were infected with *Babesia* spp., *Anaplasma* spp., *Borrelia* spp. and *Bartonella* spp.

The overall presence of vector-borne pathogens in red foxes in Europe is shown in Table 4.

Table 4. Review of vector-borne pathogens in European countries

Pathogen	Country	Presence in Lithuania	Reference
		fox	this study;
<i>Babesia</i> sp.	Poland		Karbowiak et al., 2010
	Slovakia		Koneval et al., 2017
		dog	Paulauskas et al., 2014
<i>B. canis</i>	Portugal		Cardoso et al., 2013
	Bosnia and Herzegovina		Hodžić et al., 2015
	Austria		Hodžić et al., 2018
	Slovakia		Koneval et al., 2017
<i>B. vulpes</i> (synonyms: <i>B. microti</i> , <i>B. cf.</i> <i>microti</i> , <i>B. an-</i> <i>nae</i> , <i>Theileria</i> <i>anna</i>)	Austria		Duscher et al., 2014; Hodžić et al., 2018
	Portugal		Cardoso et al., 2013
	Hungary		Farkas et al., 2015
	Bosnia and Herzegovina		Hodžić et al., 2015
	Germany		Najm et al., 2014
	Croatia		Dezdek et al., 2010
	Great Britain		Bartley et al., 2013
Italy		Zanet et al., 2014	
<i>B. venatorum</i>	Germany		Najm et al., 2014

Table 4. (Continued)

Pathogen	Country	Presence in Lithuania	Reference
<i>Hepatozoon canis</i>	Austria		Duscher et al., 2014; Hodžić et al., 2018
	Croatia		Dezdek et al., 2010
	Bosnia and Herzegovina		Hodžić et al., 2015
	Hungary		Tolnai et al., 2015
	Slovakia		Majláthová et al., 2007
	Poland		Karbowiak et al., 2010
<i>Anaplasma phagocytophilum</i>		fox, dog	this study; Tamoliūnaitė et al., 2019
	Austria		Hodžić et al., 2018
	Poland		Karbowiak et al., 2009
	Italy		Ebani et al., 2011
	Germany		Härtwig et al., 2014
	Croatia		Beck et al., 2014
	Netherlands		Jahfari et al., 2014
	Hungary		Tolnai et al., 2015
	Romania		Dumitrache et al., 2015b
Switzerland		Hofmann-Lehmann et al., 2016	
<i>A. ovis</i>	Italy		Torina et al., 2013
<i>A. bovis</i>	Croatia		Beck et al., 2014
<i>A. platys</i>	Portugal		Cardoso et al., 2015
Candidatus <i>Neoehrlichia</i> sp.	Austria		Hodžić et al., 2018
	Serbia		Sukara et al., 2019
<i>Ehrlichia canis</i>	Italy		Torina et al., 2013
<i>Bartonella</i> spp.		fox	this study
<i>B. rochalimae</i>	Austria		Hodžić et al., 2018
	France		Henn et al., 2009
	Spain		Gerrikagoitia et al., 2012
<i>Toxoplasma gondii</i>	Poland		Karbowiak et al., 2010
<i>Borrelia</i> spp.		fox, dog	this study; Tamoliūnaitė et al., 2019
<i>B. burgdorferi</i> s.l.	Romania		(Dumitrache et al., 2015b)
	Germany		Heidrich et al., 1999
	Norway		Mysterud et al., 2019
<i>B. burgdorferi</i> s.s., <i>B. lusitaniae</i> , <i>B. garinii</i>	Serbia		Sukara et al., 2019
<i>Rickettsia</i> spp.		fox	this study
<i>R. helvetica</i>	Switzerland		Hofmann-Lehmann et al., 2016
<i>R. typhi</i>	Spain		Lledó et al., 2016

Table 4. (Continued)

Pathogen	Country	Presence in Lithuania	Reference
<i>R. slovaca</i>	Spain		Lledó et al., 2016
<i>R. massiliae/Bar29</i>	Spain		Ortuño et al., 2018
<i>R. conorii</i>	Spain		Ortuño et al., 2018
<i>Mycoplasma</i> spp.	Slovakia		Koneval et al., 2017
	Spain		Millán et al., 2018
<i>M. haemofelis</i> , <i>M. haemocanis</i>	Slovakia		Koneval et al., 2017
<i>Dirofilaria repens</i>		dog	Tamoliūnaitė et al., 2019; Sabūnas et al., 2019a
	Italy		Marconcini et al., 1996; Magi et al., 2007
	Slovakia		Hurníková et al., 2012
	Serbia		Ćirović et al., 2014
	Romania		Ionică et al., 2017
<i>D. immitis</i>		imported dog	Sabūnas et al., 2019b
	Italy		Marconcini et al., 1996; Magi et al., 2007
	Hungary		Tolnai et al., 2014
	Serbia		Penezić et al., 2014
	Romania		Ionică et al., 2017
<i>Dipetabnema dracunculoides</i>	Italy		Marconcini et al., 1996
	Italy		Marconcini et al., 1996
<i>Acanthocheilonema reconditum</i>	Romania		Ionică et al., 2017

All studies point to the importance of red foxes as a reservoir of various vector-borne pathogens. Some of them were not detected in this study. However, previous studies conducted in Lithuania showed the presence of *Anaplasma* spp., *Babesia* spp., and *Dirofilaria* sp. in dogs (Paulauskas et al., 2014; Sabūnas et al., 2019a; Sabūnas et al., 2019b; Tamoliūnaitė et al., 2019).

CONCLUSIONS

Our results demonstrate that vector-borne pathogens are widespread among red foxes in Lithuania. To our knowledge, this is the first

report on the detection of infection with *Anaplasma* spp., *Bartonella* spp., *Rickettsia* spp., *Borrelia* spp. and *Babesia* spp. in red foxes from Lithuania. Further studies are needed to determine the prevalence and distribution of these vector-borne pathogens in foxes and other carnivores, and their ectoparasites. *Mycoplasma* spp. and filaroid parasites were not detected in red foxes in our study. Further studies of mycoplasma and filariasis in wildlife carnivores in Lithuania are required.

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RUDŪJŲ LAPIŲ (*Vulpes vulpes*) UŽSIKRĖTĪMAS PATOGENAIS LIETUVOJE

Santrauka

Šio tyrimo tikslas buvo patikrinti laisvai gyvenančių rudųjų lapių užsikrėtimą skirtingais vektorių pernešamais patogenais Lietuvoje. Iš viso molekuliniais metodais ištirta 31 lapė iš trijų Lietuvos apskričių. Nustatyti 5 skirtingų šeimų patogenai 83,9 % tirtų lapių: *Anaplasma* spp., *Bartonella* spp., *Rickettsia* spp., *Borrelia* spp. ir *Babesia* spp. Šio tyrimo metu *Mycoplasma* spp. ir *Dirofilaria* spp. lapėse neaptikta.

Raktažodžiai: *Vulpes vulpes*, *Anaplasma* spp., *Bartonella* spp., *Rickettsia* spp., *Borrelia* spp., *Babesia* spp., *Mycoplasma* spp., *Dirofilaria* spp.