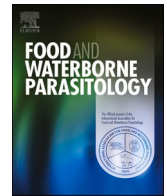


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## A review of *Trichinella* species infection in wild animals in Romania

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### ABSTRACT

Nematodes of the genus *Trichinella* are important zoonotic parasites present throughout Romania. This study aimed to assess the status of *Trichinella* species in wild animals in Romania over the past 30 years. A literature review of original studies concerning the only two species (out of the four in Europe) of *Trichinella* (*T. spiralis* and *T. britovi*) confirmed in wildlife from Romania was conducted and corroborated with the results of our original research concerning the topic. This review article has shown that, in Romania, European minks were infected with *T. spiralis*, while wolves, European wild cats, Eurasian lynx, golden jackals, stone marten, and European badgers were infected with *T. britovi*, respectively. Both *Trichinella* species have been identified in foxes, bears, wild boars, and ermines, but mixed infections have been found only in European polecats. *Trichinella* infection is still significantly present in Romania, infecting several wild omnivorous and carnivorous species in an equal manner, with different prevalence rates over the years. Regarding the spatial distribution of *T. spiralis* and *T. britovi* in Romania, both species can be found all over the country, but in wild animals, *T. britovi* is the most prevalent.

### 1. Introduction

Romania is a southeastern European country located in the north of the Balkan Peninsula. The Country is characterized by a temperate-continental climate of transitional type, with four clearly defined seasons (Trușcă and Alecu, 2005). Romania's Carpathic-Danubian-Pontic geography is defined by the Carpathian Mountains, the Black Sea, the Danube river, and its Delta. These units are in a nearly balanced combination with the hills and plains, determined by the step-like arrangement of the relief (Ilieș et al., 2017). Due to the forested mountains, wild animals are found in large numbers and show high diversity (Tănase et al., 2019). Many wild omnivorous and carnivorous species can host *Trichinella* species in Romania, thus maintaining the parasite's sylvatic life cycle (Boros et al., 2020).

Nematodes of the genus *Trichinella* are zoonotic parasites, being among the most widespread parasites in domestic and wild omnivores and predatory animals (Campbell, 1988; Pozio et al., 2009; Șuteu and Cozma, 2012). Rodents can act as a source of infection

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with *Trichinella* spp. for domestic and wild animals (Pozio and Zarlenga, 2005). The infection develops after the ingestion of raw meat, harboring the infective larvae (Pozio, 2007).

In Romania, the first information regarding trichinellosis dates back to 1866, when the supreme medical authority introduced the control of all slaughtered pigs in the country, but without any infections identified. In 1868, Schreiber had diagnosed the first case of human trichinellosis in Colțea hospital in Bucharest. In the same year, the first case of swine trichinellosis was confirmed in the southeastern part of the Country (Lupu and Cironeanu, 1960). In 1913, the use of trichinelloscopy was officially introduced in all slaughterhouses from Bucharest. Afterwards, new laws and regulations have been implemented to help reduce the number of human infections (Cironeanu, 1961).

In Romania, a priority epidemiological study on *Trichinella* spp. in domestic and wildlife hosts was conducted in the year 1960 with the use of trichinoscopy (Lupașcu et al., 1970). Since then, the knowledge regarding *Trichinella* spp. infections has significantly improved, due to the introduction of the artificial digestion method in the 1990s. This method was used initially in parallel with trichinoscopy, whereas later studies focused on the use of artificial digestion. The risk of *Trichinella* infection still remains a concern in Romania, because of local eating habits and customs (Blaga et al., 2007). Most human cases are caused by consuming undercooked meat of pigs infected with *T. spiralis* (Blaga et al., 2007). Additionally, wild boar meat consumed in several local dishes, sometimes infected with *T. britovi*, might represent another source of infestation for the local human population (Blaga et al., 2009a; Blaga et al., 2009b). According to the International Commission on Trichinellosis, Romania accounted for most cases of human trichinellosis reported worldwide in 2004 (Neghină et al., 2010a). Furthermore, an increase in the incidence of trichinellosis in Romania has been observed since the beginning of the 21st century. After the fall of communism in 1989, the annual incidence increased from 0.1 to 4.1 cases per 100,000 inhabitants (until 1989) to 6.2 cases per 100,000 inhabitants, with a range of 2–15.9 per 100,000 inhabitants between 1990 and 2007 (Neghină et al., 2009; Neghină et al., 2010b). In a more recent study from 2018, among 1347 blood donors from Timiș county, aged 18–63 years, *T. spiralis* IgG antibodies were detected only in 2.0%. However, with further development and implementation of sanitary education programs for pig farmers and meat consumers, the number of human infections is expected to further decrease in the future (Pavel et al., 2022).

The present review of studies conducted between 1991 and 2021 aimed to assess the presence of *T. spiralis* and *T. britovi* (the only two species currently present in Romania) in Romania over the past 30 years.

## 2. Prevalence of *Trichinella* spp. infections in wild animals in Romania

One of the earliest studies aiming to broaden the epidemiological knowledge on *Trichinella* spp. in Romania, was conducted in 1991 in bears (*Ursus arctos*), wolves (*Canis lupus*), foxes (*Vulpes vulpes*), wild cats (*Felis silvestris*), badgers (*Meles meles*), wild boars (*Sus scrofa*), and polecats (*Mustela putorius*) (Tables 1, 2, 3, 4; Figs. 1, 2, 3) (Nesterov et al., 1991). A further study was conducted between 1991 and 1994 in a restricted area of the Carpathian Mountains (Jiu valley), in red foxes and wild boars (Table 2, Table 3, Fig. 1, Fig. 2) (Cristea and Șuteu, 1996), indicating that these animal species play a limited role in the sylvatic cycle in that area. Afterwards, several studies focused on the detection of *Trichinella* spp. infection in wild animals from different regions of Romania. Between 1992 and 1997, wild boars and bears from Transylvania were subjected to larvae detection methods and the results are provided in Tables 1 and 2, and in Fig. 1, respectively (Gherman, 1998). The low prevalence rates detected in wild boars compared to bears show that, in the

**Table 1**  
*Trichinella* spp. infections in bears (*Ursus arctos*) from Romania between 1991 and 2021.

Year	Location (areas or counties)	Number of animals	Methods	Prevalence	* <i>Trichinella</i> species (PCR)	Reference
1991	Central Romania	50	Trichinelloscopy	18.5%		Nesterov et al., 1991
1992–1997	Transylvania	503	Trichinelloscopy	12.1%		Gherman, 1998
1997–2004	Transylvania	1062	Artificial digestion	12.4%		Blaga et al., 2009b
2000–2005	Other counties Cluj county Mureș county	2	Trichinelloscopy	100.0%	* <i>T. spiralis</i>	Blaga et al., 2009a
2000	Covasna county	6	Artificial digestion PCR	66.6%		Oprescu et al., 2007
1997–2007	Covasna county	60	Trichinelloscopy	38.3%		Oprescu et al., 2007
2010–2015	Eastern Romania	49	Artificial digestion digestion PCR	6.5% 15.6%	* <i>T. spiralis</i> * <i>T. britovi</i>	Iacob, 2017
2011–2015	Eastern Transylvania	37	Trichinelloscopy	5.4%		Borka-Vitalis et al., 2017
2015	North-Eastern, North-Western, Central regions, Western, South, and South-Eastern regions of Romania	147	Artificial digestion PCR	6.1% 4.7%	* <i>T. spiralis</i> * <i>T. britovi</i>	Nicorescu et al., 2015

**Table 2***Trichinella* spp. infections in wild boars (*Sus scrofa*) from Romania between 1991 and 2021.

Year	Location (areas or counties)	Number of animals	Methods	Prevalence	* <i>Trichinella</i> species (PCR)	Reference
1991	Central Romania	38,908	Trichinelloscopy	0.1%		Nesterov et al., 1991
1991–1994	Jiu Valley	1210	Trichinelloscopy	23.5%		Cristea and Şuteu, 1996
1992–1997	Transylvania	17,053	Artificial digestion Trichinelloscopy	0.3%		Gherman, 1998
1997–2007	Covasna county	210	Artificial digestion Trichinelloscopy	9.5%		Oprescu et al., 2007
1990–1999	Constanța county	340	Trichinelloscopy	0.1%		Olteanu, 2001
1997–2004	Transylvania Other counties	29,825	Trichinelloscopy	8.7%		Blaga et al., 2009b
1998–2011	Timiș county	823	Trichinelloscopy	0.5%		Borza et al., 2012
2010–2014	Hunedoara county	973	Trichinelloscopy	1.3%		Ciobotă et al., 2015
2000–2005	Cluj county Mureș county	5	Artificial digestion PCR	30.0% 70.0%	* <i>T. spiralis</i> * <i>T. britovi</i>	Blaga et al., 2009a
2015	North-Eastern, North-Western, Central, Western, South-Western, Southern, and South-Eastern regions of Romania	5596	Artificial digestion PCR	0.8% 0.6%	* <i>T. spiralis</i> * <i>T. britovi</i>	Nicorescu et al., 2015
2010–2015	Eastern Romania	8024	Artificial digestion PCR	* <i>T. spiralis</i> + * <i>T. britovi</i> / 0.0% 6.5% 0.4%	* <i>T. spiralis</i> + * <i>T. britovi</i> * <i>T. spiralis</i> * <i>T. britovi</i>	Iacob, 2017

mentioned region, bears have a more important role in the maintenance of the sylvatic cycle than wild boars. Furthermore, of two ten-year studies, the first one (1990–1999) focused on wild boars (Olteanu, 2001), while the other study took into consideration the prevalence of *Trichinella* infection in bears and wild boars from Covasna county in central Romania (Table 1, Table 2, Fig. 1) (Oprescu et al., 2007), highlighting the importance of these animal species for trichinellosis in Romania. The presence of *Trichinella* spp. infection in three wild carnivore species from Romania (fox, wolf, and wild cat) was assessed between October 1999 and March 2002, which brought updates regarding the epidemiology of trichinellosis in these wild carnivore species (Table 3, Fig. 2) (Gherman et al., 2002). Based on the results obtained, wild carnivores represent the most important hosts in the sylvatic cycle of *Trichinella* spp. in Romania. Routine *Trichinella* test (trichinelloscopy) was conducted with game species (wild boars, bears), between 1997 and 2004, to investigate the extent of the infection in hunted animals in Romania (Table 1, Table 2, Fig. 1). Apart from their role in the sylvatic cycle, they could represent a source of inter-foci transmission of *Trichinella* spp. due to different feeding habits compared to domestic species (Blaga et al., 2009b). An epidemiological study of *Trichinella* infection in wild boars in Timiș county was done between 1998 and 2011 (Table 2). The data were collected from the Veterinary Public Health Department of Timiș County and show a low prevalence rate in wild boars, meaning this species of animal exhibit a minor role in the local sylvatic life cycle of *Trichinella* (Fig. 1) (Borza et al., 2012).

Another study was conducted between 2010 and 2014 on the epidemiology of *Trichinella* infection in wild boars from Hunedoara county in western Romania. The highest prevalence of infection was established in 2012 (1.3%), followed by 2013 (1.1%), 2010 (0.8%), and then 2014 (0.7%), whereas all animals examined in 2011 were negative (Table 2, Fig. 1). The results indicated that wild boars from this county had a low infection rate with *Trichinella* spp. (Ciobotă et al., 2015) and that, over the years, infected animals became less and less common. Brown bears in eastern Transylvania were also tested for infection between 2011 and 2015 and the results confirmed that bears from this area contribute to the maintenance of the sylvatic life cycle of parasites (Table 1, Fig. 1) (Borka-Vitális et al., 2017). Marian et al. (2015) assessed the prevalence of *Trichinella* spp. infection in large wild carnivores from Romania between 2014 and 2015. The highest prevalence was identified in Eurasian lynx, followed by wolves, golden jackals, and wildcats, as seen in Table 3. The methods used in the detection of *Trichinella* spp. in these studies are presented in Tables 1, 2, and 3.

The present review, which included research conducted over the last 30 years, performed an analysis of the presence of *Trichinella* infection in more than 80% of Romania's territory (33 out of 41 counties), as it can be observed in the figures. Infections of wild animals were found in all studied areas during this period. As the number of examined animals and the detection methods varied drastically among the different studies, the comparative contribution of different host species to the parasite's maintenance is difficult to assess. Looking at the studies with large sample sizes, prevalences of wild canids and felids are at the higher end of the range, while bears and mustelids are less frequently affected. *Trichinella* infection in wild boars seems to be least frequent and may reflect a low proportion of mammalian carcasses in the diet (Tables 1–4 and Olteanu et al., 2014; Boros et al., 2020; Boros et al., 2021b).

**Table 3***Trichinella* spp. infections in wild carnivores from Romania between 1991 and 2021.

Animal species	Year	Location (areas or counties)	Number of animals	Methods	Prevalence	* <i>Trichinella</i> species (PCR)	Reference
Wolves ( <i>Canis lupus</i> )	1991	Central Romania	399	Trichinelloscopy	30.5%		Nesterov et al., 1991
	1999–2002	Transylvania	7	Artificial digestion	71.4%		Gherman et al., 2002
	2014–2015	Transylvania	3	Artificial digestion	66.7%		Marian et al., 2015
Foxes ( <i>Vulpes vulpes</i> )	1991	Central Romania	972	Trichinelloscopy	15.8%		Nesterov et al., 1991
	1991–1994	Jiu Valley	163	Trichinelloscopy	23.5%		Cristea and Şuteu, 1996
	1999–2002	Transylvania	50	Artificial digestion	16.0%		Gherman et al., 2002
	2000–2005	Cluj, Covasna and Harghita counties	71	Artificial digestion	14.0%	* <i>T. spiralis</i>	Blaga et al., 2009a
				PCR	57.1%	* <i>T. britovi</i>	
	2015	Arad, Hunedoara, and Timiş counties	121	Artificial digestion	96.0%	* <i>T. britovi</i>	Imre et al., 2015
				PCR	4.0%	* <i>T. spiralis</i>	
Wild cats ( <i>Felis silvestris</i> )	1991	Central Romania	158	Trichinelloscopy	31.5%		Nesterov et al., 1991
	1999–2002	Transylvania	6	Artificial digestion	16.6%		Gherman et al., 2002
	2014–2015	Buzău, Tulcea, and Maramureş counties	3	Artificial digestion	66.7%		Marian et al., 2015
Eurasian lynx ( <i>Lynx lynx</i> )	2014–2015	Transylvania	3	Artificial digestion	66.7%		Marian et al., 2015
Golden jackals ( <i>Canis aureus</i> )	2006	Tulcea county	1	Artificial digestion	100.0%	* <i>T. britovi</i>	Blaga et al., 2008
	2014–2015	Botoşani, Buzău, Brăila, Tulcea, Ialomiţa, Ilfov, Giurgiu, Teleorman, Olt, Vâlcea, Dolj, Gorj, and Timiş counties	54	Artificial digestion	53.7%		Marian et al., 2015

### 3. Species of *Trichinella* circulating in wild animals

Identifying the species of *Trichinella* in Romania is important due to the fact that *Trichinella spiralis* is more often found in domestic animals. However, this species can also appear in wild animals. Infection in humans is most often caused by *T. spiralis*. Therefore, identifying the exact species of *Trichinella* present in wild animals in Romania represented an important step in this field (Cozma et al., 2013; Cozma et al., 2016). Several studies have been conducted over the last 15 years and PCR-based methods confirmed the presence of *T. spiralis* and *T. britovi* in wild species in Romania.

#### 3.1. *Trichinella spiralis* infections in wild animals in Romania

*Trichinella spiralis* infections were found in bears, wild boars, red foxes (Blaga et al., 2009a; Nicorescu et al., 2015; Imre et al., 2015), European minks (*Mustela lutreola*) (Oltean et al., 2014), and European polecats (*Mustela putorius*) (Boros et al., 2021b), as seen in Tables 1, 2, 3, and 4.

The results show that this parasite species was identified more frequently in bears and less frequently in foxes. However, there are few studies using PCR to determine the parasite species in wild animals, so final conclusions regarding this topic still remain to be drawn.

#### 3.2. *Trichinella britovi* infections in wild animals in Romania

*Trichinella britovi* infections were found in golden jackals (Blaga et al., 2008;), wild cats, wolves, Eurasian lynx (Blaga et al., 2009a), beech martens (*Martes foina*), short-tailed weasels (*Mustela erminea*) (Oltean et al., 2014), foxes (Imre et al., 2015), wild boars, bears (Blaga et al., 2009a; Nicorescu et al., 2015; Iacob, 2017), European badgers (*Meles meles*) (Boros et al., 2021a), as seen in Tables 1, 2, 3, and 4. Mixed infections with *T. britovi* and *T. spiralis* were found in wild boars (Nicorescu et al., 2015) and polecats (Boros et al., 2021b).

The results show that *T. britovi* was identified more frequently in wild boars (Table 2) and mustelids (Table 4) but less frequently in

**Table 4**  
*Trichinella* spp. infections in mustelids from Romania between 1991 and 2021.

Animal species	Year	Location (areas or counties)	Number of animals	Methods	Prevalence	* <i>Trichinella</i> species (PCR)	Reference
European badgers ( <i>Meles meles</i> )	1991	Central Romania	166	Trichinelloscopy	6.0%		Nesterov et al., 1991
	2015–2019	Timiș, Bihor, Sălaj, Maramureș, Cluj, Alba, Mureș, Sibiu, Brașov, Harghita, Ilfov, Giurgiu, Constanța, and Tulcea counties	61	Trichinelloscopy Artificial digestion PCR	1.6%	* <i>T. britovi</i>	Boros et al., 2021a
Polecats ( <i>Mustela putorius</i> )	1991	Central Romania	157	Trichinelloscopy	5.2%		Nesterov et al., 1991
	2016–2020	Arad, Brașov, Constanța, Brăila, Călărași, Ialomița, Giurgiu, Teleorman, and Olt counties	75	Trichinelloscopy Artificial digestion PCR	1.3%	* <i>T. spiralis</i>	Boros et al., 2021b
European mink ( <i>Mustela lutreola</i> )	2009–2013	Danube Delta	3	Artificial digestion PCR	33.3%	* <i>T. spiralis</i>	Oltean et al., 2014
Beech martens ( <i>Martes foina</i> )	2009–2013	Danube Delta	4	Artificial digestion PCR	50.0%	* <i>T. britovi</i>	Oltean et al., 2014
Short-tailed weasels ( <i>Mustela erminea</i> )	2009–2013	Danube Delta	4	Artificial digestion PCR	50.0%	* <i>T. britovi</i>	Oltean et al., 2014



**Fig. 1.** The map of Romania showing the collection sites of bears and wild boars. Black circles: bear samples; Black stars: wild boar samples; Big circles and stars: general areas; Small circles and stars: counties.

golden jackals (Table 3). Regarding the mixed infection with *T. britovi* and *T. spiralis*, it was identified only two times (Table 2, Table 3), indicating that its occurrence is a rare phenomenon.

### 3.3. Serology in wild animals with *Trichinella* spp. infections

The serology approach regarding *Trichinella* infection in wild and domestic animals has been used less frequently in Romania. Nevertheless, a study from 2018 reported the seroprevalence of *Trichinella* spp. in wild boars (84 plasma samples) from Bihor county, located in western Romania. These animal samples were tested by ELISA and Western blot, although the artificial digestions of the tissue samples ( $n = 84$ ) were negative. At analysis by indirect ELISA, 65.4% ( $n = 55$ ) were positive, 7.1% ( $n = 6$ ) were doubtful, and 27.38% ( $n = 23$ ) were negative. On analysis by Western blot, from 26 samples, only 23.7% ( $n = 6$ ) were positive, whereas 76.9% ( $n = 20$ ) were negative, thus indicating the presence of anti-*Trichinella* antibodies in these animals (Boros et al., 2020). This study is important because it shows that antibodies can be found in animals that are negative in the golden standard method, thus indicating these animals probably had a very small infection or the samples (tissue) weren't taken correctly. The same situation might occur in other similar contexts and by this exposing the local population to this parasitic infection.



**Fig. 2.** The map of Romania showing the collection sites of wolves, foxes, wild cats, lynxes and golden jackals. Black circles: wolf samples; Black rectangles: fox samples; Black stars: wild cat samples; Black triangle: lynx samples; Black diamonds: golden jackal samples; Big circles, rectangles, stars, triangles, and diamonds: general areas; Small circles stars, rectangles, triangles and diamonds: counties.



**Fig. 3.** The map of Romania showing the collection sites of badgers, polecats, European minks, beech maters, and short-tailed weasels. Black circles: badger samples; Black stars: polecat samples; Black rectangles: beech matern samples; Black triangle: European minks samples; Black diamonds: short-tailed weasel samples; Big circles, rectangles, stars, triangles, and diamonds: general areas; Small circles and stars: counties; The rectangle, triangle and diamond: Danube Delta.

The results referenced above regarding *Trichinella* infection in wild species from Romania seem to reconfirm the combined statements of Campbell (1983) and Neghină et al. (2012) according to which „the saga of the helminth, destined to remain with us, both in nature and in the laboratory, will still haunt and fascinate scientists at the same time!” from both developing and developed countries, as they try to answer new questions regarding the parasite's evil nature.

#### 4. Conclusions

*Trichinella* infection is still significantly present in Romania, infecting several wild omnivorous and carnivorous species in an equal manner, with different prevalence rates over the years, thus maintaining the sylvatic focus of the parasites. Two species of *Trichinella*, namely *T. spiralis* and *T. britovi*, were identified in wild animals. Although the relative frequency of the two parasite species and the contribution of different host species are difficult to assess given the heterogenous data available, it is clear that dietary habits of the carnivores and omnivores play a major role, which needs to be addressed in future studies.

#### Declaration of Competing Interest

All authors declare no conflicts of interest regarding the content in this article.




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## Article

# European Hares, *Lepus europaeus*, Represent a Reservoir Host for *Thelazia callipaeda* in Romania

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**Abstract:** Thelaziosis caused by *Thelazia callipaeda* is an emerging disease in Europe. Only two reports of naturally infected lagomorphs have been published so far. The aim of this study was to evaluate the status of the Romanian populations of European brown hares, *Lepus europaeus* as reservoir hosts for *T. callipaeda*. Between November 2019 and November 2021, the eyes of 326 *L. europaeus* carcasses were examined for the presence of ocular parasites. Nematodes were stored in plastic vials with physiological saline, followed by morphological and molecular identification. QGIS 3.20 and EpiInfo<sup>TM</sup> 7 were used for mapping and statistical analysis. Four (1.23%) hares harbored *T. callipaeda* infection, with a total of 84 nematodes collected (mean intensity 21 nematodes/host), with 45 males, 39 females (two sexually immature, seven with only eggs, and 30 with eggs and larvae). One specimen from each host was successfully sequenced resulting in a 100% similarity with several other sequences of *T. callipaeda* haplotype 1. Statistical analysis revealed no significant results. The current study represents a first report of *T. callipaeda* in the European brown hare in Romania, and the second in Europe, also reiterating the role of lagomorphs as reservoir hosts for this zoonotic ocular nematode.

**Keywords:** *Thelazia callipaeda*; *Lepus europaeus*; reservoir host; Thelaziosis



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## 1. Introduction

Thelaziosis caused by *Thelazia callipaeda* (Spirurida, Thelaziidae) is a rapidly emerging zoonosis reported across most of Europe and Asia [1]. Domestic and wild carnivores are considered the primary vertebrate hosts of *T. callipaeda* [2]. Still, occasionally, adult nematodes were reported from other mammals such as other carnivores, lagomorphs, wild boars, and humans [3–7].

Infections in both domestic and wild carnivores are commonly reported across the distribution range of this nematode [1]. Human ocular infections follow an emerging trend in most countries where *T. callipaeda* had been reported in the main reservoir hosts [6–8]. These findings not only underline the zoonotic potential of this nematode but also highlight the clinical implications of the disease. Symptoms range from mild to severe conjunctivitis [9], further complicated by bacterial or fungal infections, which may lead to corneal ulcers [7].

In Romania, the disease was first diagnosed in 2014 [10], in a domestic dog from the western part of the country. Subsequent surveillance documented the spread across most of Romania's territory, in a wide variety of hosts: domestic dogs [11–13], domestic cats [13], jackals, wolves, wildcats [14], foxes [15], and mustelids [16]. However, despite its wide distribution in animals, no human cases have been documented in Romania, so

far. Although lagomorphs (hares, rabbits) are known as suitable hosts for *T. callipaeda* [3,4], there are no studies or reports of these hosts in Romania. Hence, we aimed to investigate the presence of *T. callipaeda* in hares, *Lepus europaeus* collected in various regions of Romania, and to evaluate their reservoir role.

## 2. Results

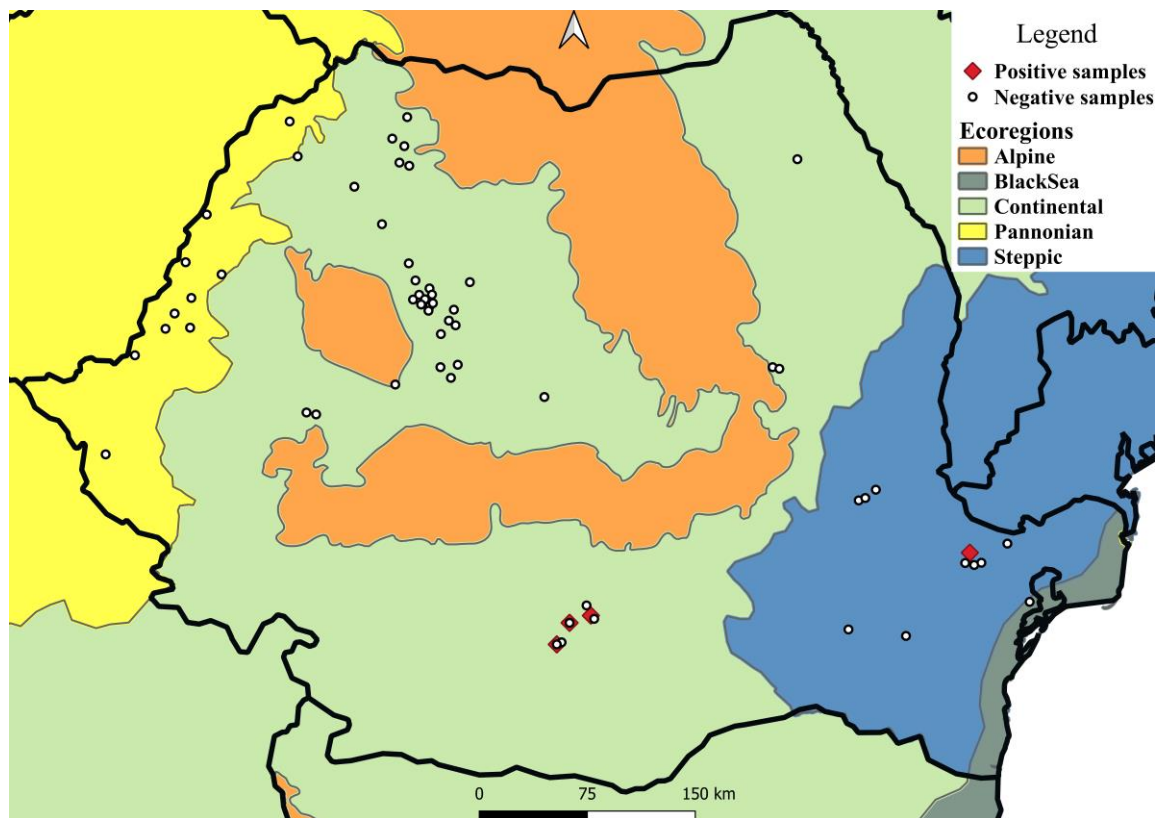
Four of the 326 European brown hares examined were positive for ocular nematodes (1.23%) (Table 1, Figures 1 and 2). A total of 84 nematodes were collected. All nematodes were morphologically identified as *T. callipaeda*. The intensity varied between 1 and 70 nematodes/hare, with a mean intensity of 21 (Table 2). Seven (18.9%) of the 37 mature females presented non-blastomerized eggs and blastomerized eggs, whereas 30 (81.1%) also presented larvated eggs as well as larvae inside the uterus.

**Table 1.** Sampled European brown hares according to the sex, altitude, and ecoregion.

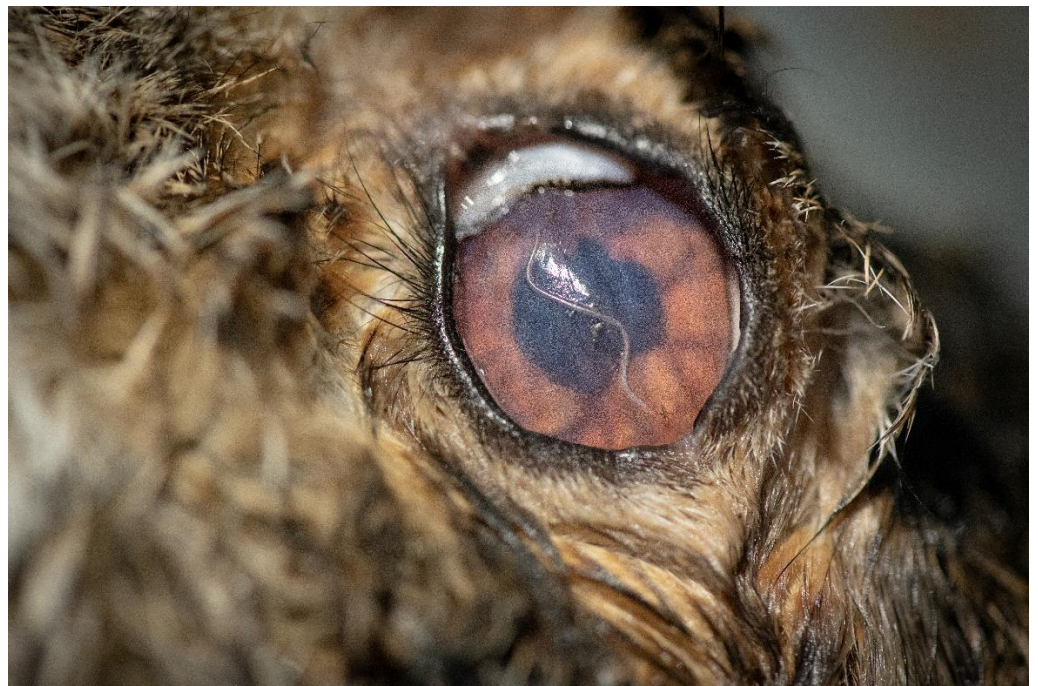
Variable		Sampled	Positive	Prevalence (%)	95% CI
Sex	Males	132	2	1.52	0.42–5.36
	Females	136	2	1.47	0.4–5.2
	Undetermined	58	0	0	0–6.21
Altitude interval (meters)	0–50	15	1	6.66	1.19–29.82
	51–100	147	0	0	0–2.55
	101–200	50	0	0	0–7.13
	201–300	63	3	4.76	1.63–13.09
	301–500	41	0	0	0–8.57
	≥501	10	0	0	0–27.75
Ecoregion	Pannonian	161	0	0	0–2.33
	Continental	146	3	2.05	0.7–5.87
	Alpine	2	0	0	0–65.76
	Steppic	17	1	5.88	1.05–26.98
	Pontic	0	0	0	0
Sample season	Winter	227	4	1.76	0.69–4.44
	Spring	5	0	0	0–43.45
	Summer	1	0	0	0–79.35
	Autumn	85	0	0	0–4.32
	Unknown	8	0	0	0–32.44
Total		326	4	1.23	0.48–3.11

All four specimens selected for molecular analysis were successfully sequenced, showing a 100% similarity with several sequences of *T. callipaeda* haplotype 1 (GenBank: MK546436–MK546439, MF578281; MG913802; AP017700; OM470911).

Statistical analysis, using Pearson's chi-squared test, correlating sex ( $p = 0.6563$ ), ecoregion ( $p = 0.1171$ ), altitude intervals ( $p = 0.1721$ ) to infection status revealed no significant results, the  $p$  values exceeding the 0.05 benchmark.



**Figure 1.** Sampling areas and distribution of *T. callipaeda* in European brown hares from Romania, by ecoregion.



**Figure 2.** *L. europaeus* with a specimen of *T. callipaeda* present in its left eye.

**Table 2.** *Thelazia callipaeda* infection intensity and population structure in European brown hares from Romania.

Positive Animals	<i>T. callipaeda</i> Collected	Infestation Type	Left Eye Intensity	Right Eye Intensity	<i>T. callipaeda</i> Population Structure		
					Male	Female	L5 Female
Hare 1	1	Unilateral	1	0	0	0	1
Hare 2	4	Unilateral	4	0	2	2	0
Hare 3	9	Bilateral	1	8	2	6	1
Hare 4	70	Bilateral	45	25	41	29	0
Median	6.5		2.5	4	2	4	0.5

### 3. Discussion

The current study serves as the first report of *T. callipaeda* in European brown hares in Romania and the second in Europe [3]. Moreover, the presence of larvae in the adult females of *T. callipaeda* is a strong indicator that hares are definitive (final) and also reservoir hosts, being able to transmit the infection in natural conditions. However, due to the low prevalence, we cannot suggest that hares are significant reservoir hosts in Romania, mainly as the area is known as hyperendemic for *T. callipaeda* in red foxes [15]. For instance, in Italy, the prevalence in hares was significantly higher (3/13, 23.1%) [3]. The higher prevalence in foxes could be linked to their crepuscular activity, which fits the one of *Phortica variegata* [17], whereas European brown hares are predominantly crepuscular and nocturnal, with a peak in the late afternoon, during the mating season, in spring [18,19]. Additionally, two wild European rabbits, *Oryctolagus cuniculus* from Portugal, also harbored *T. callipaeda* infection [4], highlighting the susceptibility of European lagomorphs to infection with this nematode.

Lagomorphs were only reported as natural hosts for *T. callipaeda* in Europe and Russia [3,4,20]. An experimental study, in Russia, concluded that the estimated life span of sexually mature forms of *T. callipaeda* in laboratory rabbits, *O. cuniculus* is of around six months [21], which, under natural conditions, could overlap with the activity period of the vectors. Moreover, the shallow burrowing behavior of brown hares during their inactive periods might leave them exposed to the activity of *P. variegata* [22].

The potential susceptibility of European brown hares as feeding hosts for *Phortica variegata* was suggested by Otranto et al. [3]. Interestingly, landscape diversity for the European hare has seen a shift towards woodlands, brushlands, unimproved grasslands, and field margins [23], potentially making them more susceptible both to predators [24] and diseases. This follows the trends of the decline of farmland biodiversity, which can be attributed to the intensification of the agricultural industry in the late 20th century in Europe, according to several studies on agri-environment schemes [25–27].

Because of the scarcity of hare carcass availability outside of the hunting season, which takes place between November and January, the current study is mainly limited to mature and immature adult stages of *T. callipaeda*. Subsequently, any larval stages present during the peak infestation season March–June [28] will have either matured or died, affecting both the overall prevalence rate as well as the intensity within the host.

Therefore, there is an increasing need to determine the complexity of the sylvatic cycle and the diversity of reservoir hosts in relation to their ecology to better understand and implement preventive measures for limiting this zoonotic disease. This latter aspect has become a key point over the past ten years, as more human cases have emerged worldwide [6–8].

### 4. Materials and Methods

Between November 2019 and November 2021, 326 carcasses of European hares, *Lepus europaeus*, were examined as part of a broader survey of their parasites (unpublished data). Of these, six were collected outside of the November–February period, whereas another

eight had an unknown collection date (Table 1). The study area comprised 17 counties covering four ecoregions (Figure 1). The carcasses originated from legally hunted individuals or roadkills. The following information was recorded for each animal: date and location of collection, and sex.

As part of the necropsy procedure, the eyes of each carcass were examined under a stereo zoom microscope, with the lateral and medial canthus dissected to uncover the entire globe. Upon detection, nematodes were placed in a vial with physiological saline (0.9%), followed by a morphological examination.

Morphological identification of the ocular nematodes was performed using the keys provided by [20,29], during which each nematode's sex and developmental stages were recorded. Intact specimens underwent detailed morphometric analysis following preservation in 4% formalin solution. All measurements were done using an Olympus microscope (Olympus BX61) and dedicated software.

One randomly selected nematode from each brown hare was stored in 70% ethanol and used for molecular characterization. DNA extraction was performed individually from each nematode using the ISOLATE II Genomic DNA Kit (Bioline Meridian Bioscience, Luckenwalde, Germany), according to the manufacturer's instructions, and stored at  $-20^{\circ}\text{C}$  until further use. The samples were processed by PCR amplification of a 670-bp gene region the cytochrome c oxidase subunit 1 (cox 1), using a C1000<sup>TM</sup> Thermal Cycler (Bio-Rad, London, UK) and the NTF/NTR primer pair, as previously described [30]. Sequencing was performed by MacroGen Europe (Amsterdam, The Netherlands), while the assembled chromatograms and consensus sequences were translated and edited using the Geneious 4.8.5 software (Biomatter Ltd., Auckland, New Zealand). Lastly, using the Basic Local Alignment Search Tool (BLAST), the consensus sequences were compared with the available data in the GenBank<sup>®</sup> database.

Mapping was performed using the free open source QGIS Geographic Information System (version 3.20 Odense, QGIS Development Team, 2021), including ecoregions as a layer. Statistical analysis was performed using the EpiInfo<sup>TM</sup> 7 software (CDC, Atlanta, GA, USA, 2021), recording and calculating values for the frequency, prevalence, as well as 95% confidence interval of infestation, according to several parameters (Table 1).

## 5. Conclusions

The current study represents the first report of the presence of *T. callipaeda* in European brown hares in Romania, while also emphasizing the role as a reservoir host of lagomorphs for the aforementioned nematode.

**Author Contributions:** Conceptualization, V.-D.C., C.M.G. and A.D.M.; methodology, V.-D.C. and A.M.I.; validation, A.D.M., A.M.I. and C.M.G.; formal analysis, V.-D.C., C.D.C. and A.M.I.; investigation, V.-D.C., K.A.H. and C.M.G.; resources, C.M.G. and A.D.M.; data curation, A.D.M. and C.M.G.; writing—original draft preparation, V.-D.C. and A.D.M.; writing—review and editing, V.-D.C., A.D.M. and C.M.G.; visualization, V.-D.C.; supervision, C.M.G.; project administration, C.M.G. and A.D.M.; funding acquisition, A.D.M. and C.M.G. All authors have read and agreed to the published version of the manuscript.

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**Data Availability Statement:** The data generated or analyzed during this study is included in this published article.

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SHORT REPORT

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# Occurrence of *Giardia duodenalis* assemblages in farmed long-tailed chinchillas *Chinchilla lanigera* (Rodentia) from Romania

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## Abstract

**Background:** *Giardia duodenalis* is a parasitic protist that infects a large number of species, being localized in the small intestine. Two of the eight recognized assemblages have zoonotic potential, but studies regarding their distribution in less important pet or farm species are scarce. Of these species, the long-tailed chinchilla is a host for *Giardia* spp., although data on the spread of infection and assemblages involved are confined. The present work aimed to determine the prevalence of *Giardia* infection and assemblage identification in farmed chinchillas in Romania. A total of 341 fecal samples were collected from 5 farms and microscopically examined using flotation test based on saturated sodium chloride solution. DNA from all positive samples was extracted and identified by PCR targeting the *gdh* gene.

**Results:** The overall prevalence of *Giardia* infection was 55.7% (190/341); there was no statistically significant difference ( $P = 0.25$ ) in prevalence between young animals (58.8%) and adults (52.6%). Assemblages B (151/190), D (33/190) and E (6/190) were identified. Among assemblage B, sub-assemblages BIII (6/151) and BIV (145/151) were determined.

**Conclusions:** This study demonstrates that *Giardia* spp. infection is highly prevalent in farmed chinchillas from Romania, and the sub-assemblages identified are potentially zoonotic.

**Keywords:** Farmed long-tailed chinchilla, *Chinchilla lanigera*, *Giardia duodenalis*, Prevalence, Assemblages, Romania

## Background

The genus *Giardia* contains six species of aerotolerant anaerobic enteric protozoan parasites isolated from mammals, birds and amphibians [1–4]. Of all these species, three infect mammals, *Giardia muris* and *G. microti* in rodents and *G. duodenalis* commonly in a broad range of mammalian hosts [5]. Within *G. duodenalis*, eight species assemblages, or genotypes, are currently recognized, named from A to G. The hosts of assemblages A and B of *G. duodenalis* are the humans and other primates, livestock, domestic carnivores and wild mammals; C and D infect canids, E is common in

hoofed livestock, F is typical for cats, G infects rodents and H was isolated from marine mammals [6]. The most important are zoonotic assemblages A and B, within each of them being isolated by protein polymorphisms or allozyme electrophoresis four sub-assemblages (AI, AII, AIII, AIV and BI, BII, BIII, BIV, respectively) [7, 8].

In Romania, limited data exist regarding the prevalence of *Giardia* infection in animals. Recently, the presence of *G. duodenalis* was reported in domestic carnivores; the overall prevalence was 8.5% in dogs and 27.9% in cats [9, 10]. Furthermore, assemblages A (AII), B, C (10/60; 16.7%), D (42/60; 70.0%), and E (7/60; 11.7%) have been identified in domestic and wild animals (dogs, cats, foxes, deer, wolves, raccoon dogs and muskrats) [11–13]. Consequently, the study of *Giardia* spp. infection in Romania is a field of high importance.

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The long-tailed chinchillas (*C. lanigera*) are mountainous and crepuscular animals native to South America. Extensively hunted for their fur during the 19th century the species is now almost extinct in the wild, several colonies being identified only in Chile [14]. Due to their complex social behavior and attractive aspect, chinchillas became increasingly popular as pets across the world. At the same time, because of the softest, longest and finest furs among wild animals, the species became of interest for animal breeders. Farming of chinchilla dates back to 1923, when M. F. Chapman began to raise chinchillas in captivity, being the inception of what has become an industry [15]. Intensive farming exposed chinchillas to different pathogens, which are probably less common in the wild animals. Of these, water-borne parasitic diseases, particularly giardiasis, may cause clinical and sanitary problems and lead to production and economic losses [16]. Currently, there are about 75 chinchilla farms in Romania, with a production of 12,500 animals exported per year. It manifests also an increasing trend of chinchillas' farming, whose debut in Romania dates back about 10 years ago (<http://agfcicr.ro/>). Due to the increasing number of farmed chinchillas in Romania, and the lack of information on the occurrence and zoonotic potential of *G. duodenalis* in these animals, the present study aimed to investigate the prevalence of the infection and preliminary genotyping of the isolates in Romanian chinchilla farms.

## Methods

### Animals and collection sites

Five farms with an overall stock of 5500 animals were involved in the study. Of these 2200 were breeding animals and the rest were kits and young of different ages. The following abbreviations were used for the farms studied: BM, RG, SB, SM and LU. All farms use the intensive growth closed system, but farms BM and RG also buy animals from small farmers who grow chinchillas in polyspecific farms exposed to contact with other species. A total of 341 fecal samples were collected, representing 6.2% of the stock. Of these, 171 samples were from chinchilla mothers and 170 from young animals (Table 1).

### Sample processing

Each fecal sample was individually examined by flotation technique using saturated sodium chloride solution (specific gravity 1.28) [17], followed by microscopic examination (light microscopy, magnification: 10×, 20×, 40×) for the identification of *Giardia* cysts. Briefly, 0.5 g of feces/sample was homogenized with 10 ml of distilled water, filtered and centrifuged at 3000× *g* for 10 min. The supernatant was discarded, and the sediment containing *Giardia* cysts was transferred to an Eppendorf tube and used for DNA extraction.

### DNA extraction and PCR analysis

DNA extraction was performed from *Giardia*-positive samples, confirmed by microscopic examination, using Isolate Fecal DNA kit (Bioline, London, UK). To increase the specificity of DNA amplification, a semi-nested PCR reaction was performed targeting the glutamate dehydrogenase (*gdh*) gene in a T100 Thermal Cycler (Bio-Rad, Hercules, USA) [18, 19]. The PCR reaction mix contained 2× Red PCR Master mix (Roalab, Teltow, Germany), 12 pmol of primers, 1 µl of genomic DNA; the reaction profile consisted of 1 cycle of initial denaturation at 95 °C for 5 min, followed by 40 cycles of 30 s each at 94 °C, annealing at 50 °C for 30 s for the primary reaction and 60 °C for secondary reaction, extension at 72 °C for 1 min and final extension at 72 °C for 5 min. Agarose gel (1.5%) electrophoresis stained with SYBR Safe DNA gel stain (Invitrogen, Carlsbad, USA) was performed for the visualization of PCR products.

### RFLP

For discrimination of all assemblages of *G. duodenalis*, RFLP analysis was performed using *Rsa* I and *Nla*IV (Biolabs, New England, US) restriction enzymes [18]. The amplified fragments were digested in a total volume of 50 µl, as recommended by the manufacturer's instructions, 5 min at 37 °C for *Rsa*I, 1 h for *Nla*IV, and the reactions were stopped by 20 min of incubation at 60 °C. The digested products were visualized by electrophoresis on 3% agarose gel.

**Table 1** Prevalence of *G. duodenalis* in fecal samples collected from long-tailed chinchillas in farms in Romania

Farm code	Total		Chinchilla mothers		Kits/young		Comparison	
	F	Prevalence (%) (95% CI)	F	Prevalence (%) (95% CI)	F	Prevalence (%) (95% CI)	Chi-square	P-value
BM	49/80	61.3 (49.7–71.9)	29/52	55.8 (41.3–69.5)	20/28	71.4 (51.3–86.8)	1.880	0.170
RG	56/80	70.0 (58.7–79.7)	24/28	85.7 (67.3–96.0)	32/52	61.5 (47.0–74.7)	5.065	0.024
SB	40/60	66.7 (53.3–78.3)	18/30	60.0 (40.7–77.3)	22/30	73.3 (54.1–87.7)	1.200	0.273
SM	19/60	31.7 (20.3–45.0)	9/30	30.0 (14.7–49.4)	10/30	33.3 (17.3–52.8)	0.077	0.781
LU	26/61	42.6 (30.0–55.9)	10/31	32.3 (16.7–51.4)	16/30	53.3 (34.3–71.7)	2.769	0.096
Total	190/341	55.7 (50.3–61.1)	90/171	52.6 (44.9–60.3)	100/170	58.8 (51.0–66.3)	1.325	0.2497

Abbreviations: F Frequency, CI confidence interval

### DNA sequencing

The PCR products were purified by using QIAquick PCR purification kit (Qiagen, Hilden, Germany) and sequenced at MacroGen Europe (Amsterdam). Nucleotide sequence data from this study were submitted to the GenBank database under the accession numbers MG432793–MG432795.

### Statistical analysis

The frequency of *Giardia*-positive samples, their prevalence and 95% confidence interval were calculated. The difference in prevalence between age groups and among farms was statistically analyzed by a Chi-square test. Statistical significance was set at a *P*-value of  $\leq 0.05$ . All statistical analyses were performed using EpiInfo software version 3.5.1. (Centers for Disease Control and Prevention: <http://www.cdc.gov/epiinfo/>).

## Results

### The occurrence of *Giardia* spp.

*Giardia* cysts were identified in 190 of 341 (55.7%, 95% CI: 50.3–61.0) fecal samples by microscopic examination. All 190 microscopically identified *Giardia*-positive samples were positive by PCR. General prevalence recorded the highest value in farm RG (56/80, 70%, 95% CI: 58.7–79.7%) and the lowest in farm SM (19/60, 31.6%, 95% CI: 20.3–45.0%) ( $\chi^2 = 28.83$ ,  $df = 4$ ,  $P < 0.001$ ). The infection was somewhat more frequent in young animals (100/170, 58.8%, 95% CI: 51.0–66.3%) compared to mother chinchillas (90/171, 52.6%, 95% CI: 44.9–60.3%) but the difference was not statistically significant ( $\chi^2 = 1.09$ ,  $df = 1$ ,  $P = 0.25$ ) (Table 1).

### *Giardia* spp. assemblages

In total, three *Giardia* assemblages (B, D and E) were found in the chinchilla farms studied. Assemblage B was the most prevalent (151/190, 79.5%), followed by D (33/190, 17.4%) and E (6/190, 3.1%). The identified sub-assemblages were BIV (145/190, 76.3%) and BIII (6/190; 3.1%) (Table 2).

Sequence analysis of fecal samples confirmed the infection with *G. duodenalis* sub-assemblages BIII, BIV, D and E (Table 2). Assemblages B (MG432795) and D (MG432793) were common in all farms in the study, in both age categories, and Assemblage E (MG432794) was identified only in farms BM and RG. No mixed assemblage infections were detected in animals in this study.

## Discussion

The study of intestinal parasites in the long-tailed chinchilla is an important field of interest due to a permanent contact of this pet or farmed animal with humans. Among parasitic diseases identified in this species, giardiasis seems to be the most significant, due to the zoonotic character and increased values of prevalence reported worldwide (Table 3).

**Table 2** Assemblages of *G. duodenalis* identified by PCR-RFLP and sequencing targeting the *gdh* gene in fecal samples of long-tailed chinchillas from farms in Romania

Farm	Age	Assemblage (RFLP)		Assemblage (sequencing) (no. of samples)			
		<i>NlaIV</i>	<i>RsaI</i>	BIII	BIV	D	E
BM	CM	BIII/BIV/E/D	BIII; BIV	3	20	4	2
	Y	BIII/BIV/D	BIV		16	4	
RG	CM	BIII/BIV/D/E	BIV		19	3	2
	Y	BIII/BIV/D/E	BIV	1	22	7	2
SB	CM	BIII/BIV/D	BIV		15	3	
	Y	BIII/BIV/D	BIII; BIV	2	17	3	
SM	CM	BIII/BIV/D	BIV		4	5	
	Y	BIII/BIV	BIV		10		
LU	CM	BIII/BIV/D	BIV		8	2	
	Y	BIII/BIV/D	BIV		14	2	
Total				6	145	33	6

Abbreviations: CM chinchilla mothers, Y young

**Table 3** Reported prevalence of *Giardia* spp. infection in the long-tailed chinchilla

Country	Husbandry system (pet/farmed/wild)	Prevalence (%)	Frequency	Detection method	Reference
Argentina	Farmed	34.42	84/244	Wet mounts, IFA	[46]
Belgium	Pet	66.3	53/80	SCF	[24]
Brazil	Farmed	8.0	20/250	ZCF	[47]
Brazil	Farmed	38.0	38/100	ZCF	[48]
Brazil	Pet	10.0	6/60	ZCF	[49]
Brazil	Farmed	31.37	80/255	ZCF	[28]
Chile	Wild	Negative	na		–
China	Pet	37.5	36/96	SF	[50]
China	Pet	27.1	38/140	PCR	[51]
Europe	Pet	61.4	326/531	ELISA	[31]
Italy	Farmed	39.4	41/104	DFA	[31]
Portugal	Pet	35.2–92.3	na	ZCF, SF	[52]
Russia	Pet	50.0	25/50	CFM	[53]
Russia	Pet	Positive	na	ANF	[29]
Peru	Wild	Negative	na		–
Romania	Farmed	55.7	190/341	NaClIF	Present study

Abbreviations: ANF ammonium nitrate flotation, CFM combined flotation method, DFA direct fluorescent assay, ELISA enzyme-linked immunosorbent assay, IFA immunofluorescence assay, na not applicable, NaClIF sodium chloride flotation, SCF sucrose gradient centrifugation-flotation technique, SF sugar flotation (Sheather's sugar solution), ZCF zinc-sulfate centrifugation-flotation

The prevalence revealed in the present study (55.7%) is slightly increased compared to that reported in farmed chinchilla from other regions (8.0–38.0% in Brazil, 34.4% in Argentina and 39.4% in Italy) but is comparable to those reported in pet animals (10.0–92.3%).

The discrepancies of prevalence recorded in existing studies can be explained by the different diagnostic value of copromicroscopic methods used, determined by the technique, less than the density of supersaturated solutions [20]. Moreover, coproscopic techniques have a lower diagnostic value, the prevalence determined by other modern serological or molecular methods (ELISA, IFA, PCR) being 2.6-fold higher in dogs and 3.7-fold higher in cats [21]. As such, we consider that the prevalence of infection revealed in this study, although high, can be appreciated as undervalued.

Prevalence of *Giardia* infection is generally influenced by many factors, such as the sensitivity of the diagnostic method used, the peculiarities of the biological cycle of the parasite (the discontinuities of cysts removal), the host, the age of host, the growth system, and the hygiene conditions (water, food, bedding) [22]. A variety of factors favor the emergence and transmission of infection in chinchilla populations. These risk factors may differ among pet and farmed chinchilla. Regarding pet chinchilla, participation in shows and contact with other pet animals, such as dogs, cats or other rodents, are significant [23, 24]. In farmed chinchillas, the age of animals, stress, poor husbandry system associated with low quality of water source, overcrowding and close contact with feces seems to act as predisposing factors. Juvenile chinchillas are more sensitive to acquire the infection [25]. Intensive rearing in plastic or metal cages, with fecal accumulation underneath and vulnerability of the drinking-water-processing system, favor the contact between animals and cysts of *Giardia* spp. [26, 27]. Captivity associated with specific stress emphasizes the sensitivity of chinchilla to *G. duodenalis* infection, an aspect demonstrated by the absence of *Giardia* spp. infection in wild animals [28, 29].

Chinchillas harbor various assemblages (A, B, C, D and E) of *G. duodenalis*, representing a potential zoonotic risk (Table 4). Assemblage B is the most common, being identified in almost all reported studies, except for an axenic isolate of *G. duodenalis* from Germany [30], in which assemblage A was identified. In our research, RFLP analysis of *G. duodenalis*-positive samples revealed a high occurrence of assemblage B isolates grouped into sub-assemblages BIII and BIV, representing the main assemblages involved in chinchilla's infection. In the present study, no mixed assemblage infections were detected, similar to previous studies [16, 31]. However, our data do differ from those reported in Belgium and Germany, which showed the presence of mixed assemblage A, B, C and E infections in chinchillas [24, 32].

**Table 4** Assemblages of *G. duodenalis* identified in the long-tailed chinchillas

Country	Type of animal (pet/farmed)/ assemblage		Reference
	Pet	Farmed	
Austria	B	–	[32]
Belgium	A, AI, All, B, BIV, C, E	–	[24]
Brazil	B	–	[16]
Brazil	BIV	–	[54]
China	AI, All, BIV, BIV-1, BIV-2	–	[51]
Croatia	B	–	[55]
Czech Republic	B	–	[56]
Germany	A	–	[30]
Germany	A, B, D	–	–
Italy	–	B, C	[31]
Romania	–	BIII, BIV, D, E	Present study

The presence of C and D assemblages typical for canids, and E from hoofed livestock, in chinchillas is quite interesting. In this work, the existence of assemblages E in farms BG and RG can be explained by acquiring animals from farms in which ruminants were also kept, the direct or indirect contact between the two species being possible.

Generally, multiple factors can explain the diversity of assemblages identified across the world. Interspecies transmission is of particular importance for the zoonotic risk of infection, domestic animals being the source of human infection. Reverse or cross-species transmission of different assemblages (BIV, E) has also been demonstrated in areas where humans, primates and livestock overlap in their use of habitat [33]. Interspecific transmission is possible between species belonging to different taxa, from rodents to carnivores and from ruminants to humans [34]. It is also proven that *G. duodenalis* from the North American beaver (*Castor canadensis*) may infect Mongolian gerbils (*Meriones unguiculatus*); in this case, the transmission was carried out between two rodent species [35]. Transmission of *Giardia* spp. between different species of rodents is also confirmed in other older studies [36]. Nevertheless, Goltz [37] demonstrated that *G. chinchillae* from *C. lanigera* were not infective to laboratory mice, rats and guinea pigs. However, the interspecies transmission may explain the presence of assemblages D and E in our study, sustained by the existence of guard dogs and small ruminants in the examined farms.

Transport vectors can also play a significant role in the transmission of giardiasis [38]. It is confirmed that assemblage E of *G. duodenalis* is carried by flies, increasing the possibility of repeated infection or cross-transmission between sensitive species, by mechanical transmission [39].

As a result, despite of the strong host specificity and narrow host range of assemblage E, which is mostly identified in cloven-hoofed mammals, the involvement of the transport hosts can ensure the transmission of this assemblage to captive chinchillas [8].

Water source is also important in the circulation of *G. duodenalis* cysts, giardiasis being recognized as one of the major waterborne diseases [40]. Although the long-tailed chinchilla is a species adapted to aridity, with low water needs, it prefers the open dish drinker [41]. The best water supply in chinchilla farming is represented by bottled water, free of pathogens and chlorine [42]. Tap and well water are also accepted sources, but they present the risk of contamination with *Giardia* cysts. Surprisingly, in Romania, bottled water seems to have an increased risk of infection compared with wells or tap water [43]. Feces of different animal species can pollute water sources, shedding cysts into the water supply [44]. These cysts can pass through water treatment, even for pristine or filtered drinking water. Furthermore, *Giardia* spp. cysts have a demonstrated effective resistance to chlorination [45]. Tap water was the source in studied farms, without an additional water filtration; chlorination and filtration performed by water plant suppliers being the unique treatments. Combining predisposing factors as interspecific transmission, the possible involvement of vectors and deficiencies in water supply, the increased prevalence of *G. duodenalis* infection in farmed chinchilla from Romania may be explained.

## Conclusions

This study revealed the increased prevalence of infection with *G. duodenalis* in farmed chinchilla from Romania and the presence of BIII, BIV, D and E assemblages. Further studies are needed to clarify the zoonotic risk for the owners and workers in chinchilla husbandry.

## Abbreviations

BM: Baia Mare; LU: Lunca; RG: Reghin; SB: Suceava-Bejenaru; SM: Suceava-Morozeanu

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## Availability of data and materials

Nucleotide sequence data from this study were submitted to the GenBank database under the accession numbers MG432793–MG432895.

## Authors' contributions

GCM collected the samples, GA and MV made the flotation and microscopic examinations, KZ performed the DNA extraction, PCR, RFLP and sequencing. All authors read and approved the final manuscript.

## Ethics approval and consent to participate

Not applicable.

## Consent for publication

Not applicable.

## Competing interests

The authors declare that they have no competing interests.

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# Validity of genus *Perostrongylus* Schlegel, 1934 with new data on *Perostrongylus falciformis* (Schlegel, 1933) in European badgers, *Meles meles* (Linnaeus, 1758): distribution, life-cycle and pathology

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## Abstract

**Background:** A century of debates on the taxonomy of members of the Metastrongyloidea Molin, 1861 led to many reclassifications. Considering the inconstant genus assignation and lack of genetic data, the main aim of this study was to support the validity of the genus *Perostrongylus* Schlegel, 1934, previously considered a synonym of *Aelurostrongylus* Cameron, 1927, based on new molecular phylogenetic data and to understand its evolutionary relationships with other metastrongyloid nematodes.

**Results:** Specimens of lungworm collected from European badgers in Germany, Romania and Bosnia and Herzegovina were morphologically and molecularly (rDNA, *cox1*) characterized. From a phylogenetic standpoint, *Perostrongylus* is grouped with high support together with the genera *Filaroides* van Beneden, 1858 and *Parafilaroides* Dougherty, 1946 and includes probably two species: *Perostrongylus falciformis* (Schlegel, 1933), a parasite of *Meles meles* in Europe and *P. pridhami* (Anderson, 1962), a parasite of *Neovison vison* in North America. *Perostrongylus* and *Aelurostrongylus* are assigned to different clades. *Aelurostrongylus* becomes a monotypic genus, with the only species *Aelurostrongylus abstrusus* (Railliet, 1898). In addition, we provide morphological and morphometric data for the first-stage (L1), second-stage (L2), and third-stage (L3) larvae of *P. falciformis* and describe their development in experimentally infected *Cornu aspersum* snails. The pathological and histopathological lesions in lungs of infected European badgers are also described. This is the first record of *P. falciformis* in Romania.

**Conclusions:** Molecular phylogenetic and morphological data support the validity of the genus *Perostrongylus*, most probably with two species, *P. falciformis* in European badgers and *P. pridhami* in minks in North America. The two genera clearly belong to two different clades: *Perostrongylus* is grouped together with the genera *Filaroides* and *Parafilaroides* (both in the family Filaroididae Schulz, 1951), whereas *Aelurostrongylus* belongs to a clade with no sister groups.

**Keywords:** *Perostrongylus*, *Aelurostrongylus*, Metastrongyloidea, European badgers, mustelids

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## Background

A century of debates on the taxonomy of members of the superfamily Metastrongyloidea Lane, 1917 led to many reclassifications of these nematodes within a variety of families, subfamilies, genera and species [1, 2]. The genus *Aelurostrongylus* Cameron, 1927 was erected to accommodate *Aelurostrongylus abstrusus* (Railliet, 1898) [3] which was originally described by Mueller in 1890 [4] as *Strongylus pusillus* and renamed to *Strongylus abstrusus* by Railliet [5], because *S. pusillus* was pre-occupied [6]. Later, the genus *Protostrongylus* Kamensky, 1905 was erected [7] and *Strongylus abstrusus* transferred to this new genus (as *Protostrongylus pusillus*), containing two other species, i.e. *Protostrongylus rufescens* (Leuckart, 1865), the type-species, and *Protostrongylus commutatus* (Diesing, 1851) [as *Protostrongylus terminalis* (Passerini, 1884)]. Interestingly, Kamensky used the early specific name as originally named by Mueller in 1890.

The definition of *Aelurostrongylus* as a new genus [3] was based mainly on the absence of cuticular bursal supports and the absence of “supporting fingers” of the spicular sheaths. Cameron [3] included only the type-species *A. abstrusus* in the newly erected genus.

*Perostrongylus falciformis* (Schlegel, 1933) was described from European badgers, *Meles meles* in Germany as *Strongylus falciformis* Schlegel, 1933 [8] due to the sickle-shaped spicules and one year later, transferred to the genus *Filaroides* van Beneden, 1858 as *Filaroides falciformis* [9]. In the same year, Schlegel [10] erected a new genus, *Perostrongylus* Schlegel, 1934 in order to include this nematode. The main characteristics to support the new genus were the reduced, truncated copulatory bursa of the males, and the presence of larvated eggs in the uterus of the females [10]. A few years later, Wetzel [11] suggested that *P. falciformis* should be transferred to the genus *Aelurostrongylus*, considering the genus *Perostrongylus* as a synonym, based on the morphology of the bursa and gubernaculum in males. In two subsequent reviews on this group of nematodes [12, 13], the genus *Perostrongylus* is listed as a synonym of *Aelurostrongylus*, based on Wetzel's suggestions, without further comments. In his taxonomic review, Dougherty [12] listed four species in the genus *Aelurostrongylus*: *Aelurostrongylus abstrusus* (Railliet, 1898); *Aelurostrongylus brauni* (von Linstow, 1897); *Aelurostrongylus falciformis* (Schlegel, 1933); and *Aelurostrongylus fengi* (Hsü, 1935). The latter has been initially described as the type-species of *Pulmostrongylus* Hsü, 1935 [14], but Dougherty [12] considered this genus as a synonym of *Aelurostrongylus* while Anderson [15] and Lesage [16] as a subgenus of *Protostrongylus*. However, Seneviratna [13] as well as the authors of later keys and reviews [17, 18] maintained the validity of *Pulmostrongylus*. The generic allocation of *A.*

*brauni* was also questioned [19]. Asakawa et al. [20] redescribed this species and assigned it to the newly established genus *Viverrostrongylus* Asakawa, 1986.

A new species belonging to genus *Aelurostrongylus*, *A. pridhami* was described by Anderson [21] in *Neovison vison* from Canada. Previously, the species was erroneously identified as *A. falciformis* [22]. The same author [19] highlighted that some species of the genus *Aelurostrongylus* (*A. abstrusus* and *A. fengi*) are oviparous, while others (*A. falciformis* and *A. pridhami*) are ovoviviparous. Moreover, *A. falciformis* and *A. pridhami* differ from *A. abstrusus* with regard to the morphology of the bursa and spicules. Based on these differences, Anderson [19] suggested that the genus *Perostrongylus* should be reinstated, but later placed it as a subgenus of *Aelurostrongylus* [15, 17]. Subsequent publications continued to use the genus name *Aelurostrongylus* (synonymy of the genus [23]; *A. falciformis* [24–29], *A. pridhami* [27, 30–33]), while others accepted and used *Perostrongylus* (*P. pridhami* [34–42], *P. falciformis* [37, 43]). It is evident, that most European studies maintained the validity of *Aelurostrongylus* while the American studies predominantly used *Perostrongylus*. However, based on the data from Anderson [19], the two species are congeneric, sharing the same features.

The life-cycles of both species of *Perostrongylus* have been described in detail. Wetzel [11] studied the development of *P. falciformis* in several snail and slug species, and described the L1-L3 larval stages, but illustrated only L1 and L3. He also established the prepatent period in experimentally infected European badgers. The development of *P. pridhami* was described in slugs as well as in various terrestrial and aquatic snails, with detailed description and illustrations for L1-L3 larval stages [21]. The development of *P. pridhami* in American minks has also been described in detail [21, 37]. Anderson [21] demonstrated the infectivity to minks of L3 of *P. pridhami* from paratenic hosts (rodents, birds, amphibians and fish).

Similarly to most metastrongyloid nematodes, *P. falciformis* has an indirect life-cycle. Females are ovoviviparous and deposit in the alveoli thin-shelled eggs with larvae which subsequently hatch. Larvae and mature adult parasites are found in the alveoli, alveolar ducts and terminal bronchioles. L1 are coughed-up, swallowed and shed through the faeces. Prepatency in experimental infections was shown to be 18–19 days. Larvae enter different species of land snails and moult twice to infective L3. European badgers become infected by eating snails or paratenic hosts. The development of L3 to adults in European badgers is not known [11]. Symptoms of infected European badgers vary from less severe to death, depending on lungworm infection rate and secondary bacterial infections. The associated lung lesions and different stages of verminous pneumonia in European badgers with minor to massive lungworm infections were

lobular bronchopneumonia, diffuse bronchitis and widespread emphysema [8, 10]. In minor infections, European badgers in good nutritional status often completely recovered after coughing out the worms, leading to the regression of inflammatory process and encapsulation and calcification of degraded worms and eggs in the form of small, cheesy calcareous nodules in the subpleura and parenchyma of lung lobes. The lungworm invasion affected predominantly young animals [8, 10, 11, 19].

Considering the rather inconstant genus assignation and lack of molecular data, the main aim of this study was to provide information to support the validity of the genus *Perostrongylus* based on new molecular phylogenetic data and to understand its evolutionary relationships with other lungworms of carnivores. In addition, morphological details of the larval stages of *P. falciformis*, as well as a detailed pathological and histopathological description of the lesions in European badgers are provided.

## Methods

### Sample collection

Thirty-two adult European badgers were collected from different localities in Europe (Table 1) and carcasses were examined by necropsy by removing the entire respiratory tract. The trachea, bronchi, and the bronchioles were longitudinally dissected and carefully examined under a stereomicroscope for the presence of parasites. Nematodes found encapsulated in small nodules on the surface of the lungs were collected, washed in saline solution and preserved in formaldehyde for morphological identification. Midbody fragments of nematodes were stored in 70% ethanol for DNA extraction and molecular identification.

### Morphological analysis

Eight males and three females collected from two European badgers in Romania (CJ005077 from Hărman, Braşov County and CJ005086, from Charlottenburg, Timiş County) were examined as temporary mounts in lactophenol. Five morphometric features in males (body length, body width, oesophagus length, length of spicules, length of gubernaculum) and six morphometric features in females (body length, body width, oesophagus length, distance between the vulva and the caudal end, distance between the anus and the caudal end, distance between

the vulva and anus) were evaluated. Furthermore, 50 L1 larvae collected from the lungs of the same European badgers were also measured (length and maximum width). Measurements were taken using an Olympus BX61 microscope, DP72 digital camera and the Cell<sup>^</sup>F imaging software (Olympus Corporation, Tokyo, Japan). One male was available for measurements in Germany. No adult specimens were available for measurement from the European badger collected in Bosnia and Herzegovina. Additionally, larvae collected from the experimentally infected snails were also examined.

### Experimental life-cycle of *P. falciformis* in *Cornu aspersum*

First-stage larvae of *P. falciformis* were recovered from the lungs of a naturally infected European badger (CJ005086), hunted in Charlottenburg, Timiş County, Romania (45.975825°N, 21.518763°E) by the Baermann method [44]. The resulted solution was collected into two 50 ml Falcon tubes, centrifuged at 600× *g* for 3 min and the sediment examined under light microscopy. Larvae obtained were morphologically and molecularly identified as *P. falciformis* (based on sequence identity with morphologically confirmed adults). Single infective doses of 200 L1 each were collected and used for the infection of snails. *Cornu aspersum* snails not exposed to any nematodes of vertebrates were purchased from a commercial provider from Puglia, Italy. The snails were kept in a plastic box, covered with a fine mesh, in a temperature-controlled room (21 ± 2 °C) and fed lettuce every second day. Water was provided *ad libitum*. Moreover, the boxes were humidified twice a day. To exclude the presence of any previous parasitic infections, a subset of 10 snails were artificially digested and microscopically examined, one day before the infection. The experimental infection took place in the Unit of Parasitology of the Department of Veterinary Medicine of the University of Bari, Italy. *Cornu aspersum* snails (*n* = 30) were deprived of food 24 h before the infection and then placed individually into infection chambers, composed of six circular cell culture wells (Corning; CellBIND; Sigma-Aldrich, St. Louis, Missouri, USA). Each well contained a potato slice (0.3–0.4 mm thick, obtained with a circular puncher) with the infective dose on the surface. The infection chambers were covered with a wet gauze cloth and secured with rubber bands. The snails were maintained in the infection chamber for 24 h and then released in the rearing box.

Larval development of *P. falciformis* was assessed by artificial digestion [45] of five randomly selected snails at 3 (T1), 6 (T2), 10 (T3), 15 (T4), 20 (T5) and 30 (T6) days post-infection (dpi). At each dpi, the suspension obtained from the gastropod digestion was microscopically examined and, when present, larvae were isolated and preserved in 70% ethanol. Larvae were then cleared

**Table 1** The examined samples and number of European badgers infected with *P. falciformis*

Country	No. of European badgers examined	Positive	Prevalence (%)
Romania	27	9	33.3
Bosnia and Herzegovina	1	1	nd
Germany	4	3	75

Abbreviation: nd not determined

and examined as temporary mounts in glycerol and digital images and measurements were taken using Leica LAS<sup>®</sup> AF 4.1 software.

### Molecular analysis

The specimens used for molecular analysis are shown in Table 2. DNA was isolated from one male, one female fragment and three pools of L1 collected separately from three infected European badgers in Germany, using the DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. The ribosomal DNA (rDNA) region including partial 18S rRNA gene, internal transcribed spacer 1 (ITS1), 5.8S rRNA gene, internal transcribed spacer 2 (ITS2) and partial 28S rRNA gene and a partial sequence of the mitochondrial cytochrome *c* oxidase subunit 1 gene (*cox1*) were all amplified using nematode-specific primers. For the rDNA region we used combinations of the forward primers N18SF1, NF1 and NC1 and the reverse primers D3B, NC2 and NC5BR [44–49]. For the *cox1* sequence we used the primers MetCOI-F1 and JB4.5 [50–52]. PCR was performed with HOT FIREPol<sup>®</sup> Blend Master Mix (Solis BioDyne, Tartu, Estonia), 200 nM final concentration of forward and reverse primers each and 100 ng of nematode DNA in a 50 µl reaction volume. PCR cycling conditions were as follows: 15 min activation/initial denaturation at 95 °C, 35 cycles of 20 s denaturation at 95 °C, 30 s annealing at 54 °C and 2 min extension at 72 °C, followed by a 5 min 72 °C final elongation. Amplicons were analysed on 1.5% agarose gels, gel-purified, cloned into pDrive vector (Qiagen, Hilden, Germany) and sequenced by an external service provider (LGC Genomics, Berlin, Germany). Sequence chromatograms were checked manually and complete sequences, assembled from overlapping amplicons, were submitted to the GenBank database under the accession numbers KY365435–KY365437.

Genomic DNA was extracted from two adult nematodes from Romania, using a commercial kit (Isolate II

Genomic DNA Kit, Bioline, UK), according to the manufacturer's instructions. For each nematode, PCR amplification of a ~700 bp fragment of the *cox1* gene and of the internal transcribed spacer 2 (ITS2, ~500 bp) of the rRNA gene were performed, using primers and protocols available in literature [47, 51]. The amplicons were purified using a commercial kit (Isolate II PCR and Gel Kit, Bioline, UK) and sequenced using an external service (performed by Macrogen Europe, The Netherlands).

Genomic DNA from L1 collected from one European badger from Bosnia and Herzegovina was extracted using a commercial kit (DNeasy Blood & Tissue Kit, Qiagen, GmbH, Hilden, Germany), in accordance with the manufacturer's instructions, and a partial fragment of the ribosomal internal transcribed spacer 2 (ITS2) was amplified as previously described [47]. Amplicons were purified and sequenced in both directions using the same primers as for PCR, employing the Taq Dye Deoxy Terminator Cycle Sequencing Kit (v.2, Applied Biosystems) in an automated sequencer (ABI-PRISM 377). Sequences were aligned using the Geneious R9 software package (<http://www.geneious.com>) and compared (BLASTn) with those available in the GenBank database (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>).

Additionally, the DNA was isolated from three specimens of each larval stage collected from experimentally infected snails, following the same protocol used for nematodes from Bosnia and Herzegovina.

### Phylogenetic analysis

For molecular phylogenetic analyses datasets of sequences obtained from BLAST searches of the NCBI nucleotide (nt/nr) database using complete and partial *Perostrongylus* sequences were trimmed to homologous ends and realigned using the multiple sequence alignment program MAFFT 7 [53] with the L-INS-i method for the 28S D2–D3 and *cox1* sequence data sets and the structure-aided Q-INS-i method for the ITS2 sequence

**Table 2** Samples used for molecular analysis

Sample type	Sample code	Locality of origin	Country	Target gene	Primers	GenBank ID
Adult nematode (f)	CJ005077	Härman	Romania	ITS2	NC1/NC2 <sup>a</sup>	MG733142
Adult nematode (f)	CJ005086	Charlottenburg	Romania			
Adult nematode (f)	CJ005077	Härman	Romania	<i>cox1</i>	LCO/HCO <sup>b</sup>	MG736730
Adult nematode (f)	CJ005086	Charlottenburg	Romania			
Adult nematode (m) + L1 pools	DE-FD-Mm3	Fulda	Germany	rDNA	NC18SF1/D3B	KY365435
Adult nematode (m) + L1 pools	DE-FD-Mm3	Fulda	Germany	<i>cox1</i>	MetCOI-F1/JB4.5	KY365437
L1	OP137/17	Semizovac	Bosnia and Herzegovina	ITS2	NC1/NC <sup>a</sup>	MG910460
L1–L3 from experimentally infected <i>Cornu aspersum</i>				ITS2	NC1/NC2 <sup>a</sup>	MG733142

<sup>a</sup>As in [47]

<sup>b</sup>As in [51]

data set. Phylogenetic trees were constructed using Bayesian analysis (MrBayes 3.2) (10,000 tree generations, sampling each 10, discarding first 250 trees) and Tree-Dyn for tree drawing at the phylogeny.fr platform [54]. The 28S D2-D3 data set included 25 taxa and sequences homologous to nucleotides (nt) 3053–3968 of the *P. falciformis* sequence (KY365435). The ITS2 data set included 26 taxa and sequences homologous to nt 2513–2983 (including 15 nt of the flanking 5.8S rRNA gene and 28S rRNA gene). The *cox1* data set included 15 taxa and sequences homologous to nt 200–650 of KY365437.

### Histological analysis

Pieces of lung tissues originating from two fresh (unfrozen) European badgers collected in Romania (CJ005077 from Hărman, Braşov County and CJ005086, from Charlottenburg, Timiş County) containing nodules with the nematodes were fixed in 10% phosphate-buffered formalin for 24 h, routinely processed, embedded in paraffin wax, cut into 4 µm sections, and stained with haematoxylin and eosin (H&E).

### Results

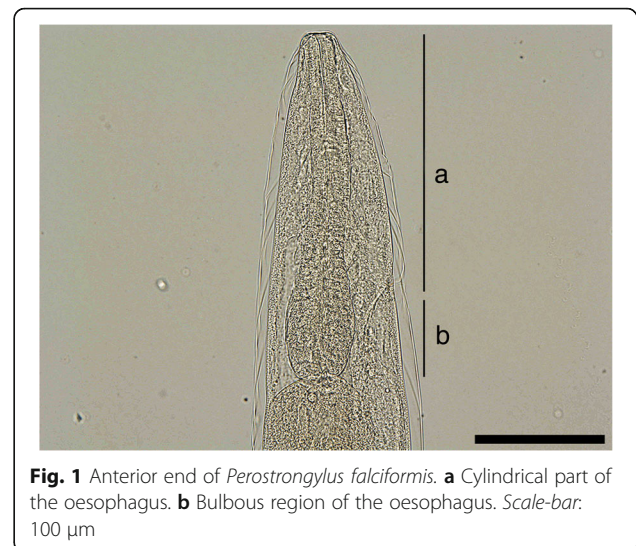
Out of the 32 examined European badgers, *P. falciformis* was found in 13 animals from all countries (Table 1).

### Morphological description of the adults

Adult worms show a pronounced sexual dimorphism, the females being larger than the males. Both sexes have a cylindrical body, uniformly coloured, elongated, thread-like, very thin and extremely coiled inside nodules, making the removal of intact specimens difficult. The cuticle at the anterior end is smooth and the mouth opening is placed terminally. The buccal cavity is small, rudimentary, and opened into a clavate oesophagus which is composed of a cylindrical part in the anterior two-thirds of its length and a posterior bulbous region (Fig. 1).

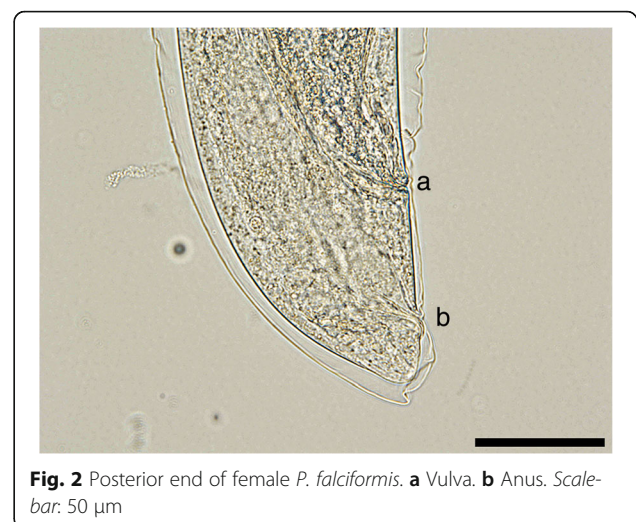
The posterior end of females is slightly curved with the vulvar and anal openings on the lower curvature (Fig. 2). Morphometric data are shown in Table 3. In the uterus, larvated eggs are clearly visible (Fig. 3), demonstrating the ovoviviparity (Fig. 4).

The morphometric data for the males are shown in Table 3. At the posterior end, the males have a small copulatory bursa, two dissimilar and highly curved spicules, and a well-developed gubernaculum (Fig. 5). The copulatory bursa (Fig. 5a, b) is undeveloped, bi-lobed, with two symmetrical, transparent, and indistinguishable lateral lobes. The lobes are supported by rays with different appearance and origins: ventral, lateral, externo-dorsal and median. The ventral ray is short and distally split into two branches, the ventro-ventral and ventro-lateral, both similar in size. The lateral ray is divided into three short branches



**Fig. 1** Anterior end of *Perostrongylus falciformis*. **a** Cylindrical part of the oesophagus. **b** Bulbous region of the oesophagus. Scale-bar: 100 µm

with lobate appearance: externo-lateral and medio-lateral having a common trunk, slightly separated from the postero-lateral branch. The externo-dorsal ray is undivided, small and lobated. The median-dorsal ray is short, thick, and has two lateral micro-lobes and a median, sharp and short expansion (Fig. 5a). The spicules are chitinous, brown, slightly dissimilar, sickle-shaped, short, but stout. The anterior end of each spicule is knob-shaped or hemispherical and is followed by a bent caudal half, sharpened on an edge and thickened on the opposite side (Fig. 6a, b). The gubernaculum is placed between the spicules, being attached to them through protractor and retractor muscles. It is triangular, with prolonged and tapered anterior half, while the posterior end is bifurcated with a bi-lobed shape at the base (Fig. 6c).



**Fig. 2** Posterior end of female *P. falciformis*. **a** Vulva. **b** Anus. Scale-bar: 50 µm

**Table 3** Comparative morphometric data for *Perostrongylus falciformis* obtained in the present study. Measurements are in micrometres unless indicated otherwise

Country	Romania	Germany <sup>a</sup>
Male	(n = 8)	(n = 1)
Body length (mm)	11.9–23.7	26.0
Body width	136–328	160
Cuticle thickness at mid-body	4–5	nd
Distance excretory pore to cephalic end	106–136	nd
Distance anus to caudal end	38–60	40
Oesophagus length (total)	207–395	209
Oesophagus length (cylindrical part)	137–145	131
Spicules length		
Shorter spicule	97–132	117 <sup>b</sup>
Longer spicule	103–150	
Spicules maximum width	17–23	18
Gubernaculum length	39–54	48
Female	(n = 3)	
Body length (mm)	23–26	–
Body width	135–314	–
Cuticle thickness at mid-body	6–7	–
Distance excretory pore to cephalic end	132–222	–
Oesophagus length	267–273	–
Distance vulva to anus	94–105	–
Distance vulva to caudal end	176–184	–
Distance anus to caudal end	77–83	–
Larva	(n = 50)	–
Body length	310–408	–
Body maximum width	14–28	–

Abbreviation: nd not determined

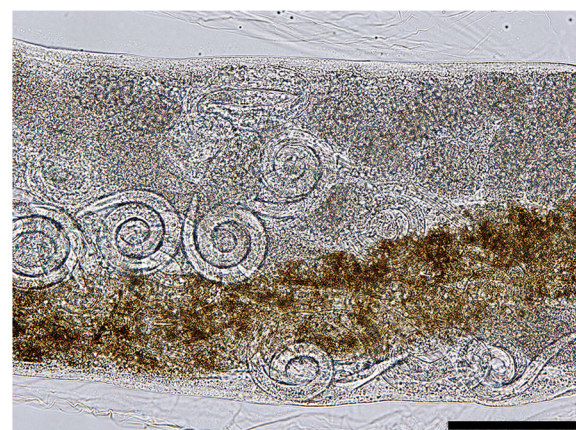
<sup>a</sup>No females and larvae were measured from Germany<sup>b</sup>The specimen was photographed from lateral view and only one spicule was visible**Development of *P. falciformis* in *Cornu aspersum***

Larval stages of *P. falciformis* were found in 27 out of 30 (90 %) experimentally infected snails. Numbers and developmental stages of larvae detected from experimentally infected snails are shown in Table 4. All control *C. aspersum* specimens digested prior to the infection ( $n = 10$ ) were negative for helminths.

A total of 293 larvae were found at the gastropod digestions. First-stage larvae were found from T1 until the end of the study period, whereas the first L3 was detected as soon as 10 dpi and increasingly found until the end of the observational period (Table 4).

**Morphology of the larval stages of *P. falciformis***

All measurements below are given in micrometres (Table 5). Metrical data are given as the range, with the mean in parentheses.

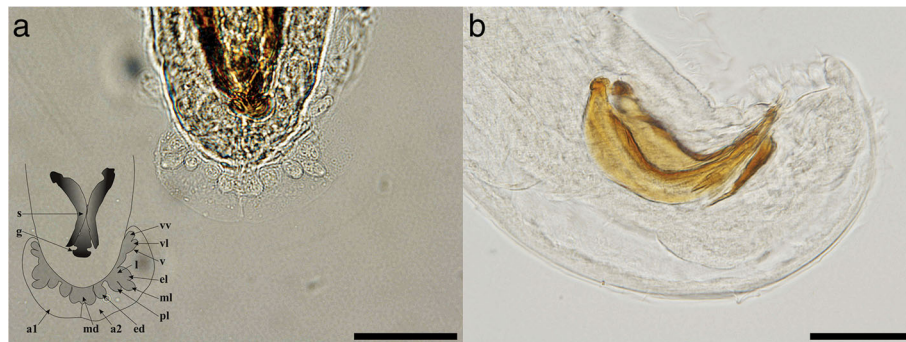
**Fig. 3** Larvated eggs are clearly visible inside the uterus. Scale-bar: 100  $\mu$ m

First-stage larvae collected from European badgers (Fig. 7a) measured 247–352 ( $317 \pm 41$ ) in length and 13–18 ( $14 \pm 1$ ) in width. The anterior extremity was featured by a narrowed, blunt end with a terminal buccal opening. The posterior extremity was 23–37 ( $32 \pm 5$ ) in length and characterized by a dorsal subterminal spine with a deep notch and a ventral bulge followed by an elongated sigmoid ending (Fig. 7a1).

Second-stage larvae (Fig. 7b) measured 403–443 ( $421 \pm 13$ ) in length and 30–33 ( $31 \pm 1$ ) in width. L2 were C-shaped and filled with granules. The button-like anterior extremity as well the tail (Fig. 7b1) resembled that of L1. The anterior and posterior extremities displayed an empty-like appearance due to the presence of the cuticle of the L2 and the sheet of the previous larval stage.

Third-stage larvae (Fig. 7c) had a ventrally curved body measuring 459–496 ( $484 \pm 12$ ) in length and 23–33 ( $27 \pm 3$ ) in width. Some L3 were still encased in the

**Fig. 4** Free L1 larva (center) and eggs with larvae of *P. falciformis*. Scale-bar: 100  $\mu$ m



**Fig. 5** Light microscopy and schematic representation of the posterior end of the males of *Perostrongylus falciformis*. **a** Copulatory bursa, dorsal view (inset: schematic representation: a1, a2, lateral lobes; v, ventral ray; vv, ventro-ventral branch of ventral ray; vl, ventro-lateral branch of ventral ray; l, lateral ray; el, externo-lateral part of lateral ray; ml, medio-lateral part of lateral ray; pl, postero-lateral branch of lateral ray; ed, externo-dorsal ray; md, median-dorsal ray; s, spicules; g, gubernaculum) **b** Copulatory bursa, lateral view. Scale-bars: 50 µm

sheets of the previous stages. The anterior end was blunt, with a distinct buccal cavity followed by two stylet-like structures (Fig. 7c1). The muscular upper part of the oesophagus was cylindrical and followed by the glandular part which gradually enlarged in the bulbar oesophago-intestinal junction. The nerve-ring and the slightly posterior excretory pore were detected at 66–76 ( $72 \pm 3$ ) and 76–92 ( $84 \pm 6$ ) from the anterior extremity, respectively. The posterior extremity was 30–43 ( $39 \pm 4$ ) in length with a digitiform tip (Fig. 7c2).

#### Molecular data and phylogenetic position of *P. falciformis*

For molecular analysis of *P. falciformis* a region of 4021 bp of the ribosomal DNA including the near complete 18S, ITS1, 5.8S, ITS2 and partial 28S and a partial region of 1075 bp of the mitochondrial cytochrome *c* oxidase subunit 1 gene (*cox1*) were sequenced from the German isolates. Furthermore, in order to compare geographical

variants, the ITS2 region for *P. falciformis* isolates from Bosnia and Herzegovina and the ITS2 region and a partial *cox1* gene for isolates from Romania were sequenced. The *cox1* sequence from Romania was 99% identical to the German isolate, leading to three residue changes in the deduced amino acid sequence. The obtained ITS2 sequences of *P. falciformis* from the three countries were 100% identical, except one clone, suggesting an overall low geographical variation. The one exceptional rDNA clone (GenBank: KY365436) of the amplicon NF1-NC2 was from a female fragment from Germany, which had 15 SNPs (1802/1817 bp identities) compared to sequences from six other clones. This could be an additional haplotype or a rare intraspecific sequence variation in the rDNA repeats.

GenBank database searches with the *P. falciformis* 18S and 28S rDNA sequences did not support the close phylogenetic relationship to *A. abstrusus* as would have been expected from the current taxonomic classification where *Perostrongylus* is considered as a subgenus of *Aelurostrongylus* [17]. Among the best matches for *P. falciformis*, according to alignment scores were species of the genera *Parafilaroides* and *Filaroides*. In contrast, the alignment score for *A. abstrusus* was lower and in the same range than to other metastrongyloid genera (not shown).

To further investigate the relationships among *Perostrongylus* and other metastrongyloid nematodes and to determine the molecular phylogenetic relation, analyses were performed with ITS2, partial 28S (domains D2-D3) (Fig. 8) and partial *cox1* sequences (Fig. 9) as biomarkers. These sequences were chosen due to their higher resolution at the species level and their length was adjusted to include a maximum of high scoring metastrongyloid nematodes from BLAST search on GenBank.

In the phylogenetic trees, *P. falciformis* and *A. abstrusus* were clearly separated, assigned to different clades,



**Fig. 6** Spicules and gubernaculum of *P. falciformis*. **a** Knob-shaped anterior end of the spicule. **b** The bent caudal half of the spicule. **c** Gubernaculum. Scale-bar: 50 µm

**Table 4** Total number (mean no. per snail  $\pm$  SD) for the developmental stages of *Perostrongylus falciformis* larvae collected from five experimentally infected snails at 3 (T1), 6 (T2), 10 (T3), 15 (T4), 20 (T5) and 30 (T6) days post-infection

	First-stage larvae	Second-stage larvae	Third-stage larvae	Total
T1	19 (3.8 $\pm$ 2.7)	–	–	19 (6.3 $\pm$ 11.0)
T2	10 (2.0 $\pm$ 1.6)	–	–	10 (3.3 $\pm$ 5.8)
T3	13 (2.2 $\pm$ 1.8)	59 (11.8 $\pm$ 2.6)	1 (0.2 $\pm$ 0.4)	73 (24.3 $\pm$ 30.6)
T4	3 (0.6 $\pm$ 0.9)	78 (15.6 $\pm$ 7.2)	1 (0.2 $\pm$ 0.4)	82 (27.3 $\pm$ 43.9)
T5	4 (0.8 $\pm$ 1.1)	37 (7.4 $\pm$ 5.7)	4 (0.8 $\pm$ 1.1)	45 (15.0 $\pm$ 19.1)
T6	5 (1.0 $\pm$ 1.7)	36 (7.2 $\pm$ 3.8)	23 (4.6 $\pm$ 4.1)	64 (21.3 $\pm$ 15.6)

which was supported by all three genetic markers. Interestingly and consistent with discussed morphological similarities and forms of reproduction, the phylogeny inferred from the two rDNA sequence analyses, grouped *P. falciformis* together with species of the genera *Parafilaroides* and *Filaroides* (both within the family Filaroididae Schulz, 1951). The phylogenetic relationships of the Metastrongyloidea rDNA sequences correspond to previous studies [2]. There was strong support for groups of congeneric species and for the exclusion of the family

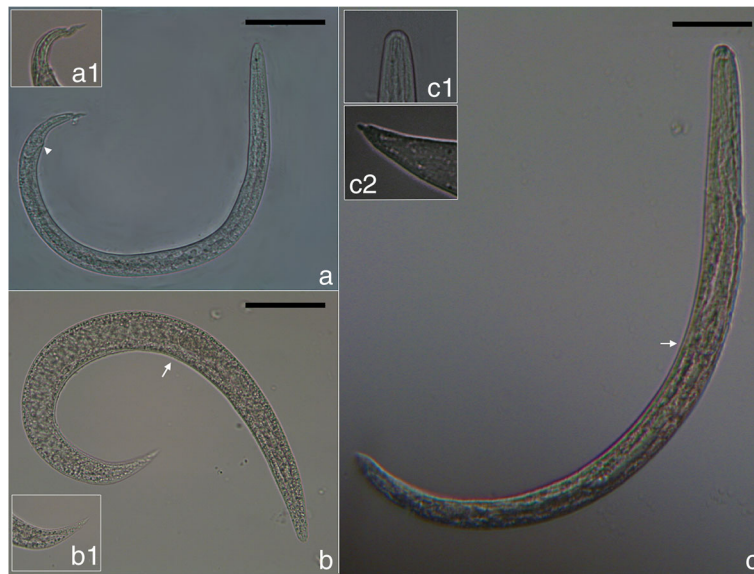
Crenosomatidae from other metastrongyloid taxa. The relations obtained here for the partial *cox1* sequence seem less consistent, because some morphologically proven congeneric species grouped with unrelated families, e.g. *A. abstrusus* with the Crenosomatidae and *A. costaricensis* with the Metastrongylidae.

#### Pathology caused by *P. falciformis* in European badgers

Grossly, multifocal, slightly elevated, well defined, small brown-black nodules were randomly distributed in the

**Table 5** Measurements (in micrometres) of first- (L1), second- (L2) and third-stage (L3) larvae ( $n = 10$  each) of *Perostrongylus falciformis*

Measurements	L1	L2	L3	Reference
Body length	247–352 (317 $\pm$ 41)	403–443 (421 $\pm$ 13)	459–496 (484 $\pm$ 12)	Present study
	270–370	350–420	340–440	[11]
	–	–	380–440	[63]
Maximum body width	13–18 (14 $\pm$ 1)	30–33 (31 $\pm$ 1)	23–33 (27 $\pm$ 3)	Present study
	10–17	26	30–32	[11]
	–	–	24–27	[63]
Tail length	23–37 (32 $\pm$ 5)	35–46 (41 $\pm$ 3)	30–43 (39 $\pm$ 4)	Present study
	33–40	–	30–46	[11]
Oesophagus length	99–163 (132 $\pm$ 25)	145–161 (153 $\pm$ 5)	162–196 (173 $\pm$ 10)	Present study
	130–150	161	130–183	[11]
Intestine length	130–150	204	176–260	[11]
Genital primordium, distance from posterior extremity	66–117 (88 $\pm$ 17)	–	109–166 (141 $\pm$ 15)	Present study
Nerve ring, distance from anterior extremity	–	–	66–76 (72 $\pm$ 3)	Present study
	85–90	–	–	[11]
Excretory pore, distance from anterior extremity	–	–	76–92 (84 $\pm$ 6)	Present study
	90–100	–	75–90	[11]
Ratio oesophagus length to body length	0.399–0.464	0.359–0.362	0.352–0.395	Present study
Ratio distance from posterior extremity to genital primordium to body length	0.267–0.331	–	0.237–0.334	Present study
Anus to posterior extremity	30	40	30	[11]



**Fig. 7** Larval stages of *P. falciformis*. **a** First-stage larva and detail of the posterior extremity (a1) and well-visible anus (arrowhead). **b** Second-stage larva and detail of the posterior extremity (b1) and oesophago-intestinal junction (arrow). **c** Third-stage larva and details of the anterior (c1) and posterior (c2) extremities and oesophago-intestinal junction (arrow). Scale-bars: 50 µm

subpleural region of both lungs (Fig. 10a). Frequently, the parasite-containing nodules were associated with multifocal to coalescing areas of moderate alveolar emphysema (Fig. 10a). On the cut section, multiple, equally thin, blackish, partially coiled, *P. falciformis* adults were embedded in the lung parenchyma (Fig. 10b), without a significant preference for certain lung lobes. The bronchi were filled with a mucinous, foamy exudate (Fig. 10a).

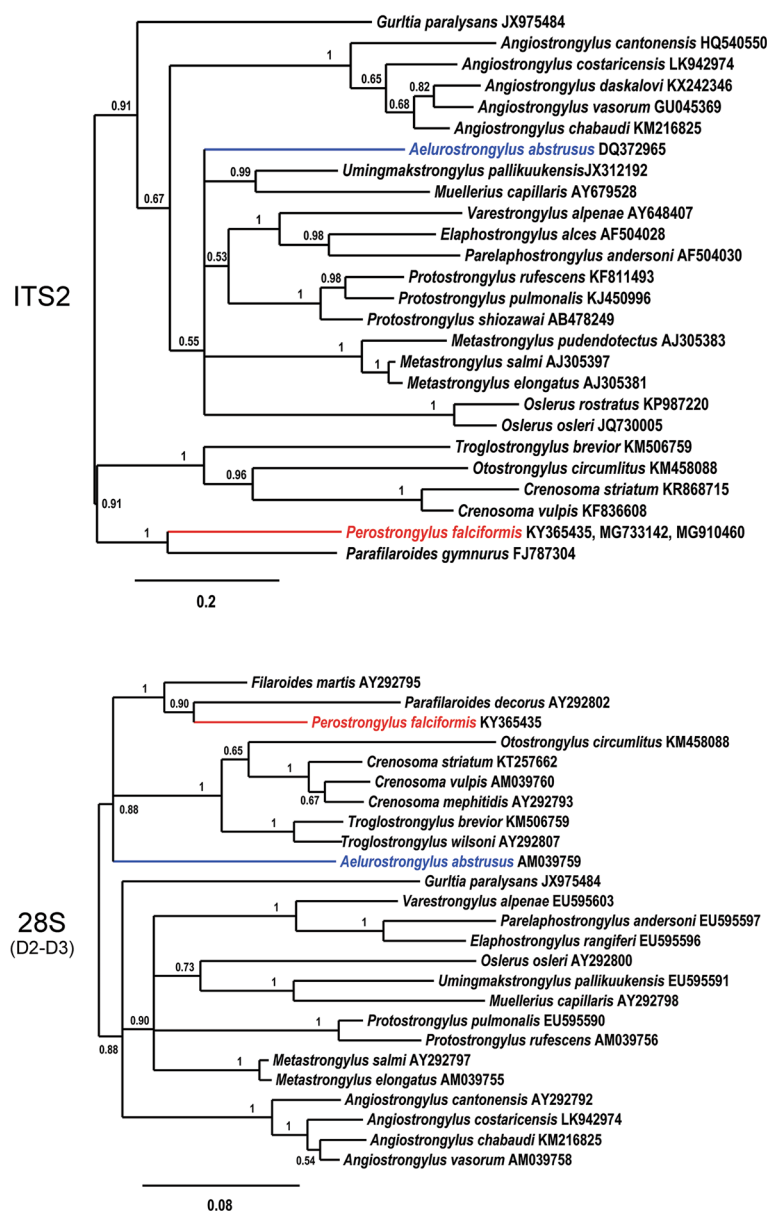
Histologically, *P. falciformis* adults embedded in the lung parenchyma were present in high number in all examined histological sections. Few larval stages were also noted, especially in the bronchioles. *Perostrongylus falciformis* adults have a thin smooth cuticle, coelomyarian-polymyarian musculature and pseudocoelom with prominent intestine lined by cells that frequently contain brown-black granular pigment, and large uterus filled with developing eggs and larvae (Fig. 11c). Viable *P. falciformis* adults induce a mild inflammatory response consisting of macrophages (frequently laden with hemosiderin), occasional multinucleate giant cells, some lymphocytes and eosinophils (Fig. 11a-c). Few fibroblasts and thin collagen bundles were scattered between the above described cells. Smooth muscle hyperplasia of the terminal airways and alveolar emphysema were occasionally associated with the foci of interstitial pneumonia. Some viable adult nematodes are directly surrounded by a thin fibrous capsule. The inflammatory infiltrate extends from the parasite to the adjacent parenchyma, markedly expanding the alveolar walls. Alveolar emphysema was also focally associated with the foci of interstitial pneumonia. Bronchus-associated lymphoid

tissue hyperplasia and alveoli filled by cellular infiltrate (as described above) and oedema were also observed.

Degenerated adult parasites (Fig. 11e) induced a marked inflammatory response consisting of poorly localized granulomas (sometimes centred on the parasite debris) and lympho-histiocytic and eosinophilic interstitial pneumonia. Occasionally, free *P. falciformis* larvae were present in the peribronchiolar and bronchiolar spaces (Fig. 11f). At these sites, the bronchiole walls were segmentally infiltrated by macrophages, epithelioid cells and multinucleate giant cells admixed with few eosinophils, fibroblasts and coiled larvae. Additionally, moderate to severe smooth muscle and bronchiolar epithelial hyperplasia with luminal obstruction by sloughed epithelial cells admixed with mucus, leukocytes (as described above) and parasite larvae were noted.

## Discussion

This study provides the first molecular evidence for the validity of the genus *Perostrongylus*, which was previously synonymized with or considered a subgenus of *Aelurostrongylus*. With the exception of *A. abstrusus*, other species previously assigned to genus *Aelurostrongylus*, namely *A. brauni* and *A. fengi* were subsequently transferred to different genera. Due to the extremely poor description of *A. brauni* (a parasite originally described as *Strongylus brauni* from the Indian civet, *Viverra zibetha*), its classification as *species inquirenda* has already been suggested [19] and is now designated as *Viverrostrongylus brauni* [20]. *Aelurostrongylus fengi* was described from Crab-eating mongoose, *Herpestes*



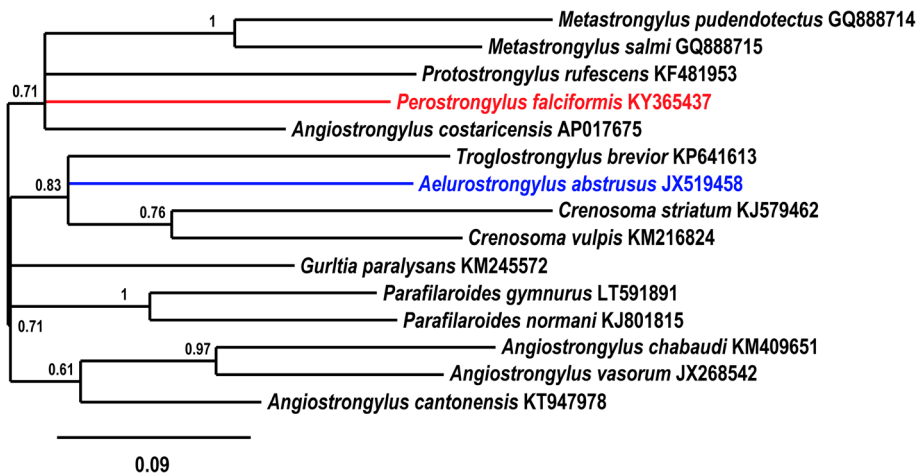
**Fig. 8** Phylogenetic relationships of *P. falciformis* (red) with *A. abstrusus* (blue) and other metastrongyloid nematodes. Phylogenetic analysis based on ITS2 and partial 28S rDNA (domains D2-D3) sequences of metastrongyloid genera. Trees are constructed using Bayesian inference. Posterior probability values are shown next to the nodes; branches with values < 0.5 are not shown. The scale-bar indicates the number of substitutions per site

*urva*, as *Pulmostrongylus fengi*. The taxonomic status of *Pulmostrongylus* (which includes already several species) is under debate, and currently it is considered a valid genus [18] or a subgenus of *Protostrongylus* [16]. Our molecular data provide evidence that *P. falciformis* and *A. abstrusus* are not congeneric. The conclusion drawn from this is the validity of the full genus status of *Perostrongylus* and the species name *P. falciformis* for the European badger lungworm.

Hence, the genus *Aelurostrongylus* becomes monotypic and includes only the type-species *A. abstrusus*.

Considering the rigorous rules of taxonomy, an interesting fact arises regarding *A. abstrusus*. As the first description of the species used the specific name *pusillus* [4], the valid name for this species should be *Aelurostrongylus pusillus* (see above). However, due its veterinary importance and worldwide use since more than a century under the name *A. abstrusus*, we suggest the latter name to be used.

From a phylogenetic standpoint, *Perostrongylus* is a valid genus and most probably includes two species: *P. falciformis*, a parasite of *M. meles* and possibly *M.*

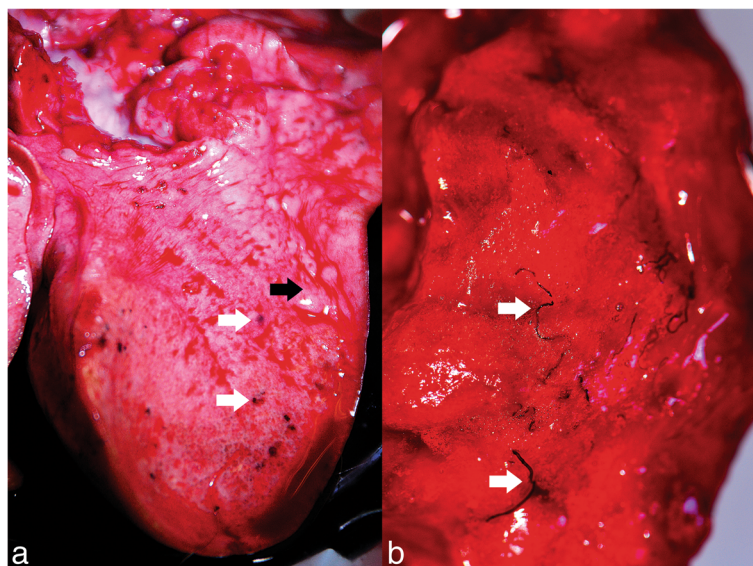


**Fig. 9** Phylogenetic tree (Bayesian inference) using *cox1* sequences for *P. falciformis* (red), *A. abstrusus* (blue) and species of other metastrongyloid genera. Posterior probability values are shown next to the nodes; branches with values < 0.5 are not shown. The scale-bar indicates the number of substitutions per site

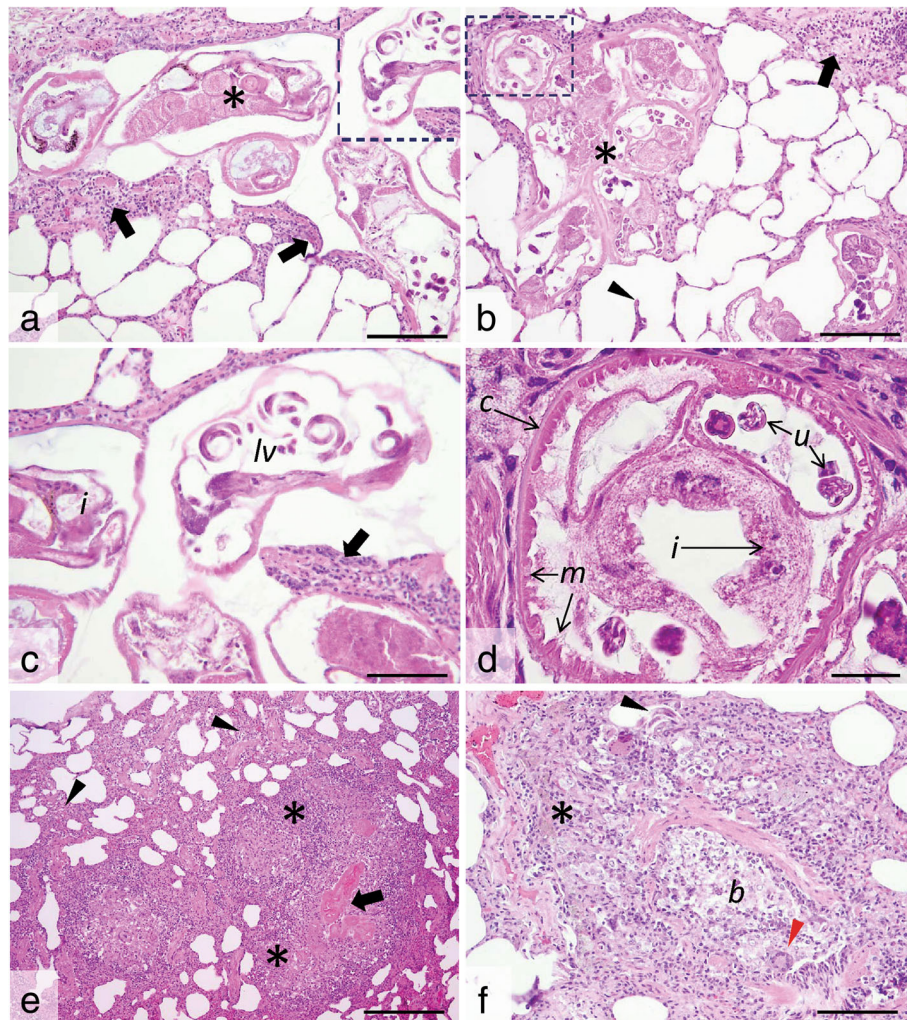
*erminea* in Europe, and *P. pridhami* [21], a parasite of *N. vison* and *Mustela erminea* in North America. Our view is strongly supported by molecular phylogenetic data currently available only for *P. falciformis*. Further molecular studies are needed also for *P. pridhami* in North America, to conclude its phylogenetic position and relationships to *P. falciformis*.

Moreover, the phylogenetic analysis of the relationships of *P. falciformis* with species of other metastrongyloid genera clearly assigned *Perostrongylus* and *Aelurostrongylus* to different clades. *Perostrongylus falciformis* was grouped with high support together with the

genera *Filaroides* and *Parafilaroides* (family Filaroididae), whereas *A. abstrusus* represented a single branch with no sister groups. Alignments of the internal transcribed spacer sequences (ITS1, ITS2) for different genera of the Metastrongyloidea are difficult because of the high variability in comparison to ribosomal RNA genes (18S, 28S). We therefore performed the ITS2 multiple sequence alignment using a method of the program MAFFT which also considers secondary structures. However, the obtained correspondence between the analyses of ITS2 and the 28S rDNA D2-D3 region corroborate the inferred phylogenetic position of *P. falciformis*



**Fig. 10** Gross lesions produced by *P. falciformis*. **a** Adults in nodules in the subpleural space (white arrows) and the presence of alveolar emphysema (black arrow). **b** Adults in the pulmonary parenchyma (white arrows)



**Fig. 11** Histological cross- and tangential sections of *P. falciformis* in the lung parenchyma. **a, b.** Viable *P. falciformis* adults (asterisks) coiled in the lung parenchyma and surrounded by a mild leukocyte reaction (many macrophages, occasional multinucleate giant cells, some lymphocytes and eosinophils) (black arrows) and smooth muscle hyperplasia. The alveolar walls are moderately expanded by the above described inflammatory cell population, with occasional alveolar wall rupture (arrowhead) and emphysema. **c, d** Detail of the marked areas in **a** and **b**. The parasites have a thin smooth cuticle (**c**) and pseudocoelom, coelomyarian-polymyarian musculature (**m**), intestine (**i**) with granular pigment and large uterus (**u**) filled with developing larvae (**lv**). The leukocyte reaction is also visible (black arrow in **c**). **e, f.** Free *P. falciformis* larvae (with thin walls and granular content) (black arrowhead in **f**) are present in the bronchiolar (**b**) and peribronchiolar spaces, associated with prominent inflammatory reaction consisting of many macrophage (some laden with hemosiderin) (asterisk in **f**), epithelioid cells and multinucleate giant cells (red arrowhead in **f**) and few eosinophils and fibroblast. Degenerated parasites (black arrow in **e**) induce a marked inflammatory response consisting of ill-defined granulomas (asterisks in **e**) and a locally-extensive interstitial lympho-histiocytic and eosinophilic pneumonia (arrowheads in **e**); H&E staining,  $\times 20$  (**a, b** and **f**),  $\times 40$  (**c**),  $\times 100$  (**d**) and  $\times 10$  (**e**). Scale-bars: **a, b, f**, 100  $\mu\text{m}$ ; **c**, 50  $\mu\text{m}$ ; **d**, 25  $\mu\text{m}$ ; **e**, 200  $\mu\text{m}$

close to the two genera of the Filaroididae within the superfamily Metastrongyloidea.

The close relationship of *Perostrongylus*, *Filaroides* and *Parafilaroides* in the molecular phylogeny is in good agreement with morphological characters and forms of reproduction. Males of species in all three genera have short, stout and arcuate spicules, a single-element gubernaculum and females are ovoviparous. In contrast, males of *A. abstrusus* have slender (half the width of *P. falciformis*) and straight spicules, a gubernaculum of two

joined equal elements and the females are oviparous [55]. The present paper also provides a very detailed morphological description of the adult stages of *P. falciformis* which was previously relatively brief [8, 10].

Both species of genus *Perostrongylus* are parasites of the Mustelidae. *Perostrongylus falciformis* has been reported so far only in European badgers from various countries in the western Palearctic, including Germany [8, 11], Ukraine [56], Russia [57], Italy [58], UK [26], Norway [27], Poland [28], and Bosnia and Herzegovina

[29]. Here we report for the first time the presence of *P. falciformis* in Romania. In a study from UK on stoats, unidentified nematodes were shown in a histological section of a lung [59]. Later, Simpson et al. [60], hypothesized, based on the morphology of the female in these histological sections that the nematodes could be *P. falciformis*. However, without morphological or genetic data, this remains only a presumption and we do not list stoats as confirmed hosts for *P. falciformis*.

*Perostrongylus pridhami* has been reported mainly in the American mink, *N. vison* in North America: Ontario, Canada [21, 22, 37, 42], Newfoundland, Canada [30], and Montana, USA [40] and in stoats, *M. erminea* from Newfoundland [30]. Torres et al. [32] mentioned *P. pridhami* in European badgers in Spain. However, this is highly unlikely, as it probably represents a misidentification of *P. falciformis*.

Interestingly, one study on invasive American minks in Spain [33] reported a specimen identified as *Aelurostrongylus* spp. As the specimen was not identified to the species level, it is not known if this represents *P. pridhami*, a natural parasite of this host in North America, but in an invasive population, or *P. falciformis*, which could suggest an adaptation from European badgers to invasive American minks.

Lungworms of genus *Perostrongylus* seem to occur with variable prevalence in mustelids across their distribution range (Table 6). Additionally to the overview in this table, unidentified lungworms were reported in 18% (8/45) of European badgers in Germany, with pathological lesions consistent with those produced by *P. falciformis* [61]. In our opinion, a low prevalence or total absence of these parasites in studies with a reasonably large number of samples are likely the result of a rather superficial examination; probably *P. falciformis* is present in European badgers across their distribution range.

The data presented here indicate that *C. aspersum* is a suitable intermediate host of *P. falciformis*. However, in

a series of laboratory infection studies, larval development from L1 to L3 was demonstrated to occur in two slug species [*Deroceras agreste* (Linnaeus, 1758) and *Arion hortensis* (Férussac, 1819)] and five species of terrestrial snails [*Trochulus hispidus* (Draparnaud, 1801), *Cepaea hortensis* (Müller, 1774), *C. nemoralis* (Linnaeus, 1758), *Euomphalia strigella* (Draparnaud, 1801) and *Succinea putris* (Linnaeus, 1758)] [11, 62].

After 24 hours, the L1 were found coiled between the muscle fibres of the snails' foot and the first moult occurred at 6–8 dpi at room temperature (or as long as 14 days at lower temperatures) [11, 62]. In the present study, the first L2 larvae were found at 10 dpi (however, the previous examination time was 6 dpi). Wetzel [11] mentions the second moult at 10–12 dpi. In our study, the first L3 were found at 10 dpi, but the largest numbers were present in snails at 30 dpi. Wetzel [11] also mentioned that these time frames are slightly variable according to the species of snail used, but no other details were provided. Wetzel [11, 62] described in detail L1–L3 larval stages and provided drawings for L1 and L3. These morphological details are largely consistent with our results (Table 5), with only minor differences. In addition, our present work provides the first detailed photomicrographs of L1–L3.

The life-cycle of *P. pridhami* described in North America [21] showed a role as potential intermediate hosts for several experimentally infected species of aquatic snails [*Physa integra* (Haldeman, 1841), *Gyraulus deflexus* (Sandberger, 1858), *G. crista* (Linnaeus, 1758), *Ampullaria cuprina* Reeve, 1856] as well as terrestrial snails [*Zonitoides arboreus* (Say, 1816), *Discus cronkhitei* (Newcomb, 1865), *Novisuccinea ovalis* (Say, 1817), *Anguispira alternata* (Say, 1816)] or slugs [*Deroceras gracile* (Müller, 1774)] [21]. As in *P. falciformis* [62], larvae of *P. pridhami* penetrate the foot of snails [21]. Stockdale [37] succeeded to infect terrestrial snails by

**Table 6** Reported prevalence for *Perostrongylus* spp.

Species	Host	Country	Prevalence (%) (infected/examined)	Reference
<i>P. falciformis</i>	<i>Meles meles</i>	Germany	50.0 (6/12)	[10]
<i>P. falciformis</i>	<i>Meles meles</i>	Poland	22.2 (2/9)	[28]
<i>P. falciformis</i>	<i>Meles meles</i>	Norway	33.3 (3/9)	[27]
<i>P. falciformis</i>	<i>Meles meles</i>	UK	0.8 (1/118)	[26]
<i>P. falciformis</i>	<i>Meles meles</i>	Italy	52.6 (10/19)	[58]
<i>P. falciformis</i>	<i>Meles meles</i>	Spain	3.5 (3/85)	[32]
<i>P. falciformis</i>	<i>Mustela erminea</i>	UK	13.5 (5/37)	[59]
<i>P. pridhami</i>	<i>Neovison vison</i>	Canada	8.6 (13/152)	[42]
<i>P. pridhami</i>	<i>Neovison vison</i>	Canada	2.1 (1/48)	[30]
<i>P. pridhami</i>	<i>Mustela erminea</i>	Canada	12.5 (8/40)	[30]
<i>Perostrongylus</i> sp.	<i>Neovison vison</i>	Spain	2.0 (1/50)	[33]

injection. The dynamics of larval development in snails is not known for *P. pridhami*. The prepatent period for this species was 23–28 days in experimentally infected minks [21], slightly longer than for *P. falciformis* in European badgers [11, 62]. As demonstrated for other lungworms of carnivores, *P. pridhami* can be transmitted to minks after ingestion of paratenic hosts (mice, birds, amphibians and fish) [21] but no such information is available for *P. falciformis*.

Additional information is provided on the development of *P. pridhami* in minks experimentally infected *via* gastric tube with L3 from terrestrial snails [37]. The first moult in minks (L3 to L4) occurred 3 dpi and the final moult (L4 to L5) at 7 dpi [37]. The migration in the minks included penetration of the stomach wall, crossing the peritoneal cavity and the diaphragm, followed by penetration of the visceral pleura of the lungs, all these occurring within the first 24 hours [37]. The migration pattern and last two moults for *P. falciformis* in European badgers are not known. Anderson [21] also described the morphology of L1–L3 of *P. pridhami* which seem to be similar to that of the larvae of *P. falciformis* ([11, 62]; present study). L1–L3 of *P. pridhami* are all illustrated in detail [21].

As concluded by Hancox [25], although the European badger is affected by a wide range of parasites, average rates of infection will not have a significant effect on host population regulation. However, individuals may be affected by a high parasite load. Lesions and symptoms produced by *P. falciformis* in European badgers have been described previously [8, 10, 27, 29, 60]. Additionally, lesions consistent with a possible *P. falciformis* infection in *M. erminea* were found in the UK [59, 60]. In North America, lesions produced by *P. pridhami* in minks have also been described [21, 37, 38]. Generally, the pathology caused by the two species of *Perostrongylus* is similar and results in vomiting (though after experimental infection), coughing (usually when large numbers of parasites are present) and can be complicated by the presence of co-infections [i.e. with *Filaroides martis* (Werner, 1782) in minks]. However, the clinical signs are known only from experimental infections. The importance of co-infections with *Angiostrongylus daskalovi* Janchev & Genov, 1988 in European badgers [63] on the clinical outcome is unknown.

The lesions are produced either by infective larval migration and are located at various levels (stomach, peritoneum, pleura) or by larvae migrating through the lung parenchyma and adults. Generally, adults of *P. falciformis* are found either in subpleural granulomas or embedded in the lung parenchyma (present study). Similar subpleural nodules were found also in minks infected with *P. pridhami* [37, 38]. The histological lesions in our study are to date the most detailed and largely similar to

the lesions observed in other studies on *P. falciformis* [27, 29, 59] or *P. pridhami* [38].

## Conclusions

Molecular phylogenetic and morphological data support the validity of the genus *Perostrongylus*, with probably two species: *P. falciformis* in European badgers in Europe and *P. pridhami* in minks in North America. Moreover, *Aelurostrongylus* becomes a monotypic genus, with *A. abstrusus* as the type- and only species. Interestingly, the two genera clearly belong to two different evolutionary branches: *Perostrongylus* is grouped together with the genera *Filaroides* and *Parafilaroides* (both in family Filaroididae), whereas *Aelurostrongylus* belongs to a single branch, with no sister groups. The present study also demonstrated for the first time that *C. aspersum* snails are suitable intermediate hosts. Several aspects remain unknown. One question is which species of *Perostrongylus* is found in American minks invasive to Europe. The role of paratenic hosts in the life-cycle of *P. falciformis* is also a matter to be explored. Moreover, molecular data from *P. pridhami* will bring further proof for the phylogenetic position of *Perostrongylus* among metastrongyloids.

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## Availability of data and materials

The data supporting the conclusions of this article are included within the article. Representative sequences were submitted to the GenBank database under the accession numbers KY365435–KY365437. Voucher specimens are available in the collection of the Museum of Parasitology, Department of Parasitology and Parasitic Diseases, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Romania under accession numbers CJ005077, CJ005086. The dataset and reference materials are available from the corresponding author upon request.

## Authors' contributions

GD collected samples, performed necropsies and wrote the manuscript. ADM collected samples, wrote the manuscript and coordinated the study. JH: collected samples and performed the phylogenetic analysis. VC performed the experimental life-cycle; FAT carried out the histopathology analysis; MAC performed the larval morphological description and illustrations. FGB collected samples, participated in necropsies and revised the manuscript. CB collected samples, carried out the phylogenetic analysis, provided critical comments on the manuscript. AMI participated in the sample collection and performed the molecular analyses. AA essentially contributed to the sample collection and performed necropsies. DO critically revised the text, coordinated the experimental life-cycle. CMG performed the morphological identification, collected samples and coordinated the study. All authors read and approved the final manuscript.

## Ethics approval and consent to participate

The study was performed in accordance with the national and European rules and regulations for research ethics. No live vertebrates were used in this study.

## Consent for publication

Not applicable.

## Competing interests

The authors declare that they have no competing interests.

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REVIEW

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# A synoptic overview of golden jackal parasites reveals high diversity of species

Călin Mircea Gherman and Andrei Daniel Mihalca\*

## Abstract

The golden jackal (*Canis aureus*) is a species under significant and fast geographic expansion. Various parasites are known from golden jackals across their geographic range, and certain groups can be spread during their expansion, increasing the risk of cross-infection with other carnivores or even humans. The current list of the golden jackal parasites includes 194 species and was compiled on the basis of an extensive literature search published from historical times until April 2017, and is shown herein in synoptic tables followed by critical comments of the various findings. This large variety of parasites is related to the extensive geographic range, territorial mobility and a very unselective diet. The vast majority of these parasites are shared with domestic dogs or cats. The zoonotic potential is the most important aspect of species reported in the golden jackal, some of them, such as *Echinococcus* spp., hookworms, *Toxocara* spp., or *Trichinella* spp., having a great public health impact. Our review brings overwhelming evidence on the importance of *Canis aureus* as a wild reservoir of human and animal parasites.

**Keywords:** Golden jackal, *Canis aureus*, Parasites

## Background

The golden jackal, *Canis aureus* (Carnivora: Canidae) is a medium-sized canid species [1] also known as the common or Asiatic jackal [2], Eurasian golden jackal [3] or the reed wolf [4]. Traditionally, *Canis aureus* has been regarded as a polytypic species (Table 1), with 14 subspecies distributed across a vast geographical territory in Europe, Asia and Africa [5, 6]. Recently, phylogenetic studies have demonstrated that at least two of the African subspecies need a formal recognition as distinct species. Koepfli et al. [3] suggested that *C. aureus anthus* forms a distinct monophyletic lineage to *C. aureus* and should be recognized as a separate species. Similarly, the phylogenetic comparison of the Egyptian jackal (*C. aureus lupaster*) with other wolf-like canids showed a close relationship with the gray wolf species complex rather than with other subspecies of golden jackals [7]. Nevertheless, because most of the studies dealing with parasites of golden jackals do not mention the subspecies, for the purpose of this review we have considered the entire group, without excluding the two former subspecies.

The distribution of golden jackals is limited to the Old World [8]. Molecular evidence supports an African origin for all wolf-like canids including the golden jackal [8]. It is considered that the colonization of Europe by the golden jackal took place during the late Holocene and early Neolithic, through the Balkan Peninsula [9]. During the last century, the species has recorded at least two geographic expansion events. A notable expansion started in the 1950s, with a second one following during the 1980s. This is particularly evident in Europe. Stable reproductive populations have been recorded in about 20 European countries, while in other nine, vagrant specimens were observed [10]. The factors that facilitate the territorial expansion of golden jackals are unclear, but land use [11], climate change [12, 13], and the lack of intra-genus competition have been suggested [12–14].

Golden jackals have an opportunistic nutritional behaviour with an extremely varied diet [15]. They prey or scavenge on small mammals, birds and their eggs, amphibians, reptiles, even invertebrates, and they take carrion when available. Occasionally, jackals also feed on vegetables or fruits. Additionally, their relatively broad home range, varying from 1.1 to 20.0 km<sup>2</sup> [16, 17], increases the chance of contact with various parasites but also with other hosts.

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**Table 1** Subspecies and geographical distribution of the golden jackal, *Canis aureus*

Subspecies	Common name	Range	Synonyms
<i>Canis a. aureus</i> Linnaeus, 1758	Common jackal	Middle Asia; Afghanistan; Iran; Iraq; Arabian Peninsula; Baluchistan; northwestern India	<i>C. balcanicus</i> ; <i>C. caucasica</i> ; <i>C. dalmatinus</i> ; <i>C. hadramauticus</i> ; <i>C. hungaricus</i> ; <i>C. kola</i> ; <i>C. lanka</i> ; <i>C. maroccanus</i> ; <i>C. typicus</i> ; <i>C. vulgaris</i>
<i>Canis a. algirensis</i> Wagner, 1841	Algerian wolf	Algeria; Morocco; Tunisia	<i>C. barbarus</i> ; <i>C. grayi</i> ; <i>C. tripolitanus</i> ;
<i>Canis a. anthus</i> Cuvier, 1820	Senegalese wolf; grey jackal; slender jackal	Senegal	<i>C. senegalensis</i>
<i>Canis a. bea</i> Heller, 1914	Serengeti wolf; Serengeti jackal	Kenya; northern Tanzania	
<i>Canis a. cruesemanni</i> Matschie, 1900	Siamese jackal; South East Asian jackal	Thailand; Myanmar; East India	
<i>Canis a. ecdensis</i> Kretzoi, 1947	Pannonian jackal	Pannonian Basin	<i>C. minor</i> ; <i>C. balcanicus</i> ; <i>C. hungaricus</i>
<i>Canis a. indicus</i> Hodgson, 1833	Indian jackal; Himalayan jackal	Pakistan; India; Nepal; Bhutan; Burma	
<i>Canis a. lupaster</i> Hemprich & Ehrenberg, 1833	African wolf; Egyptian wolf; Egyptian jackal	Egypt; Algeria; Mali; Ethiopian Highlands; Senegal	<i>C. lupaster</i> ; <i>C. lupus lupaster</i> ; <i>C. sacer</i>
<i>Canis a. moreoticus</i> Geoffroy Saint-Hilaire, 1835	European jackal; Caucasian jackal; Reed wolf	Southeastern Europe; Asia Minor; Caucasus	<i>C. graecus</i>
<i>Canis a. naria</i> Wroughton, 1916	Sri Lankan jackal	Southern India; Sri Lanka	<i>C. lanka</i>
<i>Canis a. palaestina</i> Khalaf, 2008		Palestine; Israel	
<i>Canis a. riparius</i> Hemprich & Ehrenberg, 1832	Somali wolf	Somalia; Ethiopia; Eritrea	<i>C. hagenbecki</i> ; <i>C. mengesi</i> ; <i>C. somalicus</i>
<i>Canis a. soudanicus</i> Thomas, 1903	Variagated wolf; Nubian wolf	Sudan; Somalia	<i>C. doederleini</i> ; <i>C. nubianus</i> ; <i>C. thooides</i> ;
			<i>C. variegatus</i>
<i>Canis a. syriacus</i> Hemprich & Ehrenberg, 1833	Syrian jackal	Israel; Lebanon; Jordan	

All these biological and behavioural features create premises for their infection with a broad range of pathogens, including parasites. Golden jackals are known to host a large spectrum of viral, bacterial and parasitic pathogens [18–20]. The literature survey indicates that the studies published on golden jackal parasites are usually limited to a country or, more commonly to a region, and there is no synoptic overview on this potentially important topic. The aim of the present work was to review all the published data on the parasite fauna of golden jackals in a comprehensive and updated list. The goal is consistent with the demographic and territorial expansion tendency of this species and increased contact with domestic animals and humans.

### Literature survey methodology

The list of the golden jackal parasites was compiled on the basis of an extensive literature search published from historical times until April 2017. Abstracts in conference proceedings and theses were also considered. The search queries were performed in the several databases: Pub Med [21], Science Direct [22], Web of Science [23], Helminthological Abstracts [24], Biological Abstracts [25], BioOne [26], Host-Parasite Database of the Natural History Museum (London) [27] and the web search engine Google Scholar [28]. Additionally, two Russian databases, namely the Russian Scientific Electronic Library [29] and the Scientific Library Earth Papers [30] were also used as sources of information.

The parasites are listed in tables, organized according to their taxonomic rank, and species within families are alphabetically listed. Taxonomy follows Adl et al. [31] for protists; Gibson et al. [32], Jones et al. [33], and Bray et al. [34] for trematodes; Kahlil et al. [35] and Nakao et al. [36] for cestodes; De Ley & Blaxter [37] for nematodes; Amin [38] for acanthocephalans; and the database “Catalogue of Life: 2016 Annual Checklist” by Roskov et al. [39] for arthropods. The names of the species were updated according to the current taxonomy, but synonyms used by different authors are also indicated. Each species is indexed together with the country of the report, the method of examination and reference. The records within a species are listed according to the alphabetical order of the country name. If two or more reports for the same country are registered, the ranking was made chronologically, according to the year publication. The prevalence, frequency and intensity of infection are also given, when available. The prevalence was provided or calculated only when the sample size was at least 10. In the case of experimental infection studies, the country has not been specified. Articles that report infections in captive jackals and doubtful records are mentioned and/or discussed accordingly.

### Protists

Eight families with 21 species were reported in golden jackals in 23 countries. Additionally, several protists were identified only to the generic level or were doubtfully considered as parasites of golden jackals (Table 2) [40–85].

#### *Leishmania*

The sand fly-borne kinetoplastids of the genus *Leishmania* were reported in golden jackals from 13 countries (Table 2), showing a large geographical distribution in Asia, Africa and Europe. At least three species of *Leishmania* have been identified by molecular methods in naturally infected golden jackals (*L. donovani*, *L. infantum* and *L. tropica*). Additionally, golden jackals were experimentally shown to be receptive for the infection with *L. major* [85], but this species has never been found in naturally infected specimens. The multiple records of *Leishmania* spp. in golden jackals suggest a reservoir role for this carnivore, for both visceral and cutaneous leishmaniasis in humans, as well as for canine leishmaniasis. Infected jackals have been found also at the margin of the endemic area for canine leishmaniasis (i.e. Romania), where this finding has been temporally correlated with the re-emergence of the disease in domestic dogs [86]. Although there is no clear link between the emergence of leishmaniasis in dogs and the spreading of jackals, this is an issue to be further investigated, mainly as the jackal continues to spread into areas at the margin of canine leishmaniasis endemicity. This was previously demonstrated when infected dogs were newly introduced to non-endemic areas in Europe [87].

#### Tick-borne protists (Babesiidae, Theileriidae and Hepatozoidae)

Experimental evidence showed that golden jackals are receptive to the infection with *Babesia canis* [40] and *B. gibsoni* [43]. However, there are surprisingly few records of natural infections with piroplasms in golden jackals (Table 2) despite the large variety and number of studies on ticks (see below). In Europe, the only *Babesia* species molecularly confirmed in golden jackals is *B. canis*, recently reported in Romania [42]. The other report of *B. canis* in jackals is from Nigeria [41], but the species identification was based on blood smears and in captive animals. We consider this record doubtful, as the typical vector for *B. canis*, *Dermacentor reticulatus*, does not occur in Nigeria. Probably the species in this case belongs to the same complex group of large canine *Babesia* known in this area, *B. rossi* or *B. vogeli* [88]. *Babesia gibsoni*, which is widely distributed in Asia, has been reported only once in golden jackals, in India. Although *Babesia rossi* is common in domestic and wild carnivores in Africa [89], so far there are no records of this species in golden jackals. The scarcity of reports of *Babesia* spp. in this wild canid is probably related to the low number of studies and the lack of

**Table 2** Protist parasites of the golden jackal, *Canis aureus*

Family	Species	Origin	Prevalence (%)	Frequency	Method	Reference
Phylum Apicomplexa						
Class Aconoidasida						
Babesiidae	<i>Babesia canis</i> (syn. <i>Piroplasma canis</i> )	na (as <i>P. canis</i> )	na	na	El	[40]
		Nigeria <sup>a</sup>	na	1/6	BS	[41]
		Romania	9.2	5/54	MI	[42]
	<i>Babesia gibsoni</i>	na	na	na	El	[43]
		India	na	na	BS	[44]
Theileriidae	"Theileria annae"	Romania	3.7	2/54	MI	[42]
Class Conoidasida						
Eimeriidae	<i>Eimeria</i> sp. <sup>b</sup>	Bulgaria	5.8	3/56	CO	[45]
	<i>Eimeria aurei</i> <sup>b</sup>	India	na	na	CO	[46]
	<i>Isospora</i> sp.	Bulgaria	5.8	3/56	CO	[45]
		India <sup>a</sup>	case report		CO	[47]
		Iran	7.1	4/56	CO	[48]
		Serbia	6.6	4/60	CO	[49]
	<i>Isospora dutoiti</i>	former USSR	na	na	CO	[50]
		Turkmenistan	na	na	CO	[51]
	<i>Isospora kzilordiniensis</i>	Kazakhstan	na	2/9	CO	[52]
	<i>Isospora neorivolta</i>	Russia	9.3	14/150	CO	[53]
	<i>Isospora ohioensis</i>	Russia	5.3	8/150	CO	[53]
	<i>Isospora theileri</i>	Azerbaijan	na	na	CO	[54]
		Turkmenistan	na	na	CO	[51]
Hepatozoidae	<i>Hepatozoon</i> sp.	Algeria	na	2/5	MI	[55]
		Mauritania	25.0	4/16	MI	[55]
	<i>Hepatozoon canis</i>	Austria	case report		MI	[56]
			case report		MI	[42]
		Croatia	30.4	14/46	MI	[57]
		Czech Republic	na	1/1	MI	[42]
		Hungary	57.9	33/57	MI	[57]
			60.0	na	MI	[58]
		Israel	2.1	1/46	BS	[19]
		Montenegro	na	2/2	MI	[57]
		Romania	72.2	39/54	MI	[42]
		Serbia	67.5	140/206	MI	[57]
Sarcocystidae	<i>Cystoisospora canis</i>	Hungary	15.0	3/20	CO	[59]
	<i>Neospora caninum</i>	Israel	1.7	2/114	IFAT	[60]
	<i>Sarcocystis</i> sp.	Bulgaria	1.9	1/56	CO	[45]
	<i>Sarcocystis cruzi</i> (syn. <i>S. bovicanis</i> )	Russia (as <i>S. bovicanis</i> )	20.0	30/150	CO	[53]
	<i>Sarcocystis tenella</i> (syn. <i>S. ovis</i> )	Russia (as <i>S. ovis</i> )	34.0	51/150	CO	[53]
	<i>Sarcocystis tropicalis</i> (syn. <i>Isospora tropicalis</i> )	India (as <i>I. tropicalis</i> )	case report		CO	[61]
		India	case report		CO	[62]
	<i>Toxoplasma</i> -type oocysts	Hungary	5.0	1/20	CO	[59]
	<i>Toxoplasma gondii</i>	Iran	33.3	na	LAST	[63]

**Table 2** Protist parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Method	Reference
			77.5	31/40	ELISA	[64]
“Flagellates” <sup>c</sup>						
Hexamitidae	<i>Giardia</i> sp.	Iraq <sup>a</sup>	100	4/4	CO	[65]
	<i>Giardia duodenalis</i> (syn. <i>G. canis</i> )	Croatia	12.5	1/8	IF, MI	[66]
		Iran	7.1	4/56	CO	[48]
		Russia (as <i>G. canis</i> )	1.3	2/150	CO	[53]
Trichomonadidae	<i>Pentatrichomonas hominis</i> (syn. <i>P. canis aurī</i> )	India (as <i>P. canis aurī</i> )	case report		CO	[67]
Trypanosomatidae	<i>Leishmania</i> sp.	Iran	2.5	4/161	SIO	[68]
			12.5	6/48	IFA	
		Serbia	6.9	15/126	MI	[69]
		Spain <sup>a</sup>	case report		H	[70]
		Bangladesh	5 cases	na	MI	[71]
		Georgia	na	1/4	SIO	[72]
		Kazakhstan	na	na	na	[73]
		Iran	5.0	1/20	SIO	[74]
		na	na	na	El	[75]
	<i>Leishmania infantum</i>	Algeria	case report		IFI, MI	[76]
		Georgia	2.5	1/39	IA	[77]
		Iran	10.0	1/10	DAT, ELISA, IFAT	[78]
			11.6	7/60	DAT	[78]
			1.6	1/60	SIO	
		Iraq	59.6	90/151	SIO, Cult, IFAT, ELISA	[79]
		Israel	7.6	4/53	ELISA	[80]
			6.5	3/46	ELISA	[19]
			1.3	1/77	MI	[81]
		Kazakhstan	na	na	na	[82]
		Romania	2.7	1/36	MI	[42]
		Tajikistan	na	na	na	[83]
		Turkmenistan	2 specimens	na	na	[84]
	<i>Leishmania major</i>	na	na	na	El	[85]
	<i>Leishmania tropica</i>	Israel	6.5	5/77	na	[81]

**Abbreviations:** BS blood smear May-Grünwald-Giemsa stained, CO coprological examination, Cult cultures from the viscera, blood and other tissues, DAT direct agglutination test, El experimental infection, ELISA enzyme-linked immunosorbent assay, H histopathology, IA immunochromatographic assay, IF immunofluorescence assay, IFAT indirect fluorescent antibody test, IFI indirect fluorescent immunoassay, LAST latex agglutination slide test, MI- molecular identification, SIO smears from internal organs stained with standard Giemsa, na not applicable/unknown

<sup>a</sup>Animals kept in captivity

<sup>b</sup>Doubtful record

<sup>c</sup>Various opinions on the higher taxonomy of these groups are available, hence we keep the generic term “flagellates”

more sensitive/specific methods, as the typical vector ticks [*D. reticulatus* for *B. canis*, *Rhipicephalus sanguineus* (*sensu lato*) for *B. vogeli* and *Haemaphysalis leachi* for *B. rossii*] have been reported on various occasions on these hosts.

An interesting recent report indicates the presence of “*Theileria annae*” in golden jackals from Romania [42]. Currently, the taxonomic status of this species is debated and it is most commonly referred to as “*Babesia microti*-like”.

This group has been reported predominantly in red foxes, but also in several other wild carnivores in North America, Asia and Europe [89]. However, so far, the role of golden jackals in its ecology remains unknown.

The first report of *Hepatozoon canis* in golden jackals is relatively recent [19] and has been followed in the last years by several records, mainly in Europe and North Africa (Table 2). Surprisingly, despite the wide distribution

of *H. canis* in canids [90], this tick-borne apicomplexan has never been found in jackals from sub-Saharan Africa or Asia. Nevertheless, the large number of records and the presence of its main vector, *R. sanguineus* (s.l.) suggest a reservoir role of golden jackals for *H. canis* at least in Europe, Middle East and North Africa.

#### Intestinal homoxenous coccidia (Eimeriidae)

Various species of intestinal coccidia of the family Eimeriidae have been found in, or even described from jackals (Table 2). We consider all records of *Eimeria* as pseudoparasites, as previously suggested [91]. Three species of the genus *Isoospora* have been described from golden jackals but currently their taxonomic status is listed as doubtful [91]: *Isoospora dutoiti* is a misidentification with *Hammondia* spp. or *Neospora caninum*, while *I. theileri* and *I. kizilordiniensis* are probably invalid names (as they might be synonyms with other *Isoospora* species from canids). Two other species, *I. neorivolta* and *I. ohioensis*, which are known to infect several species of canids [91], were reported in golden jackals. Interestingly, all these *Isoospora* reports in golden jackals are from countries in the former USSR, and this probably reflects a greater interest of researchers from this area for this group of parasites rather than the real geographical distribution. Few reports of unnamed *Isoospora* sp. in golden jackals are known from Asia and the Balkans (Table 2).

#### Heteroxenous coccidia (Sarcocystidae)

Various records list golden jackals host to Sarcocystidae. Sporocysts of *Sarcocystis* (*S. cruzi*, *S. tenella* and *S. tropicalis*) and oocysts of *Cystoisospora canis* have been reported in the faeces of golden jackals in Europe, Russia and India, suggesting their role as definitive hosts (Table 2). Although antibodies against *Neospora caninum* have been detected in *C. aureus* in Israel [60], the role of golden jackals as definitive hosts for this parasite has never been demonstrated and needs to be investigated. So far, various canid species were demonstrated to shed oocysts of *N. caninum*: dogs (*Canis familiaris*) [92], coyotes (*C. latrans*) [93], dingoes (*C. lupus dingo*) [94], and gray wolves (*C. lupus*) [95]. Interestingly, Takacs et al. [59] reported “*Toxoplasma*-like” oocysts in the faeces of jackals but, unfortunately, no morphometric data were provided and there was no attempt to characterize them molecularly. We can only assume that these were small oocysts which, in our opinion, could represent any of the small canine coccidia *N. caninum*, *Besnoitia* spp. or *Hammondia* spp., none of them confirmed so far in golden jackals.

#### Helminths

The highest number of studies on the parasitic fauna of golden jackals are related to helminths. Our literature survey found at least 178 publications in 38 countries

reporting helminths in golden jackals, with 119 species belonging to three phyla: Platyhelminthes, Nematoda and Acanthocephala [96–119].

#### Trematodes

The diversity of trematodes in golden jackals is relatively high (27 species from nine families) (Table 3). Most of the studies originate in the countries of the former USSR, Asia and North Africa, with few scattered records in Europe. There are no trematodes recorded in golden jackals in sub-Saharan Africa. This situation reflects probably the impact of the Russian helminthological school and the lack of studies in other regions rather than the influence of ecological factors or feeding behaviour of jackals. Among the various records of trematodes in golden jackals, two groups could be identified: the canid- or Carnivora-specific trematodes and other trematodes (specific rather to other mammal groups or birds).

The most commonly reported and widely distributed trematode in golden jackals is *Alaria alata*, found in Caucasus, Russia and Central Asia to Middle East and the Balkans (Table 3). We consider the report of *Alaria americana* in Iran doubtful, as the species is known otherwise only in canids from North America [120].

Jackals have been commonly reported as hosts for fish-borne trematodes typically associated with carnivores. Such examples include species of the genera *Ascocotyle*, *Cryptocotyle*, *Heterophyes*, *Metagonimus* (Heterophyidae), *Echinochasmus*, *Euparyphium* (Echinostomatidae), *Pseudamphistomum*, *Opisthorchis* (Opisthorchiidae) mainly in Asia and northern Africa. The fish-borne *Nanophyetus salmincola* was identified in India, but its geographical distribution is limited to the Pacific Northwest of the USA [121]; with high probability, the report might represent a misidentification with *N. schikhalowi*, an Asian troglotrematid [122]. The diversity of trematode species in golden jackals is completed by other groups which use various invertebrates (i.e. arthropods) (*Plagiorchis massino*, *Microphallus narii*) or non-fish small vertebrates (i.e. amphibians) (*Pharyngostomum cordatum*) as second intermediate hosts, reflecting the wide diet composition of this carnivore.

Interestingly, *Dicrocoelium dendriticum*, a hepatic fluke typically associated with herbivores, has been found on several occasions in the bile ducts of golden jackals [97, 98] in Russia. As the infection source for this parasite is represented by ant second intermediate hosts, the infection of jackals is probably accidental.

Several of these trematodes reported in golden jackals have zoonotic potential. Human alariosis caused by *Alaria mesocercariae* manifests in various clinical signs which range from cutaneous symptoms to respiratory disorders, a diffuse unilateral neuroretinitis even to an anaphylactic shock with fatal outcome [123]. However,

**Table 3** A comprehensive list of trematode parasites of the golden jackal, *Canis aureus*

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Phylum Platyhelminthes							
Class Trematoda							
Dicrocoeliidae	<i>Dicrocoelium dendriticum</i> (syn. <i>D. lanceatum</i> )	Russia	5.0	1/20	5.00 ± 4.45	necropsy	[96] <sup>a</sup>
			26.1	na	na	necropsy	[97]
			na	na	na	necropsy	[98]
			22.4	20/89	2–30	necropsy	[99]
			na	na	na	necropsy	[100]
			9.0	na	na	necropsy	[101]
			1.9	1/56	na	necropsy	[45]
			na	na	na	na	[102]
Diplostomidae	<i>Alaria alata</i>	Azerbaijan	100	16/16	22–268	necropsy	[103]
		Bulgaria	20.0	1/5	na	necropsy	[104]
			10.0	2/20	na	necropsy	[59]
			na	na	na	necropsy	[105]
			10.0	2/20	3.00 ± 2.68	necropsy	[96]
			34.8	na	na	necropsy	[97]
			na	na	na	necropsy	[98]
			13.3	8/60	na	necropsy	[106]
			na	na	na	necropsy	[107]
			26.0	39/150	2–23	necropsy	[53]
			0.9	4/447	19.00 ± 3.63	necropsy	[108]
			30.0	18/60	na	necropsy	[49]
			na	na	na	na	[109]
			5.0	1/20	34	necropsy	[110]
			10.0	1/10	na	necropsy	[111]
			na	na	na	necropsy	[100]
			8.3	1/12	2	necropsy	[99]
			na	na	na	necropsy	[100]
			6.6	4/60	na	necropsy	[106]
			na	na	na	na	[112]
			na	na	na	necropsy	[105]
			na	na	na	necropsy	[105]
			16.6	10/60	na	necropsy	[106]
Echinostomatidae	<i>Echinochasmus corvus</i>	Russia	na	na	na	na	[112]
	<i>Echinochasmus schwartzi</i>	Iran	na	na	na	necropsy	[105]
	<i>Euparyphium</i> sp.	Iran	na	na	na	necropsy	[105]
	<i>Euparyphium melis</i>	Russia	na	na	na	necropsy	[106]

**Table 3** A comprehensive list of trematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Heterophyidae	<i>Ascoctyle italica</i> (syn. <i>Parascocotyle italica</i> )	Russia	8.3	5/60	na	necropsy	[106]
	<i>Ascoctyle sinoecum</i> (syn. <i>Phagicola sinoecum</i> )	Iran	na	na	na	necropsy	[105]
	<i>Cryptocotyle lingua</i> <sup>b</sup>	Russia	2.7	4/150	3–18	necropsy	[53]
	<i>Heterophyes</i> sp.	Egypt	na	3/5	na	necropsy	[113]
	<i>Heterophyes aequalis</i>	Egypt	na	na	na	necropsy	[113]
	<i>Heterophyes dispar</i>	Egypt	na	na	na	necropsy	[113]
	<i>Heterophyes heterophyes</i>	Egypt	2 specimens	na	na	necropsy	[113]
	<i>Metagonimus ciureanus</i> (syn. <i>Dexiogonimus ciureanus</i> )	Georgia	na	na	na	necropsy	[114]
	<i>Metagonimus yokogawai</i>	Iran	14.2	4/28	na	necropsy	[115]
		Italy	case report		6	necropsy	[116]
Microphallidae		Serbia	1.6	1/60	na	necropsy	[49]
	<i>Microphallus narii</i> (syn. <i>Spelotrema narii</i> )	India	na	na	na	na	[117]
			na	na	na	na	[112]
		Russia	21.8	na	na	necropsy	[97]
Opisthorchiidae	<i>Metorchis xanthosomus</i> <sup>b</sup>		na	1/5	na	necropsy	[118]
	<i>Opisthorchis</i> sp.	Bangladesh	0.2	1/447	2	necropsy	[108]
	<i>Pseudamphistomum truncatum</i>	Serbia	3.3	2/60	na	necropsy	[49]
		Iran	na	na	na	necropsy	[105]
Plagiorchiidae	<i>Plagiorchis</i> sp.	Russia	3.3	2/60	na	necropsy	[106]
	<i>Plagiorchis elegans</i> <sup>b</sup>	Uzbekistan	na	na	na	na	[109]
	<i>Plagiorchis massino</i>	India	case report		na	CO	[119]
Schistosomatidae	<i>Schistosoma spindale</i> <sup>b</sup>		case report		na	CO	[119]
Troglotrematidae	<i>Nanophyetus salmincola</i> <sup>b</sup>	India	case report		na	CO	[47]

Abbreviations: na not applicable/unknown, CO coprological examination

<sup>a</sup>Unknown site of infection<sup>b</sup>Doubtful record

all human cases originate in North America (and are probably caused by *A. americanum*). The zoonotic potential of *A. alata* in Eurasia remains unknown. Adults *Heterophyes dispar* and *H. heterophyes* may produce diarrhoea, abdominal pain and discomfort in humans [124], while *Metagonimus yokogawai* is considered to be the most common intestinal trematode infection in the Far East, highly important due to the ability of their eggs to invade the blood stream thus causing serious complications [125]. Hence, golden jackals might have a significant role in the environmental contamination with such parasites and represent an indirect source for human contamination. Hepatic and biliary trematodes *D. dendriticum*, *Pseudamphistomum truncatum* and *Opisthorchis felineus* are also able to infect humans, causing abdominal pain, weight loss, chronic relapsing watery diarrhea and hepatobiliary system damages [126, 127].

However, for many other trematode species, golden jackals, as other carnivores, are probably accidental hosts, or most likely, present a pseudoparasitism following ingestion of birds or rodents, as they typically infect other vertebrate groups. For instance, *Cryptocotyle lingua* is mainly a parasite of different gull species in Europe, North America and Japan [128]; *Plagiorchis elegans* is a parasite of raptors, waterfowl, passerines and several mammals as the wood mouse, rat, gerbil and hamster [129]; *Metorchis xanthosomus* is specific for birds in Anseriformes, Gaviiformes, Podicipediformes and Gruiformes [130]; and *Schistosoma spindale* has been described in ruminants and rodents in southeastern Asia [131].

### Cestodes

Cestode infections in golden jackals have been recorded across all their distribution range, with a relatively high species diversity (Table 4) [132–152].

Among all the cestode species, *Aelurotaenia cameroni* is the only one known exclusively in the golden jackal. However, as the species was only recently described [132], its absence from other carnivores cannot be excluded until further studies. It is not surprising that all other identified tapeworm species are characteristic to carnivores, confirming the low specific affinity of the adult parasites [153]. As such species infect usually a wider range of canid or non-canid carnivores, this demonstrates a close environmental connection between multiple carnivore species and the use of the same trophic source.

The most commonly reported tapeworms in golden jackals are *Dipylidium caninum*, *Mesocestoides* spp., *Echinococcus granulosus* and *Taenia* spp., found across a wide geographical range (Europe, Asia and Africa). The cosmopolitan character of all these cestodes is attributed to the abundance and diversity of intermediate hosts and the lack of specificity for the definitive hosts [153]. Hence, the jackal, together with other carnivores, represents an

important source of environmental contamination. Several of these species are known to be zoonotic, some with a minor impact (i.e. *D. caninum*), but other being a major public health threat (i.e. *E. granulosus*).

*Dipylidium caninum* occurs across the globe, human cases being reported in European and Asian countries after accidental ingestion of the infected cat and dog fleas with cysticeroid larvae [154]. Although the jackal is not a domestic species, hence not a direct source of infection to humans, it may transmit fleas to hunting, shepherd or stray dogs and participates together with other wild canids in the natural cycle of this cestode.

Several species of the genus *Mesocestoides* have been found in golden jackals in various regions. *Mesocestoides lineatus* is spread in Africa, Asia and Europe; it was rarely found in humans, with about 20 cases being described to date across the world [155]. Although the main definitive hosts are carnivores, humans can also act as accidental final hosts following ingestion of raw or undercooked meat of birds, amphibians, reptiles or small mammals [156]. The zoonotic potential of the other species of *Mesocestoides* is unknown.

The most well-represented family of tapeworms found in jackals is the Taeniidae. The high diversity of the Taeniidae in golden jackals reflects furthermore the wide range of mammalian prey species on which they feed. Golden jackals are hosts to both zoonotic species of *Echinococcus*. *Echinococcus granulosus* and *E. multilocularis* have been reported in this wild canid on multiple occasions and across a wide geographical range. The unilocular or cystic hydatidosis produced by larvae of *E. granulosus* (*sensu lato*) is a ubiquitous infection with high prevalence in various parts of the world [157]. Human multilocular or alveolar echinococcosis caused by *E. multilocularis* has recorded a significant increase in the incidence in northern Eurasia since 1990 [157, 158]. In several regions, high prevalences with both species were reported in golden jackals (Table 4). Reports of *Echinococcus* spp. in areas where this canid has recently spread or increased in abundance (i.e. central and eastern Europe) raise the important question on its role as a potentially new natural reservoir and infection source for humans and livestock.

Among species of genus *Taenia* and *Multiceps*, the most commonly reported species in golden jackals are *T. hydatigena*, *T. pisiformis*, *T. ovis* and *M. multiceps*. Other species (*T. polyacantha*, *T. taeniaeformis*, *T. krabbei*, *T. krepkogorski*, *T. crassiceps* and *M. serialis*) have been also found but only occasionally, mainly within the limited geographical range of Caucasus and central Asia (Table 4). The zoonotic potential of these species is limited, and only few human cases have been reported so far: *T. taeniaeformis* [159–162], *T. crassiceps* [163], *T. hydatigena* [164], *T. ovis* [165, 166], *M. multiceps* and *M. serialis* [167]. *Taenia krabbei*, *T. krepkogorski* and *T. polyacantha* are considered non-zoonotic

**Table 4** A comprehensive list of cestode parasites of the golden jackal, *Canis aureus*

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Phylum Platyhelminthes							
Class Cestoda							
Dilepididae	<i>Aelurotaenia cameroni</i>	India	na	na	na	na	[132]
Diphylobothriidae	<i>Diphylobothrium</i> sp.	India <sup>a</sup>	na	na	na	CO	[133]
	<i>Diphylobothrium latum</i>	Bangladesh	20.0	6/30	na	necropsy	[134]
		India	na	na	na	na	[112]
	<i>Spirometra</i> sp.	India <sup>a</sup>	na	na	na	CO	[135]
		Iran	7.1	1/14	4	necropsy	[136]
	<i>Spirometra erinaceieuropaei</i> (syn. <i>S. erinacei</i> )	Azerbaijan	25.0	19/76	1–19	necropsy	[99]
			na	na	na	necropsy	[100]
		Azerbaijan (as <i>S. erinacei</i> )	3.5	4/114	2–21	necropsy	[137]
		Iran (as <i>S. erinacei</i> )	na	na	na	necropsy	[105]
	<i>Spirometra houghtoni</i>	Iran	na	na	na	necropsy	[105]
	<i>Spirometra mansoni</i> (syn. <i>Bothriocephalus mansoni</i> )	Italy	case report	na	necropsy	[138]	
Dipylidiidae	<i>Dipylidium noelleri</i>	Iran	5.0	na	na	necropsy	[139]
		Tunisia	16.0	5/31	1–66	necropsy	[140]
	<i>Dipylidium caninum</i> (syns <i>Taenia elliptica</i> , <i>T. cucumerina</i> )	Azerbaijan	na	na	na	necropsy	[100]
		Bangladesh	26.6	8/30	na	necropsy	[134]
		Bulgaria	3.8	na	na	necropsy	[141]
			63.6	7/11	na	necropsy	[142]
		Chechnya	100	16/16	3–12	necropsy	[103]
		Hungary	5.0	1/20	4	necropsy	[59]
		India	na	na	na	na	[143]
			na	na	na	na	[112]
		India <sup>a</sup>	5.0	3/60	na	CO	[144]
		Iran	7.1	1/14	4	necropsy	[136]
			10.0	4/40	na	necropsy	[145]
			20.0	2/10	na	necropsy	[111]
			10.1	8/79	na	necropsy	[139]
			33.9	19/56	na	necropsy	[48]
		Israel	46.6	7/15	na	necropsy	[146]
			5.8	1/17	na	CO	[19]
		Italy	na	na	na	necropsy	[138]
		Kazakhstan	16.6	3/18	2–8	necropsy	[147]
		Russia	47.8	na	na	necropsy	[97]
			5.0	1/20	1.00 ± 0.25	necropsy	[96]
			10.0	6/60	na	necropsy	[106]
			na	na	na	necropsy	[107]
			8.0	12/150	1–13	necropsy	[53]
		Serbia	1.6	7/447	4.8 ± 0.6	necropsy	[108]
		Tajikistan	na	na	na	necropsy	[148]
		Tunisia	na	1/5	na	necropsy	[149]
			16.0	5/31	4–67	necropsy	[140]
		Turkey	na	na	na	necropsy	[150]
		Uzbekistan	na	na	na	necropsy	[151]

**Table 4** A comprehensive list of cestode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Mesocestoididae	<i>Joyeuxiella echinorhynchoides</i>	Azerbaijan	na	na	na	necropsy	[152]
			30.2	23/76	1–30	necropsy	[99]
			na	na	na	necropsy	[100]
		Iran	27.8	5/18	na	necropsy	[334]
			7.5	3/40	na	necropsy	[145]
	<i>Joyeuxiella pasqualei</i>	Turkey	na	na	na	necropsy	[150]
		Iran	30.0	3/10	na	necropsy	[111]
		Israel	8.1	7/86	na	necropsy, ME	[335]
	<i>Mesocestoides</i> sp. group A (oval to elongate cirrus-pouch and short cirrus)	Israel	15.2	13/85	na	necropsy, ME	
	<i>Mesocestoides</i> sp.	Greece	na	3/5	na	necropsy	[104]
		Tunisia	na	2/5	na	necropsy	[149]
		Iran	na	1/1	na	necropsy	[336]
		Bulgaria	34.6	na	na	necropsy	[45]
	<i>Mesocestoides corti</i>	Azerbaijan	na	na	na	necropsy	[100]
		Tunisia	12.9	4/31	1–10	necropsy	[140]
	<i>Mesocestoides lineatus</i> (syn. <i>M. carnivoricolus</i> )	Azerbaijan	2.6	3/114	9–47	necropsy	[137]
			37.7	37/98	2–63	necropsy	[99]
			na	na	na	necropsy	[100]
		Bulgaria	27.0	na	na	necropsy	[101]
			72.7	8/11	na	necropsy	[142]
			20.0	4/20	na	necropsy	[59]
		Hungary	na	na	na	na	[112]
		India	na	na	na	na	[112]
		India (as <i>M. carnivoricolus</i> )	na	na	na	necropsy	[337]
		Ingushetia	na	1/2	na	necropsy	[338]
		Iran	15.0	3/20	na	necropsy	[110]
			70.0	7/10	na	necropsy	[111]
			36.7	29/79	na	necropsy	[139]
			30.3	17/56	na	necropsy	[48]
			61.1	11/18	na	necropsy	[334]
		Russia	26.1	na	na	necropsy	[97]
			5.0	1/20	1.00 ± 0.53	necropsy	[96]
			40.0	24/60	na	necropsy	[106]
			na	na	na	necropsy	[339]
			na	na	na	necropsy	[98]
			40.0	60/150	1–128	necropsy	[53]
		Serbia	5.8	26/447	69.7 ± 9.3	necropsy	[108]
		Tajikistan	na	na	na	necropsy	[148]
		Tunisia	74.0	23/31	na	necropsy	[140]
		Turkey	na	na	na	necropsy	[340]
		Ukraine	na	1/1	5	necropsy	[341]
		Uzbekistan	na	na	na	necropsy	[151]
			na	na	na	necropsy	[152]

**Table 4** A comprehensive list of cestode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Taeniidae	<i>Mesocestoides litteratus</i>	Serbia	4.7	21/447	64.3 ± 15.1	necropsy	[108]
		Tunisia	23.0	7/31	6–130	necropsy	[140]
	<i>Mesocestoides petrowi</i>	Azerbaijan	na	na	na	necropsy	[100]
		Russia	na	na	na	necropsy	[342]
	<i>Mesocestoides zacharovae</i>	Azerbaijan	case report	na	necropsy	[343]	
	<i>Echinococcus granulosus</i>	Azerbaijan	16.3	16/98	2–400	necropsy	[99]
			na	na	na	necropsy	[100]
		Bangladesh	20.0	6/30	na	necropsy	[134]
		Bulgaria	23.0	na	na	necropsy	[101]
			na	3/3	na	PCR	[344]
			9.0	1/11	na	necropsy	[142]
			1.9	na	na	necropsy	[45]
		Ceylon	case report	7	necropsy	[345]	
		Chad	1.2	1/82	na	necropsy	[346]
		Chechnya	na	na	na	necropsy	[347]
			12.0	2/16	8–16	necropsy	[103]
		Chechnya, Ingushetia	na	2/7	74–217	necropsy	[348]
		Hungary	10.0	2/20	na	necropsy	[59]
		India	na	na	na	CO	[349]
		Iran	5.0	1/20	48	necropsy	[110]
			na	na	na	necropsy	[105]
			16.0	na	na	necropsy	[350]
			2.3	2/86	na	necropsy	[351]
			40.0	16/40	na	necropsy	[145]
			40.0	16/40	na	necropsy	[352]
			8.9	7/79	na	necropsy	[139]
			20.0	2/10	na	necropsy	[353]
			66.7	6/9	na	CO	[353]
			na	1/1	na	PCR	[354]
			3.5	2/56	na	necropsy	[48]
			na	na	na	PCR	[355]
		Italy	case report	1	necropsy	[356]	
		Kazakhstan	5.9	na	3–29	necropsy	[147]
		Kenya	27.2	6/22	< 200	necropsy	[357]
		Palestine	na	na	na	na	[358]
		Pakistan	9.0	9/100	na	necropsy	[359]
		Russia	12.5	2/16	na	necropsy	[360]
			82.6	na	na	necropsy	[97]
			69.8	na	na	necropsy	[361]
			5.0	1/20	4.00 ± 2.36	necropsy	[96]
			66.0	10/15	na	CO	[362]
			3.3	2/60	na	necropsy	[106]
			na	na	na	necropsy	[107]
		Tajikistan	30.7	4/13	> 1,000	necropsy	[363]
		Tunisia	na	1/5	72	necropsy	[149]
			na	2/2	na	PCR	[364]

**Table 4** A comprehensive list of cestode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
			9.7	3/31	11–98	necropsy	[140]
	<i>E. multilocularis</i> (syn. <i>Alveococcus multilocularis</i> )	Azerbaijan	3.7	2/54	3–5	necropsy	[99]
		Hungary	9.0	1/11	412	necropsy	[365]
		Ingushetia	na	1/2	na	necropsy	[338]
		Iran	16.0	4/25	na	necropsy	[366]
			50.0	5/10	na	necropsy	[353]
			na	9/9	na	CO	[353]
		Russia (as <i>Alveococcus multilocularis</i> )	18.7	3/16	na	necropsy	[360]
		Serbia	14.3	4/28	4–57	necropsy	[367]
		Tajikistan	7.7	1/13	na	necropsy	[363]
		Uzbekistan	na	1/4	na	necropsy	[368]
	<i>Multiceps multiceps</i> (syn. <i>Taenia multiceps</i> )	Azerbaijan	8.9	8/89	2–11	necropsy	[99]
			na	na	na	necropsy	[100]
		Bangladesh (as <i>T. multiceps</i> )	10.0	3/30	na	necropsy	[134]
		Bulgaria	9.0	na	na	necropsy	[101]
			9.0	1/11		necropsy	[142]
		Chechnya	na	na	na	necropsy	[347]
		Iran	7.5	3/40		necropsy	[145]
		India	na	na	na	necropsy	[369]
		Kazakhstan	11.1	2/18	4–16	necropsy	[147]
		Russia	39.1	na	na	necropsy	[97]
		Serbia	1.6	7/447	3.00 ± 0.53	necropsy	[108]
		Tajikistan	na	2/6	na	necropsy	[370]
		Ukraine	na	1/1	na	necropsy	[341]
	<i>Taenia serialis</i>	Kazakhstan	5.5	1/18	10	necropsy	[147]
		Kenya	na	2/2	42	PCR	[371]
		Serbia	1.1	5/447	2.7 ± 0.2	necropsy	[108]
	<i>Taenia</i> sp.	Bulgaria	23.0	na	na	necropsy	[141]
		Greece	na	1/5	na	necropsy	[104]
		India	na	na	na	na	[143]
		India <sup>a</sup>	11.6	7/60	na	CO	[144]
		Iran <sup>a</sup>	na	2/2	11 ± 2 epg	CO	[372]
		Kenya	60.0	3/5	na	necropsy	[373]
		Tunisia	19	6/31	1–29	necropsy	[140]
	<i>Taenia crassiceps</i>	Azerbaijan	na	na	na	necropsy	[100]
		Hungary	40.0	8/20	na	necropsy	[59]
		Russia	25.0	15/60	na	necropsy	[106]
	<i>Taenia hydatigena</i> (syn. <i>T. marginata</i> )	Azerbaijan	15.3	14/91	1–18	necropsy	[99]
			na	na	na	necropsy	[100]
		Bulgaria	55.0	na	na	necropsy	[101]
			27.2	3/11	na	necropsy	[142]
		Chechnya	na	na	na	necropsy	[347]
			50.0	8/16	3–6	necropsy	[103]
		Hungary	15.0	3/20	na	necropsy	[59]
		India	na	na	na	necropsy	[369]

**Table 4** A comprehensive list of cestode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
		Iran	7.1	1/14	2	necropsy	[136]
			40.0	16/40	na	necropsy	[145]
			10.0	1/10	na	necropsy	[111]
			7.6	6/79	na	necropsy	[139]
			7.1	4/56	na	necropsy	[48]
			5.6	1/18	na	necropsy	[334]
			na	na	na	na	[138]
			22.0	4/18	2–8	necropsy	[147]
			6.2	1/16	na	necropsy	[360]
			36.8	14/38	1–3	necropsy	[374]
		Italy (as <i>T. marginata</i> )	34.8	na	na	necropsy	[97]
			5.0	1/20	3.00 ± 2.18	necropsy	[96]
			1.6	1/60	na	necropsy	[106]
			na	na	na	necropsy	[98]
			na	na	na	necropsy	[107]
			0.9	4/447	3.75 ± 1.80	necropsy	[108]
			na	na	na	necropsy	[148]
			na	na	na	necropsy	[152]
			0.8	1/114	3	necropsy	[137]
			na	na	na	necropsy	[100]
		Serbia	na	na	na	necropsy	[100]
			na	na	na	necropsy	[100]
		Tajikistan	na	na	na	necropsy	[100]
			na	na	na	necropsy	[100]
		Uzbekistan	na	na	na	necropsy	[100]
			na	na	na	necropsy	[100]
		Azerbaijan	na	na	na	necropsy	[100]
			na	na	na	necropsy	[100]
		Azerbaijan	na	na	na	necropsy	[100]
			na	na	na	necropsy	[100]
		Azerbaijan	na	na	na	necropsy	[100]
			na	na	na	necropsy	[100]
		Bulgaria	case report		na	necropsy	[375]
			5.6	1/18		necropsy	[334]
		Iran	39.1	na	na	necropsy	[97]
			na	na	na	necropsy	[148]
		Russia	na	na	na	necropsy	[376]
			na	na	na	necropsy	[376]
		Tajikistan	na	na	na	necropsy	[376]
			na	na	na	necropsy	[376]
		USSR (former)	na	na	na	necropsy	[376]
			na	na	na	necropsy	[376]
		Azerbaijan	15.7	14/89	1–6	necropsy	[99]
			na	na	na	necropsy	[100]
		Bulgaria	18.0	na	na	necropsy	[101]
			54.5	6/11		necropsy	[142]
		Chechnya	100	16/16	3–18	necropsy	[103]
			na	1/5	na	necropsy	[104]
		Greece	20.0	4/20	na	necropsy	[59]
			na	na	na	na	[377]
		Hungary	na	na	na	na	[377]
			na	na	na	na	[377]
		India (as <i>T. serrata</i> )	na	na	na	na	[377]
			na	na	na	na	[377]
		Iran	na	na	na	necropsy	[105]
			5.5	1/18	3	necropsy	[147]
		Kazakhstan	17.4	na	na	necropsy	[97]
			3.3	2/60		necropsy	[106]
		Russia	na	na	na	necropsy	[107]
			16.7	25/150	1–3	necropsy	[53]
		Serbia	1.8	8/447	10.1 ± 2.1	necropsy	[108]
			na	na	na	necropsy	[148]
		Tajikistan	na	na	na	necropsy	[148]
			na	na	na	necropsy	[148]

**Table 4** A comprehensive list of cestode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
		Tunisia	3.2	1/31	1	necropsy	[140]
	<i>Taenia polyacantha</i> (syn. <i>Tetratirotaenia polyacantha</i> )	Azerbaijan (as <i>Tetratirotaenia polyacantha</i> )	na	na	na	necropsy	[100]
		Turkey	na	na	na	necropsy	[340]
	<i>Taenia taeniaeformis</i> (syn. <i>Hydatigera taeniaeformis</i> )	Azerbaijan (as <i>H. taeniaeformis</i> )	na	na	na	necropsy	[100]
		Tajikistan	na	na	na	necropsy	[148]
		Uzbekistan	na	na	na	necropsy	[152]

Abbreviations: CO coprological examination; ME microscopic/morphological examination; PCR polymerase chain reaction; *egg* eggs per gram faeces; *na* not applicable/not available

<sup>a</sup>Animals kept in captivity

tapeworms [158, 168]. Considering the common findings of a wide range of Taeniidae in golden jackals, the high spatial mobility of these hosts and the high resistance of taeniid eggs in the environment [169], the role of jackals as natural reservoirs and infection source for humans and domestic animals should be considered potentially important.

Species of *Spirometra* (Diphylobothriidae) identified in golden jackals from Europe and Asia (*S. mansoni*, *S. houghtoni* and *S. erinaceieuropaei*) cause sparganosis in intermediate hosts. Humans may acquire the infection after drinking water contaminated with infected copepods or by ingestion of uncooked meat, and occasionally may lead to blindness, paralysis, and death [170, 171]. *Diphylobothrium latum* is also reported in humans due to consumption of raw or undercooked fish, in cold water areas from the Holarctic Eurasia, overlaid to those regions where the species is recorded in jackal [172]. However, due to the limited number of reports, the role of golden jackals in the natural cycle of these diphylobothriid cestodes remains unknown.

Tapeworm species with a limited geographic distribution are also reported in jackals. *Diplopylidium noelleri* and *Joyeuxiella* spp. are spread only in warm regions from Asia and Europe, probably due to the high abundance and diversity of reptiles, known as common intermediate hosts [173].

#### Acanthocephalans

Although the diet of golden jackals generally includes invertebrates, wild birds, reptiles and small mammals which are intermediate or paratenic hosts in the life-cycle of thorny-headed worms [174–176], compared to other groups of helminths, there are only few and geographically limited reports of acanthocephalans in golden jackals. The diversity of acanthocephalans identified in this canid includes at least six species (Table 5) [176–181].

*Macracanthorhynchus catulinus* has been reported on several occasions in jackals in former USSR and Bulgaria, while the congeneric species *M. hirudinaceus* was found only in Tunisia and Iran. It is unclear if the reports of *M. hirudinaceus* (a parasite typically found in pigs; [155])

represent cases of pseudoparasitism or misidentifications with *M. catulinus* (a parasite typically found in canids), as most papers referring to these findings do not provide details on the identification methods. There are few scattered records of other carnivore-specific acanthocephalan species in golden jackals (*Oncicola canis*, *Pachysentis canicola*, *Centrorhynchus itatsinis* and *Echinorhynchus pachyacanthus*) in central Asia and Italy (Table 5).

#### Nematodes

Nematodes constitute the most well-represented group of parasites in golden jackals, with 41 species identified (28 species in Chromadorea and 13 species in Enoplea) (Table 6) [182–256].

#### Ascarids

Ascarids, primarily considered heteroxenous nematodes, have lost their intermediate hosts and have adapted to direct transmission or through paratenic hosts [257]. Four species are reported in golden jackals, with *Toxocara canis* and *Toxascaris leonina* being ubiquitous. *Baylisascaris devosi* is a species typically found in mustelids inhabiting the northern hemisphere [258]. Its presence in golden jackals has been reported only once, in Azerbaijan [99]. This broad distribution and common presence of ascarids in this wild canid can be explained by the intervention of numerous paratenic hosts, possible preys for jackals, in the life-cycle of these nematode species (mostly rodents and invertebrates such as earthworms and insects) [259].

#### Strongyloides

The cosmopolitan and zoonotic *Strongyloides stercoralis* infects about 200 million people, more commonly in tropical and subtropical climates [260]. Despite the large number of records in domestic dogs from various countries, the species has been reported only once in golden jackals (Table 6). The lack of reports in other parts of the jackal's range could be explained by a low receptivity of this host or by failures of finding the parasites during necropsy due to their small size. A moderate prevalence of 5.6% is also recorded in dogs from northeastern Iran [261]

**Table 5** Acanthocephalan parasites of the golden jackal, *Canis aureus*

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Class Archiacanthocephala							
Oligacanthorhynchidae	<i>Macracanthorhynchus</i> sp.	Iran	10.0	1/10		necropsy	[111]
	<i>Macracanthorhynchus catulinus</i>	Azerbaijan	0.8	1/114	24	necropsy	[137]
			17.0	14/82	1–6	necropsy	[99]
			na	na	na	necropsy	[100]
		Bulgaria	3.8	na	na	necropsy	[45]
		Kazakhstan	5.5	1/18	3	necropsy	[147]
		Russia	6.6	4/60	n/a	necropsy	[106]
			6.7	10/150	1–6	necropsy	[53]
		Tajikistan	na	na	na	necropsy	[148]
		Turkmenistan	na	na	na	necropsy	[177]
	<i>Macracanthorhynchus hirudinaceus</i> <sup>a</sup>	Tunisia	na	1/5	na	necropsy	[149]
			3.2	1/31	6	necropsy	[140]
		Iran	case report		na	necropsy	[178]
			62.5	25/40	na	necropsy	[179]
			30.0	3/10	na	necropsy	[111]
			5.0	4/79	na	necropsy	[139]
			3.5	2/56	na	necropsy	[48]
	<i>Oncicola</i> sp.	Iran	na	na	na	necropsy	[178]
	<i>Oncicola canis</i>	Iran	case report		na	necropsy	[178]
			12.6	10/79	na	necropsy	[139]
	<i>Pachysentis canicola</i>	Iran	case report		na	necropsy	[180]
Class Palaeacanthocephala							
Centrorhynchidae	<i>Centrorhynchus itatsinis</i>	Azerbaijan	1.4	1/71	na	necropsy	[181]
			na	na	na	necropsy	[100]
<i>Incertae sedis</i>	<i>Echinorhynchus pachyacanthus</i>	Italy	na	na	na	necropsy	[138]

Abbreviation: na not applicable/not available/no answer

<sup>a</sup>Doubtful record

which is higher than estimated prevalence in humans across the country that ranges between 0.1 and 0.3% [262]. Although carnivores can be a source of infection for humans via larvae that develop in the environment, the principal reservoirs of *S. stercoralis* are humans. The role of domestic and wild carnivores in the epidemiology of strongyloidiasis remains to be clarified [155].

#### Hookworms and other digestive tract strongylids

Several hookworm (Ancylostomatidae) species have been reported in golden jackals, with *Ancylostoma caninum* and *Uncinaria stenocephala* commonly reported across the entire geographical range of these hosts. Additionally, *A. guentini* was described from golden jackals in India, being so far the only known host for this parasite [191]. The remaining two records (*Placoconus lotoris*, known otherwise only from new world procyonids, and *Ancylostoma braziliense*, typically found in the Americas) we list as doubtful and as these are probably misidentifications of

other hookworm species. The opportunistic behaviour of the golden jackals leads them to venture close to human habitats to feed [2]. The proximity with domestic dogs allows interspecific transmission of ancylostomid species, due to the high rate of soil and grass contamination [263]. In this regard, increased prevalence recorded in Russia, ranging between 5.0 and 52.2%, is correlated with similar values in dogs, between 2.06 and 62.3% [264]. *Ancylostoma caninum* and *U. stenocephala* possess a zoonotic potential causing dermal larva migrans in humans [260]. Although a direct relationship between the numerous reports in golden jackals and the presence of disease in humans cannot be established, this carnivore species probably contributes to the presence of Ancylostomatidae larvae in rural and peri-urban areas.

*Molineus patens* is a hookworm commonly reported in a wide range of carnivores in the Palaearctic and Nearctic [265], including two records from jackals in Russia. However, its zoonotic role has not been documented.

**Table 6** Nematode parasites of the golden jackal, *Canis aureus*

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Phylum Nematoda							
Class Chromadorea							
Ancylostomatidae	<i>Ancylostoma</i> sp.	India <sup>a</sup>	na	3/3	na	CO	[182]
			na	5/5	na	CO	[183]
			31.6	19/60	na	CO	[144]
			case report		700 epg	CO	[184]
			case report		na	CO	[47]
		Iran <sup>a</sup>	na	2/2	10.5 epg	CO	[372]
	<i>Ancylostoma/Uncinaria</i> sp.	Bulgaria	84.6	na	na	necropsy	[141]
		India <sup>a</sup>	na	na	na	CO	[135]
		India	na	3/6	na	CO	[185]
		Iran	na	na	na	necropsy	[105]
		Serbia	33.3	20/60	na	necropsy	[49]
		Tunisia	na	5/5	na	necropsy	[149]
		India	na	na	na	na	[117]
	<i>Ancylostoma braziliense</i> <sup>b</sup>	Azerbaijan	17.3	17/98	1–20	necropsy	[99]
	<i>Ancylostoma caninum</i>		na	na	na	necropsy	[100]
		Bangladesh	46.6	14/30	na	necropsy	[134]
		Bulgaria	54.5	6/11	na	necropsy	[142]
			11.5	na	na	necropsy	[45]
		Chechnya	50.0	8/16	3–18	necropsy	[103]
		Egypt	na	na	na	necropsy	[186]
		Greece	na	1/5	na	necropsy	[104]
		Hungary	40.0	8/20	na	necropsy	[59]
		India	na	na	na	na	[187]
			na	na	na	na	[143]
			na	na	na	na	[188]
		India <sup>a</sup>	na	na	na	CO	[189]
			100	12/12	100–400 epg	CO	[190]
		Iran	100	20/20	27.1	necropsy	[110]
			7.1	1/14	4	necropsy	[136]
			2.5	2/79	na	necropsy	[139]
			case report		na	necropsy	[155]

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
		Israel	3.5	2/56	na	necropsy	[48]
			33.3	5/15	na	necropsy	[146]
		Russia	76.0	13/17	50–800 epg	CO	[19]
			52.2	na	na	necropsy	[97]
			5.0	3/60	na	necropsy	[106]
			na	na	na	necropsy	[107]
			12.0	18/150	3–265	necropsy	[53]
		Serbia	0.2	1/447	2	necropsy	[108]
		Tajikistan	na	na	na	necropsy	[148]
		Tunisia	9.7	3/31	2–4	necropsy	[140]
		Uzbekistan	na	na	na	necropsy	[151]
		India	na	na	na	necropsy	[191]
		Russia	16.6	2/12	4	necropsy	[98]
	<i>Ancylostoma guentini</i>						
	<i>Placoconus lotoris</i> (syn. <i>Uncinaria lotoris</i> ) <sup>b</sup>						
	<i>Uncinaria stenocephala</i>						
		Afghanistan	na	na	na	necropsy	[192]
		Azerbaijan	50.0	49/98	1–404	necropsy	[99]
			na	na	na	necropsy	[100]
		Bulgaria	64.0	na	na	necropsy	[101]
			na	na	na	necropsy	[237]
			45.4	5/11	na	necropsy	[142]
			84.6	na	na	necropsy	[45]
		Chechnya	50.0	8/16	4–23	necropsy	[103]
		Greece	na	4/5	na	necropsy	[104]
		Hungary	40.0	8/20	na	necropsy	[59]
		Iran	85.0	17/20	11.1	necropsy	[110]
			6.3	5/79	na	necropsy	[139]
		Russia	34.8	na	na	necropsy	[97]
			na	na	na	necropsy	[339]
			30.0	18/60	na	necropsy	[106]
			na	na	na	necropsy	[107]
			89.3	134/150	3–550	necropsy	[53]
		Tajikistan	na	na	na	necropsy	[148]
		Tunisia	68.0	21/31	1–54	necropsy	[140]

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Ascarididae	<i>Baylisascaris devosi</i>	Turkey	na	na	na	necropsy	[150, 194]
		Uzbekistan	na	na	na	necropsy	[151]
			na	na	na	necropsy	[152]
	<i>Toxascaris</i> sp.	Azerbaijan	17.7	14/79	1–16	necropsy	[99]
		Kazakhstan	11.1	2/18	2–8	necropsy	[147]
	<i>Toxascaris leonina</i>	Afghanistan	na	na	na	necropsy	[192]
		Armenia <sup>a</sup>	case report		na	CO	[195]
		Azerbaijan	0.8	1/114	1	necropsy	[137]
			31.8	29/91	1–19	necropsy	[99]
			na	na	na	necropsy	[100]
		Bulgaria	36.0	na	na	necropsy	[101]
			5.8	na	na	necropsy	[141]
		Chechnya	100	16/16	1–12	necropsy	[103]
		Egypt	na	na	na	necropsy	[186]
		Hungary	15.0	3/20	na	necropsy	[59]
		Iran	30.0	3/10	na	necropsy	[111]
		Iran <sup>a</sup>	na	2/2	166.5 epg	CO	[372]
		Kazakhstan	11.1	2/18	2–11	necropsy	[147]
		Russia	43.5	na	na	necropsy	[97]
<i>Toxocara</i> sp.			10.0	2/20	4.00 ± 3.14	necropsy	[96]
			15.0	9/60	na	necropsy	[106]
			na	na	na	necropsy	[98]
			na	na	na	necropsy	[107]
		Tajikistan	4.7	7/150	2–23	necropsy	[53]
		Tunisia	na	na	na	necropsy	[148]
		Turkey	6.5	2/31	1–7	necropsy	[140]
		Uzbekistan	na	na	na	necropsy	[150]
			na	na	na	necropsy	[151]
			na	na	na	necropsy	[152]
		India <sup>a</sup>	21.6	13/60	na	CO	[144]
			na	na	na	CO	[196]
			na	2/2	40–700 epg	CO	[197]

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
<i>Toxocara canis</i> (syn. <i>Belascaris marginata</i> )		Azerbaijan	na	3/6	na	CO	[185]
			32.6	32/98	1–21	necropsy	[99]
		Bangladesh	na	na	na	necropsy	[100]
			40.0	12/30	na	necropsy	[134]
			na	2/5	na	CO	[118]
		Bulgaria	54.5	6/11	na	necropsy	[142]
			7.7	na	na	necropsy	[45]
		Chechnya	50.0	8/16	3–18	necropsy	[103]
		Greece	na	2/5	na	necropsy	[104]
		Hungary	20.0	4/20	na	necropsy	[59]
		India (as <i>B. marginata</i> )	na	na	na	na	[187]
			na	na	na	na	[143]
			na	na	na	na	[112]
		India <sup>a</sup>	na	na	na	CO	[189]
		Iran	10.0	2/20	na	necropsy	[110]
			7.1	1/14	10	necropsy	[136]
			10.0	1/10	na	necropsy	[111]
			5.0	4/79	na	necropsy	[139]
			12.5	7/56	na	necropsy	[48]
		Iran <sup>a</sup>	na	2/2	25 ± 5 epg	CO	[372]
		Russia	60.9	na	na	necropsy	[97]
			5.0	1/20	2.00 ± 2.13	necropsy	[96]
			6.6	4/60	na	necropsy	[106]
			na	na	na	necropsy	[98]
			na	na	na	necropsy	[107]
			23.3	35/150	1–22	necropsy	[53]
		Serbia	1.6	7/447	7.8 ± 2.1	necropsy	[108]
			23.3	14/60	na	necropsy	[49]
		Tajikistan	na	na	na	necropsy	[148]
		Tunisia	16.0	5/31	1–9	necropsy	[140]
		Turkey	na	na	na	necropsy	[150]
		Uzbekistan	na	na	na	necropsy	[151]

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Crenosomatidae	<i>Toxocara cati</i> (syns <i>Ascaris mystax</i> , <i>T. mystax</i> ) <sup>b</sup>	Italy	na	na	na	necropsy	[152]
		Russia	na	na	na	necropsy	[138]
		Russia	26.1	na	na	necropsy	[97]
	<i>Crenosoma vulpis</i>	Uzbekistan	5.0	1/20	2.0 ± 1.9	necropsy	[96]
		Azerbaijan	na	na	na	necropsy	[152]
		Azerbaijan	14.6	12/82	1–19	necropsy	[99]
		Bangladesh	na	na	na	necropsy	[100]
	Chechnya	Bangladesh	na	1/5	na	necropsy	[118]
		Chechnya	100	16/16	10–23	necropsy	[103]
		Hungary	30.0	6/20	na	necropsy	[59]
Diaphanocephalidae	<i>Dracunculus medinensis</i>	Russia	26.1	n/a	na	necropsy	[97]
		Russia	10.0	6/60	na	necropsy	[106]
		Russia	na	na	na	necropsy	[107]
	<i>Grenosoma petrowi</i>	Chechnya	12.0	18/150	6–297	necropsy	[53]
		Chechnya	37.5	6/16	16–38	necropsy	[103]
		India	na	na	na	necropsy	[198]
	<i>Kalicephalus schadi fotedari</i> <sup>b</sup>	India	na	na	na	na	[112]
		Kazakhstan	16.6	3/18	2–4	necropsy	[147]
		Tajikistan	na	na	na	necropsy	[148]
Gnathostomatidae	<i>Gnathostoma spinigerum</i>	India, Bangladesh, Burma	na	na	na	na	[112]
		Bangladesh	26.6	8/30	na	necropsy	[134]
		Serbia	0.4	2/447	1	necropsy	[108]
	<i>Gongylonema</i> sp. <sup>b</sup>	na	na	1/1	na	El	[199]
		Hungary	10.0	2/20	na	necropsy	[59]
		Russia	8.3	5/60	na	necropsy	[106]
	<i>Angiostrongylus vasorum</i>	Russia	26.0	39/150	3–104	necropsy	[53]
		Bulgaria	30.0	3/10	na	K	[200]
		Kenya (as <i>Dipetalonema reconditum</i> )	na	na	na	na	[201]
Molineidae	<i>Molineus patens</i>	Azerbaijan	na	na	na	necropsy	[100]
		Bangladesh	na	4/5	na	necropsy	[118]
		Bulgaria	8.9	5/56	2–16	necropsy/K	[202]
	<i>Acanthocheilonema reconditum</i> (syn. <i>Dipetalonema reconditum</i> )	Bulgaria	9.6	na	na	necropsy	[45]
		Bulgaria	na	na	na	na	[201]
		Kenya (as <i>Dipetalonema reconditum</i> )	na	na	na	na	[201]
	<i>Dirioflaria immitis</i>	Azerbaijan	na	na	na	necropsy	[100]
		Bangladesh	na	4/5	na	necropsy	[118]
		Bulgaria	8.9	5/56	2–16	necropsy/K	[202]
	<i>Onchocercidae</i>	Bulgaria	9.6	na	na	necropsy	[45]

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
			70.0	7/10	na	K	[200]
		Greece	37.5	122/325	1–19	necropsy	[203]
		Hungary	case report	2/27	4	necropsy	[204]
		India <sup>a</sup>	7.4	na	1–10	necropsy	[205]
		Iran	na	na	na	na	[206]
			28.5	4/14	13	necropsy	[136]
			na	na	na	necropsy	[207]
			11.4	9/79	na	necropsy	[139]
			1.7	1/56	na	necropsy	[48]
			8.9	4/45	1–10	necropsy, molecular	[208]
		Romania	18.52	10/54	1–7	necropsy	[209]
			9.26	5/54	na	molecular	[209]
		Russia	8.3	1/12	29	necropsy	[98]
			8.3	5/60	na	necropsy	[106]
			20.0	na	na	necropsy	[339]
			22.7	34/150	2–23	necropsy	[53]
		Serbia	7.3	32/437	na	necropsy	[210]
		Uzbekistan	na	na	na	necropsy	[152]
		Egypt	na	na	na	necropsy	[186]
		Iran	10.0	2/20	na	necropsy	[110]
		Romania	1.8	1/54	na	molecular	[209]
		Russia	3.3	2/60	na	necropsy	[106]
		Uzbekistan	na	na	na	necropsy	[152]
		Kazakhstan	5.5	1/18	7	necropsy	[147]
Oxyuridae	<i>Syphacia</i> sp. <sup>b</sup>	Iran	na	na	na	necropsy	[105]
Physalopteridae	<i>Physaloptera</i> sp.	Kazakhstan	5.5	1/18	4	necropsy	[147]
	<i>Physaloptera sibirica</i>	Azerbaijan	na	na	na	necropsy	[100]
		Kazakhstan	11.1	2/18	1–3	necropsy	[147]
Rictulariidae	<i>Rictularia</i> sp.	Egypt	na	na	na	necropsy	[186]
		Greece	na	1/5	na	necropsy	[104]
	<i>Rictularia affinis</i> (syn. <i>Pterygodermatites affinis</i> )	Azerbaijan	36.3	28/77	1–29	necropsy	[99]
			na	na	na	necropsy	[100]

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Spiroceridae	<i>Rictularia cahirensis</i>	Bulgaria	7.7	na	na	necropsy	[45]
		India (as <i>P. affinis</i> )	na	na	na	na	[117]
			na	na	na	na	[188]
			na	na	na	na	[112]
		Iran	50.0	5/10	na	necropsy	[111]
			5.0	4/79	na	necropsy	[139]
		Kazakhstan	11.1	2/18	1–3	necropsy	[147]
		Tunisia (as <i>P. affinis</i> )	6.5	2/31	1	necropsy	[140]
		Turkmenistan	na	na	na	necropsy	[177]
		Uzbekistan	na	na	na	necropsy	[151]
	<i>Spirocerca arctica</i>		na	na	na	necropsy	[152]
		Egypt	na	na	na	necropsy	[186]
		Iran	10.0	2/20	na	necropsy	[110]
		Turkey	na	na	na	necropsy	[340]
		Uzbekistan	na	na	na	necropsy	[151]
		Azerbaijan	16.6	2/12	5–14	necropsy	[99]
			na	na	na	necropsy	[100]
		Azerbaijan	23.4	23/98	1–29	necropsy	[99]
			na	na	na	necropsy	[100]
		India	case report		na	necropsy	[211]
Strongyloididae	<i>Spirocerca sanguinolenta</i>	India <sup>a</sup>	case report		na	na	[112]
		Iran	2.5	2/79	na	necropsy	[212]
		Italy (as <i>F. sanguinolenta</i> )	na	na	na	necropsy	[139]
		Uzbekistan	na	na	na	necropsy	[138]
		India	na	na	na	necropsy	[151]
		India <sup>a</sup>	na	na	na	CO	[213]
		Iran <sup>a</sup>	na	na	na	CO	[214]
		Iran	na	2/2	5.5 ± 0.7 epg	CO	[372]
			na	na	na	necropsy	[105]
		Tunisia	3.2	1/31	2	necropsy	[140]
Thelaziidae	<i>Thelazia callipaeda</i>	Romania	1.6	1/64	70	necropsy	[215]

Class Enoplea

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
Capillariidae	<i>Capillaria</i> sp.	India <sup>a</sup>	na	na	na	CO	[214]
		Russia	2.7	4/150	1–45	necropsy	[53]
	<i>Eucoleus aerophilus</i> (syn. <i>Thominx aerophilus</i> )	Azerbaijan (as <i>T. aerophilus</i> )	na	na	na	necropsy	[100]
		Hungary	5.0	1/20	na	necropsy	[59]
		Russia	8.3	5/60	na	necropsy	[106]
			37.3	56/150	1–6	necropsy	[53]
	<i>Capillaria boehmi</i>	Russia	30.0	45/150	1–11	necropsy	[53]
	<i>Capillaria plica</i>	Azerbaijan	14.8	4/27	1–4	necropsy	[99]
			na	na	na	necropsy	[100]
		Bulgaria	16.4	na	na	necropsy	[45]
Diectophymatidae		Hungary	45.0	9/20	na	necropsy	[59]
		Russia	11.6	7/60	na	necropsy	[106]
			33.3	50/150	1–123	necropsy	[53]
	<i>Capillaria putorii</i>	Azerbaijan	na	na	na	necropsy	[100]
	<i>Diectophyme renale</i>	Azerbaijan	3.5	4/114	1	necropsy	[137]
		Iran	35.0	7/20	na	necropsy	[110, 216]
		Russia	3.3	2/60	na	necropsy	[106]
		Tajikistan	na	na	na	necropsy	[148]
		Uzbekistan	na	na	na	necropsy	[151]
			na	na	na	necropsy	[152]
Trichinellidae	<i>Diectophyme skrjabini</i>	Russia	17.4	na	na	necropsy	[97]
	<i>Trichinella</i> sp.	Armenia	33.3	5/15	na	TRIC	[217]
		Azerbaijan	30.1	na	na	TRIC	[218]
			28.6	na	na	TRIC	[219]
		Bulgaria	50.0	na	na	TRIC	[220]
			33.3	15/45	na	TRIC	[221]
			21.2	7/33	na	TRIC	[222]
		Croatia	na	na	na	AD	[102]
		Georgia	80.0	na	na	TRIC	[218]
		Romania	53.7	29/54	na	TRIC	[223]
	Russia	14.3	na	na	TRIC	[224]	
		case report		na	AD	[225]	

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
<i>Trichinella britovi</i>	Tajikistan	Tajikistan	25.0	75/302	na	TRIC	[226]
			case report		na	AD	[227]
	Thailand	Thailand	na	na	na	TRIC	[228]
			case report		na	TRIC	[229]
	USSR (former)	USSR (former)	case report		na	TRIC	[230]
			36.5	na	na	TRIC	[231]
	Yugoslavia (former)	Yugoslavia (former)	25.0	na	na	TRIC	[232]
			case report		na	PCR	[233]
	Algeria	Algeria	case report		na	AD	[234]
			case report		na	AD, PCR	[235]
	Iran	Iran	11.1	2/18	na	TRIC	[234]
			na	na	na	AD, PCR	[235]
	Kazakhstan	Kazakhstan	na	3/4	0.9–1.4 lpg	AD, PCR	[236]
			case report		55 lpg	AD, PCR	[237]
	Romania	Romania	4.7	2/42	na	AD, PCR	[238]
			15.4	2/13	na	AD, PCR	[239]
	Serbia	Serbia	27.8	25/90	1.1–57.6 lpg	AD, PCR	[240]
			case report		na	AD	[234]
<i>Trichinella nativa</i>	Turkmenistan	Turkmenistan	case report		na	AD	[234]
			case report		na	AD	[234]
	Kazakhstan	Kazakhstan	18.9	4/18	7 lpg	AD	[147]
			n/a	1/4	0.9–1.4 lpg	AD, PCR	[236]
<i>Trichinella nelsoni</i>	Lithuania	Lithuania	61.5	na	na	TRIC	[241]
			na	2/2	na	TRIC	[242]
	Iran	Iran	16.2	3/18	6 lpg	na	[147]
			2.7	4/150	na	TRIC	[53]
<i>Trichinella pseudospiralis</i>	Russia	Russia	case report		214 lpg	TRIC	[243]
			20.4	17/83	1–7 lpg	TRIC	[244]
	Afghanistan	Afghanistan	21.1	25/114	1–22 lpg	TRIC	[137]
			17.5	16/91	1–44 lpg	TRIC	[99]
<i>Trichinella spiralis</i>	Bulgaria	Bulgaria	na	na	na	TRIC	[245]
			45.0	na	na	TRIC	[101]
	Georgia	Georgia	40.0	na	na	AD	[45]
			36.6	na	na	TRIC	[246]

**Table 6** Nematode parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species (synonym)	Origin	Prevalence (%)	Frequency	Intensity	Method	Reference
		Hungary	9.0	1/11	na	AD, PCR	[365]
		Iran	60.3	38/63	na	TRIC	[247]
			55.5	10/18	na	TRIC	[248]
			na	3/3	na	TRIC	[249]
			55.7	59/106	na	TRIC	[250]
			84.0	na	na	TRIC	[251]
		Kazakhstan	5.5	1/18	3 lpg	TRIC	[147]
		Russia	43.5	na	na	TRIC	[97]
			21.6	13/60	na	TRIC	[106]
			55.3	83/150	na	TRIC, AD	[53]
		Senegal	33.0	na	na	TRIC	[252]
		Serbia	na	3/3	1.9–21.4 lpg	AD, PCR	[253]
			8.3	1/12	3 lpg	AD, PCR	[254]
			7.9	3/38	3 lpg	AD, PCR	[255]
			14.2	6/42	na	AD, PCR	[238]
			38.4	5/13	na	AD, PCR	[239]
			71.1	64/90	0.59–152.8 lpg	AD, PCR	[240]
		Tunisia	na	2/2	na	TRIC	[256]
		India <sup>a</sup>	15.0	9/60	na	CO	[144]
		Azerbaijan	14.4	12/83	1–12	necropsy	[99]
			na	na	na	necropsy	[100]
		Azerbaijan (as <i>Trichocephalus vulpis</i> )	11.2	11/98	1–11	necropsy	[99]
			na	na	na	necropsy	[100]
		Bangladesh	na	1/5	na	CO	[118]
		Bulgaria	30.7	na	1–156	necropsy	[141]
			36.3	4/11	na	necropsy	[142]
		Russia (as <i>Trichocephalus vulpis</i> )	21.6	13/60	na	necropsy	[106]
			35.3	53/150	1–70	necropsy	[53]
		Serbia	11.6	4/60	na	necropsy	[49]
		Hungary	10.0	2/20	na	necropsy	[59]

Abbreviations: AD artificial digestion, CO coprological examination, EI experimental infection, epg eggs per gram faeces, lpg larvae per gram tissue, K Knott test, PCR polymerase chain reaction, TRIC trichinelloscopy, na not applicable/not available

<sup>a</sup>Animals kept in captivity

<sup>b</sup>Doubtful record

### Metastrongyloids

Compared to foxes, little is known about the respiratory and cardiovascular strongylids of golden jackals. *Crenosoma vulpis* has been reported on several occasions in Asia and Europe, with variable prevalence (Table 6). There is a single report of *Crenosoma petrowi* in golden jackals, a parasite otherwise known mainly from mustelids in North America [266], one report from bears (also in North America) and another one from stone martens in Italy [267]. Surprisingly, there is only one record of *Angiostrongylus vasorum* in golden jackals, suggesting either a lack of habitat overlap or a low detection sensitivity during necropsy.

### Filarioids

Zoonotic filarioids *Acanthocheilonema reconditum*, *Dirofilaria immitis* and *D. repens* have been all reported in golden jackals in various countries (Table 6). They have been found both as adults during necropsies but also as microfilariae demonstrating the reservoir role of jackals. *Dirofilaria* spp. are responsible in humans of conjunctivitis, focal pulmonary infarction with granuloma formation and subcutaneous and submucosal lesions in the lung and conjunctiva [268–270]. A recent review listed 1782 human *Dirofilaria* spp. infections, out of which 372 were pulmonary (in Australia, North and South America) and 1410 were subcutaneous/ocular cases (mostly in Europe and Asia) [271]. *Acanthocheilonema reconditum* is considered non-pathogenic for canids [155], but a single human case is well documented as being caused by this species and at least other two, by other *Acanthocheilonema* species [270, 272, 273]. The recorded prevalence of *D. immitis* has significantly varied in different areas between 7.3% in Serbia and 80.0% in Bangladesh, and seems to be consistent with the prevalence registered in dogs, generally between 40 and 70% in endemic areas [155]. The prevalence of *D. repens* in golden jackals ranged between 3.3 and 10.0%, resembling that recorded in dogs, generally varying from 5 to 20% [155].

The oriental eye-worm *Thelazia callipaeda* has been identified in golden jackals only in Romania [215], but this is probably due to lack of proper examinations of the eyes during the necropsy in other studies rather than a resistance of this host. Dogs originating in the Far East were initially considered the main host of the nematode [257]. Over the last 15 years, *T. callipaeda* has shown an increase in the distribution area mainly in Europe, with many new host records [274]. Human thelaziosis followed the same geographical spreading, with recent cases of infection diagnosed [274]. In this epidemiological picture, the golden jackal occurs as a new reservoir host.

### Capillariids

Respiratory capillariids of carnivores (*C. aerophila*, *C. boehmi* and *C. putorii*) are considered primarily

homoxenous, but the earthworms often act as facultative intermediate hosts [1, 275]. Along with the heteroxenous species *Capillaria plica* found in the urinary bladder, all species are cosmopolitan [257]. They have been found in golden jackals in Russia and other former Soviet Union countries. Only *C. plica* and *C. aerophila* are known to be zoonotic [276, 277], but their public health impact is minor. As the primary source of infection with *Capillaria* is the soil contaminated by infective eggs [155], the jackal can play an epidemiological role and secondary source of infection for domestic carnivores and humans.

### Trichinella

Trichinellids are an important group of meat-borne zoonotic parasites [278] for which the golden jackals represent an important reservoir. Five species, *T. britovi*, *T. nativa*, *T. nelsoni*, *T. pseudospiralis* and *T. spiralis*, were recorded in mountainous and lowland regions across the distribution range of the golden jackal in Europe and Asia. However, only three of these (*T. britovi*, *T. nativa* and *T. spiralis*) have been confirmed molecularly (Table 6). We consider all the records by artificial digestion or trichinelloscopy (see Table 6) where the species is named as hypothetical, as there is no reliable morphological means of differentiation between species, hence we recommend to consider these as *Trichinella* sp. Nevertheless, the zoonotic potential have been shown for most *Trichinella* species, hence, the golden jackal represents an important natural sylvatic reservoir for these nematodes [240].

### Other nematodes

Various other groups of nematodes have been found in golden jackals (families Spirocercidae, Dracunculidae, Gnathostomatidae, Physalopteridae, Rictulariidae, Subuluridae), but the reports are occasional (Table 6). Other groups (*Kalicephalus*, *Syphacia* and *Gongylo-nema*) are with high probability pseudoparasites, originating in prey hosts.

*Spirocerca lupi* is a rare zoonotic nematode species also identified in golden jackals in Europe, central and southern Asia (Table 6). Although a single human infection has been reported [279], the jackal may represent a reservoir host that maintains the life-cycle of the parasite in a certain region. Two other species of the genus *Spirocerca* (*S. arctica* and *S. sanguinolenta*, both described from domestic dogs) have been also reported in jackals, but their taxonomic status and biology are unknown.

*Dracunculus medinensis* has been identified in the golden jackal from several central and southern Asian countries. Currently the disease in humans has been declared extinct in the vast majority of the countries, with only three (Chad, South Sudan and Ethiopia) reporting cases in 2016 [280]. Dogs are considered to be important reservoirs for human infection [155, 281, 282]. In 2016,

more than 1000 dogs in Chad, 14 dogs in Ethiopia, and 11 dogs in Mali were reported with guinea-worm [280]. In this context, understanding the role of wild canids (including golden jackals) remains a crucial aspect in the management of the ongoing eradication campaign.

Another zoonotic species identified in golden jackals from tropical Asian countries (India, Bangladesh, Myanmar) is *Gnathostoma spinigerum*. Gnathostomiasis, a major food-borne parasitic zoonosis and a significant public health problem, is considered an emerging imported disease in Europe and a common human infection in central and South America, and Asia [283]. Domestic and wild mammals are the final hosts and numerous intermediate and paratenic hosts are the source for the human infection. The golden jackals maintain the sylvatic focus of the parasites and interfere with the domestic cycle, at least in several Asian countries (Table 6).

Various other carnivore-specific spirurids have been found in golden jackals (*Physaloptera sibirica*, *Rictularia affinis*, *R. cahirensis* and *Oxyntema linstowi*), but the role of this host species in their natural cycle remains unknown.

The cosmopolitan species *Diocotophyme renale* causes a severe kidney destruction in the carnivore definitive hosts. Although with limited zoonotic importance, so far around 20 human cases have been reported [284]. American minks seem to be the main reservoirs of the parasite [257], but an increased prevalence is also recorded in other wild and domestic carnivores. In golden jackals, *D. renale* has been reported in Asia, where the prevalence ranged between 3.3–35.0% (Table 6). Interestingly, this wild canid has shown a twice higher prevalence than stray dogs in the same geographical region [110], demonstrating the role of the jackal in the development of parasite's cycle in nature.

*Trichuris vulpis* has been found on various occasions in golden jackals in Europe and Asia (Table 6). The high prevalence of *T. vulpis* infection in golden jackals (10.0–36.3%) is in line with the value recorded in dogs originating from the same areas: 25% in India [285], 20% in Bulgaria [286] and 8.95% in Russia [264]. Although the prevalence of *T. vulpis* in domestic and wild canids is generally high, only around 60 human cases have been recorded [155].

## Arthropods

A great variety of Arthropods have been found in golden jackals (Table 7) [287–328].

### Ticks

Due to the large geographical range, the diversity of ticks parasitizing golden jackals is high. Ticks from 37 species belonging to six genera have been recorded in jackals throughout Europe, Asia and Africa. Nevertheless, the number of studies on tick-borne pathogens is surprisingly

low. The common tick species found in golden jackals in Europe, i.e. *Dermacentor reticulatus*, *D. marginatus*, *Haemaphysalis concinna*, *H. punctata*, *Ixodes canisuga*, *I. hexagonus*, *I. ricinus* and *Rhipicephalus sanguineus* (s.l.), show that they share these ticks with other wild canids, like foxes [329] or with domestic dogs [330]. The two most commonly reported ticks in golden jackals from Europe are *D. reticulatus* and *I. ricinus*. These ticks are known to be important vectors for *Babesia canis* and important tick-borne bacteria, *Borrelia burgdorferi* (s.l.) and *Anaplasma phagocytophilum*. However, the reports of these pathogens in *C. aureus* are scarce (a single report of *Babesia canis* from Romania [42]). In Asia, the most common ticks on jackals are several species of genus *Haemaphysalis*, with a high diversity of species reported: *H. leachi*, *H. adleri*, *H. bispinosa*, *H. canestrinii*, *H. flava*, *H. indoflava*, *H. intermedia*, *H. kutchensis* and *H. parva*. However, studies on the pathogens they might transmit are absent. Several of these *Haemaphysalis* species are shared with domestic dogs or other wild carnivores, raising the question of the reservoir role of jackals for certain tick-borne pathogens. Except for *Haemaphysalis* ticks, another commonly reported tick on golden jackals from Asia is *Rhipicephalus haemaphysaloides*, a tick which prefers ungulates and known as vector of several viral and protozoan diseases [331]. Studies in golden jackals from arid regions (northern Africa and Middle East) demonstrated the predominant presence of ticks from the genus *Rhipicephalus*: *R. sanguineus* (s.l.), *R. turanicus* and *R. leporis*. Surprisingly, there are no reports of ticks on golden jackals in sub-Saharan Africa.

### Mites

Compared to foxes, jackals seem to be less affected by mange-causing mites (Table 7). So far, there is a single report of *Sarcoptes scabiei* in golden jackals, in Israel [287] and a single report of *Otodectes cynotis*, in Iran [295]. It is unclear if the scarcity of data regarding *Sarcoptes* is because of the low prevalence or because of the lack of studies and/or reports. Except sarcoptid mites, there are few records of *Demodex* in golden jackals, but its clinical significance is not known (Table 7).

### Fleas and lice

The diversity of fleas reported in golden jackals is relatively high, with at least seven species reported (Table 7), with the most common being *Pulex irritans*, *Ctenocephalides canis* and *C. felis*. Most of the reports of fleas in golden jackals originate in Russia and other former USSR countries and western and southern Asia. Surprisingly, there are no reports of fleas in golden jackals in Europe. The reports of lice in golden jackals are scarce with only three species occasionally reported (Table 7).

**Table 7** Arthropod parasites of the golden jackal, *Canis aureus*

Family	Species	Origin	Prevalence (%)	Frequency	Intensity (A, ♂, ♀, N, L) <sup>b</sup>	Reference
Class Arachnida						
Demodecidae	<i>Demodex</i> spp.	Israel	na	1/1	na	[287]
	<i>Demodex canis</i>	Russia	3.3	5/150	na	[53]
	<i>Demodex folliculorum</i>	Bangladesh	na	na	na	[118]
Ixodidae	<i>Amblyomma</i> sp.	Nepal	na	na	na	[288]
	<i>Amblyomma varanense</i> (syn. <i>Aponomma gervaisi lucasi</i> )	India	na	na	na	[289]
	<i>Amblyomma variegatum</i>	Haute-Volta	na	na	7 N	[290]
		Senegal	na	na	54 L	[291]
	<i>Dermacentor marginatus</i>	Russia	15.3	23/150	1–26	[53]
		Serbia	45.0	9/20	na	[292]
	<i>Dermacentor reticulatus</i>	Austria	na	1/1	17 ♂; 2 ♀	[56]
		Hungary	na	4/4	10 A	[293]
		Italy	na	1/1	na	[116]
		Romania	12.6	10/79	46 ♂; 25 ♀	[294]
		Russia	62.0	93/150	1–26	[53]
	<i>Haemaphysalis</i> sp.	Iran	1.7	1/56	na	[48, 295, 296]
		Nepal	na	na	na	[288]
	<i>Haemaphysalis adleri</i>	Iraq	na	na	na	[297]
		Israel	na	2/2	4 ♂; 1 ♀	[298]
			na	3/3	na	[299]
	<i>Haemaphysalis bispinosa</i>	India	na	na	na	[300]
		Nepal	na	na	na	[288]
	<i>Haemaphysalis canestrinii</i>	India	na	1/1	9 ♂; 3 ♀	[301]
			na	na	na	[300]
		Pakistan	na	3/3	3 ♂; 1 ♀	[301]
	<i>Haemaphysalis concinna</i>	Austria	na	1/1	1 N	[56]
		Hungary	na	4/4	7 N; 4 L	[293]
		Romania	1.2	1/79	1 N	[294]
	<i>Haemaphysalis flava</i>	India	na	na	A	[289]
	<i>Haemaphysalis indoflava</i>	India	na	na	na	[302]
	<i>Haemaphysalis intermedia</i>	India	na	2/2	8 ♂; 17 ♀; 28 N; 13 L	[303]
			na	na	na	[300]
	<i>Haemaphysalis kutchensis</i>	India	na	na	10 ♂; 1 ♀	[348]
	<i>Haemaphysalis leachii</i> (syns <i>H. leachii leachii</i> , <i>H. leachii indica</i> )	Egypt (as <i>H. leachii leachii</i> )	na	na	na	[305]
		India	na	1/1	9 ♂; 3 ♀	[306]
		India (as <i>H. leachii indica</i> )	na	na	na	[289]
			na	2/2	7 ♂; 2 ♀; 4 N; 1 L	[307]
		Nepal (as <i>H. leachii indica</i> )	na	3/3	6 N	[307]
	<i>Haemaphysalis longicornis</i> (syn. <i>H. neumanni</i> )	Ceylon	na	na	na	[308]
	<i>Haemaphysalis paraleachi</i>	Sudan	100	10/10	42 ♂; 4 ♀	[309]

**Table 7** Arthropod parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity (A, ♂, ♀, N, L) <sup>b</sup>	Reference
	<i>Haemaphysalis parva</i> (syn. <i>H. otophila</i> )	India	na	na	na	[310]
		Israel	na	3/3	na	[299]
		Israel (as <i>H. otophila</i> )	na	6/6	37	[311]
	<i>Haemaphysalis punctata</i>	Romania	na	4/4	na	[312]
			2.5	2/79	1 ♂; 2 N	[294]
	<i>Hyalomma</i> sp.	Russia	0.7	1/150	1	[53]
		Tajikistan	na	na	na	[148]
	<i>Hyalomma aegyptium</i>	USSR (former)	na	na	na	[313]
	<i>Hyalomma anatolicum</i>	Tajikistan	na	na	na	[148]
	<i>Hyalomma asiaticum</i>	Tajikistan	na	na	na	[148]
	<i>Hyalomma scupense</i>	Tajikistan	na	na	na	[148]
	<i>Ixodes</i> sp.	Iran	na	1/1	na	[314]
		Russia	na	na	na	[339]
		Tajikistan	na	na	na	[148]
	<i>Ixodes acuminatus</i> (syn. <i>I. redikorzevi theodori</i> )	Israel	na	6/6	1	[311]
	<i>Ixodes canisuga</i>	Hungary	na	4/4	1 N	[293]
	<i>Ixodes hexagonus</i>	Romania	10.1	8/79	2 ♂; 11 ♀; 24 N; 12 L	[294]
	<i>Ixodes ovatus</i>	Nepal	na	1/1	6 ♀	[315]
	<i>Ixodes ricinus</i>	Hungary	na	4/4	3 A	[293]
		Iran	3.5	2/56	na	[48, 295, 296]
		Italy	na	1/1	na	[116]
		Romania	na	1/1	na	[316]
			na	4/4	na	[312]
			26.5	21/79	54 ♂; 45 ♀; 3 N; 4 L	[294]
		Russia	68.7	103/150	1–62	[53]
		Serbia	55.0	11/20	na	[292]
	<i>Rhipicephalus</i> sp.	Iran	1.7	1/56	na	[48, 295, 296]
		Tajikistan	na	na	na	[148]
	<i>Rhipicephalus annulatus</i> (syn. <i>Boophilus calcaratus</i> )	Russia	1.3	2/150	1–2	[53]
	<i>Rhipicephalus cuspidatus</i>	Haute-Volta	na	na	na	[290]
	<i>Rhipicephalus haemaphysaloides</i>	India	na	na	na	[289]
			na	1/1	4 ♂	[306]
			na	2/2	1 ♀; 2 N	[303]
			na	na	na	[300]
		Nepal	na	na	na	[288]
	<i>Rhipicephalus leporis</i>	Iraq	na	na	na	[297]
		Tajikistan	na	na	na	[148]
	<i>Rhipicephalus pumilio</i>	Tajikistan	na	na	na	[148]
		Uzbekistan	na	na	na	[152]
	<i>Rhipicephalus rossicus</i>	Tajikistan	na	na	na	[148]
	<i>Rhipicephalus sanguineus</i>	Algeria	na	2/2	15 ♂; 8 ♀	[317]
		Burma, Ceylon, India	na	na	na	[289]

**Table 7** Arthropod parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity (A, ♂, ♀, N, L) <sup>b</sup>	Reference
		India	na	na	na	[300]
		Iran	na	na	na	[314]
		Israel	na	6/6	na	[311]
		Nepal	na	na	na	[288]
		Nigeria <sup>a</sup>	na	3/6	na	[41]
		Romania	na	1/1	na	[316]
			na	4/4	na	[312]
			1.2	1/79	1 ♂	[294]
		Serbia	0.5	1/20	na	[292]
		Tajikistan	na	na	na	[148]
		Turkey	na	na	na	[150]
			na	na	na	[318]
	<i>Rhipicephalus schulzei</i>	Tajikistan	na	na	na	[148]
	<i>Rhipicephalus simus</i>	Kenya	na	na	na	[319]
	<i>Rhipicephalus sulcatus</i>	Haute-Volta	na	na	5 ♂	[290]
	<i>Rhipicephalus turanicus</i>	Iraq	na	na	na	[320]
			100	14/14	na	[297]
		Tajikistan	na	na	na	[148]
		Uzbekistan	na	na	na	[152]
Psoroptidae	<i>Otodectes cynotis</i>	Iran	1.7	1/56	na	[48, 295, 296]
Sarcoptidae	<i>Sarcoptes scabiei</i>	Israel	na	1/1	na	[287]
Class Insecta						
Boopidae	<i>Heterodoxus spiniger</i>	Africa (North, East); Asia (South); Europe (Southeast)	na	na	na	[321]
		Uganda	na	1/1	1 ♂; 2 ♀	[322]
Ceratophyllidae	<i>Paraceras melis</i>	Russia	10.0	15/150	1–12	[53]
			3.3	5/150	na	[323]
Coptosyllidae	<i>Coptosylla lamellifer dubinini</i>	Uzbekistan	na	na	na	[152]
Hippoboscidae	<i>Hippobosca longipennis</i>	Russia	2.7	4/150	1–2	[53]
Linognathidae	<i>Linognathus setosus</i>	Afrotropical Region	na	na	na	[324]
		Nepal	na	na	na	[288]
Pediculidae	<i>Pediculus</i> sp.	Bangladesh	na	na	na	[118]
Pulicidae	<i>Pulex irritans</i>	Afghanistan	na	na	2 ♂; 1 ♀	[325]
		Iran	na	na	3 ♂; 1 ♀	[326]
		Israel	na	6/6	36	[311]
		Russia	24.0	36/150	1–15	[53]
			14.0	21/150	na	[323]
		Tajikistan	na	na	na	[148]
		Uzbekistan	na	na	na	[152]
	<i>Ctenocephalides canis</i>	Afghanistan	na	na	10 ♂; 38 ♀	[325]
		Iran	na	na	13 ♂; 25 ♀	[326]
			10.8	6/56	na	[48, 295, 296]
		Israel	na	4/6	27	[311]

**Table 7** Arthropod parasites of the golden jackal, *Canis aureus* (Continued)

Family	Species	Origin	Prevalence (%)	Frequency	Intensity (A, ♂, ♀, N, L) <sup>b</sup>	Reference
		Nigeria <sup>a</sup>	na	1/6	na	[41]
		Russia	48.0	72/150	1–28	[53]
			17.3	30/150	na	[323]
		Tajikistan	na	na	na	[148]
		Turkey	na	na	na	[150]
		Uzbekistan	na	na	na	[152]
	<i>Ctenocephalides felis</i> (syn. <i>C. felis felis</i> )	Ethiopia	na	na	na	[327]
		India (as <i>C. felis felis</i> )	na	na	na	[328]
		Iran (as <i>C. felis felis</i> )	na	na	2 ♂; 2 ♀	[326]
		Israel	50.0	3/6	6	[311]
		Russia	3.3	5/150	1–4	[53]
		Tajikistan	na	na	na	[148]
		Uzbekistan	na	na	na	[152]
	<i>Echidnophaga gallinacea</i>	Afghanistan	na	na	1 ♂	[325]
		Ethiopia	na	na	na	[327]
	<i>Xenopsylla nesokiae</i>	Tajikistan	na	na	na	[148]
Trichodectidae	<i>Trichodectes canis</i>	Russia	13.3	20/150	1–34	[53]
		Tajikistan	na	na	na	[148]
Vermipsyllidae	<i>Chaetopsylla globiceps</i>	Russia	27.3	41/150	1–19	[53]
			6.7	10/150	na	[323]
Class Maxillopoda						
Linguatulidae	<i>Linguatula serrata</i>	Romania	1.3	1/73	1 ♂	Our unpublished data

Abbreviation: na not applicable/not available

<sup>a</sup>Animals kept in captivity

<sup>b</sup>A, adults; ♂, male; ♀, female; N, nymphs; L, larvae

### Other arthropods

Although relatively common in most wild carnivores and domestic dogs (Mihalca, personal observation), there is only a single report of *Hippobosca longipennis* in golden jackals (Table 7). This species is an important vector for *Acanthocheilonema dracunculoides*, a filarioid widely distributed in canids across Africa [332]. However, this vector-borne nematode was never reported in golden jackals.

### Conclusions

This is the first comprehensive checklist summarizing the data on parasites of golden jackals. The large variety of parasites reported in golden jackals is caused by multiple factors, including their large geographical range, their extensive territorial mobility and wide food spectrum. Moreover, like in other carnivores, the predator behaviour of golden jackals is the cause of common records of pseudoparasites. Nevertheless, even in such cases, although these parasites do not infect jackals, they can be spread and can remain infective for their natural hosts. Considering that jackals share their habitats with domestic dogs and a wide variety of wild carnivores

across their distribution range and the high similarity with canine parasites [333], the risk of interspecific transmission among canid species, and the continued spread of the species, is likely to be associated with future territorial expanding of different parasitic diseases. The vast majority of parasites recorded in golden jackals are shared with domestic dogs or even domestic cats. Other parasites of jackals can use a wide variety of other domestic species, including livestock, as intermediate hosts. Hence, jackals are an important source of infection for domestic animals and might be directly or indirectly responsible for economic losses. Probably the most important aspect regarding the parasites of golden jackal is the large number and common occurrence of zoonotic parasites. Among these, several are with high public health impact: *Leishmania*, *Echinococcus*, hookworms, *Toxocara*, and *Trichinella*. Our review brings overwhelming evidence on the importance of *Canis aureus* as wild reservoir of human parasites.

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**Authors' contributions**

CMG collected the information from databases, systematized information in tables and wrote the manuscript. ADM had the initial idea of this review and critically revised the manuscript for important intellectual content. Both authors read and approved the final manuscript.

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# *Angiostrongylus chabaudi* (Biocca, 1957) in wildcat (*Felis silvestris silvestris*, S) from Romania

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**Abstract** *Angiostrongylus chabaudi* is a rare cardio-pulmonary nematode infecting felids. Although almost 60 years have passed since the original description of the species in Italy, this parasite has been seldom found in domestic and wildcats in southern Europe. The present study aims to report a new case of patent *A. chabaudi* infection in a road-killed wildcat from Maramureș County in Northern Romania. The necropsy revealed the presence of parasites in the pulmonary arteries and the right ventricle, and the fecal examination showed the presence of L1 larvae. Parasites were morphologically and morphometrically characterized as *A. chabaudi*, showing 100 % nucleotide similarity to an *Angiostrongylus* sp. originating from a wildcat from Germany and 99 % to *A. chabaudi* from Italy. This study reports *A. chabaudi* for the first time in Eastern Europe, expanding knowledge about the distribution range of this species.

**Keywords** *Angiostrongylus chabaudi* · Wildcat · Romania

## Introduction

Except for *Dirofilaria immitis* and *Aelurostrongylus abstrusus*, feline cardio-pulmonary nematodes have been for a long time

considered minor parasites, though they have recently gained the interest of veterinarians, due to clinical diseases in domestic cats as well as to the increasing number of case reports in new geographic regions (Brianti et al. 2014a; Traversa and Di Cesare 2013). These nematodes belong to several genera included in the superfamilies Metastrongyloidea, Trichuroidea, and Filarioidea.

The superfamily Metastrongyloidea, also known as “lungworms” comprise the genus *Aelurostrongylus*, with its main species, *A. abstrusus*, parasitizing deeply in the lung tissues of domestic cats (*Felis catus*), the typical definitive hosts (Traversa and Di Cesare 2013). The genus *Troglostrongylus* is represented by four species, namely, *T. troglostrongylus*, *T. subcrenatus*, *T. brevior*, and *T. wilsoni*, which have been sporadically found in wild felids around the world, inhabiting the frontal sinuses, trachea, bronchi, and bronchioles (Brianti et al. 2012, 2014a). The genus *Oslerus*, with the most common species *O. rostratus*, is localized in peribronchial tissues and in the lung parenchyma in wild felid species and in domestic cats (Brianti et al. 2014b). The superfamily Trichuroidea is represented by *Eucoleus aerophilus*, which has a low host specificity, parasitizing the upper respiratory tract of wild and domestic carnivores worldwide (Traversa et al. 2009). Finally, *Dirofilaria immitis* (Filarioidea), the heartworm, parasitizes the heart and pulmonary blood vessels and has a significant clinical importance as it can cause serious life-threatening conditions in domestic and wild felids across the world (McCall et al. 2008). The genus *Angiostrongylus* (Metastrongyloidea) includes 21 known species, affecting various species of mammals, including felids and canids (Spratt 2015). Three species infect domestic and wild felids: *A. felineus*, recently described in the egyptian cat, *Puma (Herpailurus) yagouaroundi*, in Brazil (Vieira et al. 2013); *A. vasorum*, common in dogs, while the cat is considered a permissive host (Dias et al. 2008); and

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*A. chabaudi* in domestic and wildcats in Europe (Biocca 1957; Varcasia et al. 2014; Diakou et al. 2015). Additionally, sequences of an *Angiostrongylus* sp. recovered from the pulmonary artery of a wildcat in Germany have recently become available in the GenBank [KM409651.1 and KM216825.1].

*A. chabaudi* is a rare cardio-pulmonary nematode localizing in the right heart and pulmonary arteries, initially recorded in wildcats (*Felis silvestris*) from the forests of the provinces of Rome and Grosseto, Italy (Biocca 1957). It has a rather limited geographical distribution, being identified in domestic cats in Italy (Varcasia et al. 2014; Traversa et al. 2015) and more recently in wildcats from Greece (Diakou et al. 2015; Spratt 2015). The life cycle is unknown (Varcasia et al. 2014).

There are many uncertainties regarding the geographical distribution range, host spectrum, and pathogenicity of angiostrongylids in felids. Due to all these gaps in the current scientific knowledge, it is pivotal to add new data regarding the infection caused by this nematode. In this context, the present paper reports the first case of patent *A. chabaudi* infection in a wildcat in Romania, emphasizing the existence of sylvatic foci throughout Europe.

## Materials and methods

### Sample origin and collection

A road-killed, young female wildcat (*F. silvestris*) was collected in the area of omcuta Mare village, Maramureş County (47.413595° N, 23.405743° E, 474 m altitude). Based on morphological and morphometric characteristics (Krüger et al. 2009), the animal was identified as a pure European wildcat (*F. s. silvestris*). During the necropsy, 12 slender and roundworms were collected from the right ventricle of the heart ( $n=1$ ) and pulmonary artery ( $n=11$ ) (Fig. 1). Parasites were temporarily mounted on microscope slides in saline, examined, photographed, and measured under an optical microscope (Olympus BX51; Soft Imaging solution GMBH LG20, Munster, Germany). The classical Baermann method (Willcox and Coura 1989) was performed on the feces, and the metastrongyloid first-stage larvae (L1) were collected. The morphological and morphometric characteristics of adults and larvae were analyzed, eight parameters being compared to other reports of angiostrongylid parasites in felids.

### Molecular analysis and species identification

Genomic DNA was extracted from an adult female using a commercial kit (Isolate II Genomic DNA Kit, Bioline, UK) according to the manufacturer's instructions. PCR reactions were performed to amplify a partial mitochondrial *cytochrome c oxidase* subunit 1 (*cox 1*, ~700 bp) gene and the internal transcribed spacer 2 (ITS2, ~500 bp) of the rRNA gene, using

primers and protocols available in literature (Gasser et al. 1993; Caldeira et al. 2003). Amplicons were purified using a commercial kit (QIAquick PCR Purification Kit, QIAGEN) and sequenced through an external service (performed by Macrogen Europe, Amsterdam). The sequences were compared to those available in the GenBank® by Basic Local Alignment Search Tool (BLAST) analysis.

Species identification was based on morphological characteristics, correlated with molecular analysis (Biocca 1957; Costa et al. 2003; Varcasia et al. 2014).

## Results

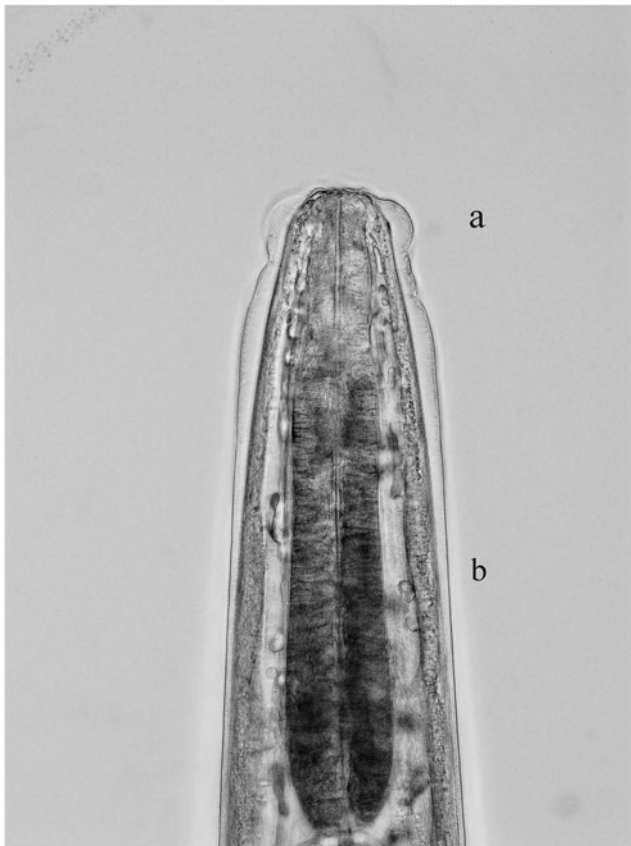
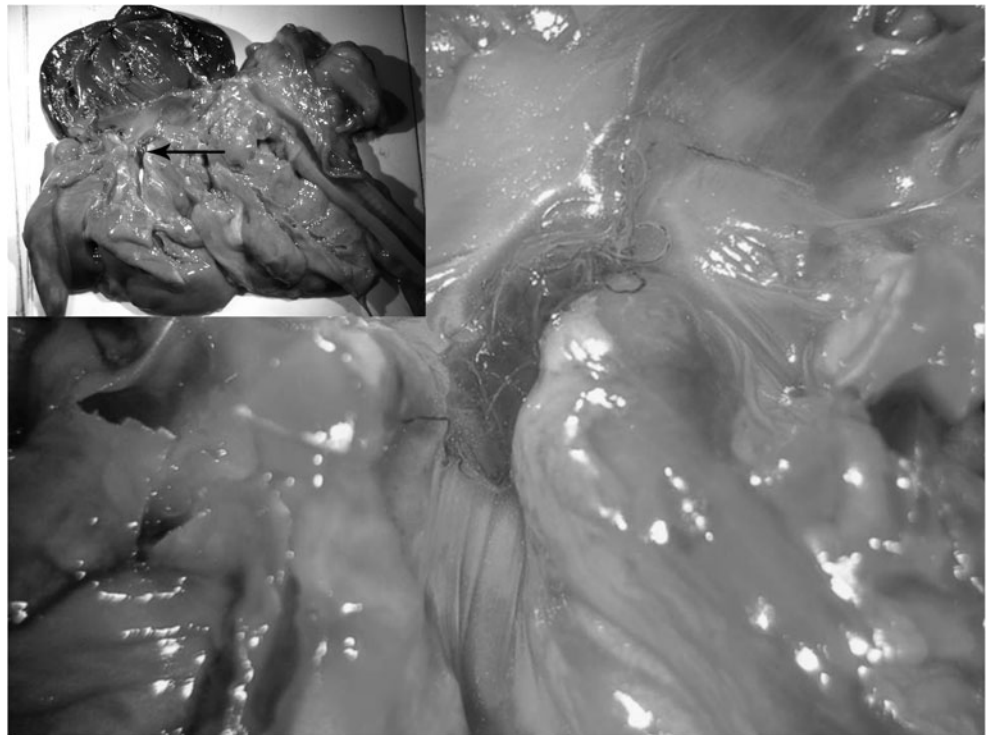
### Morphology and morphometry of parasites

Three male and nine female specimens were collected from the pulmonary arteries. The anterior end in both sexes was tapered, with a slightly dilated cuticle appearing as a small cephalic vesicle (Fig. 2). The mouth opening was annular, being surrounded by six labial papillae originally called perityles (Biocca 1957). The posterior end of females was curved, and a small trilobated copulatory bursa was observed in males. The cuticle showed transverse striation, more visible at the posterior extremity and flattened to the anterior end.

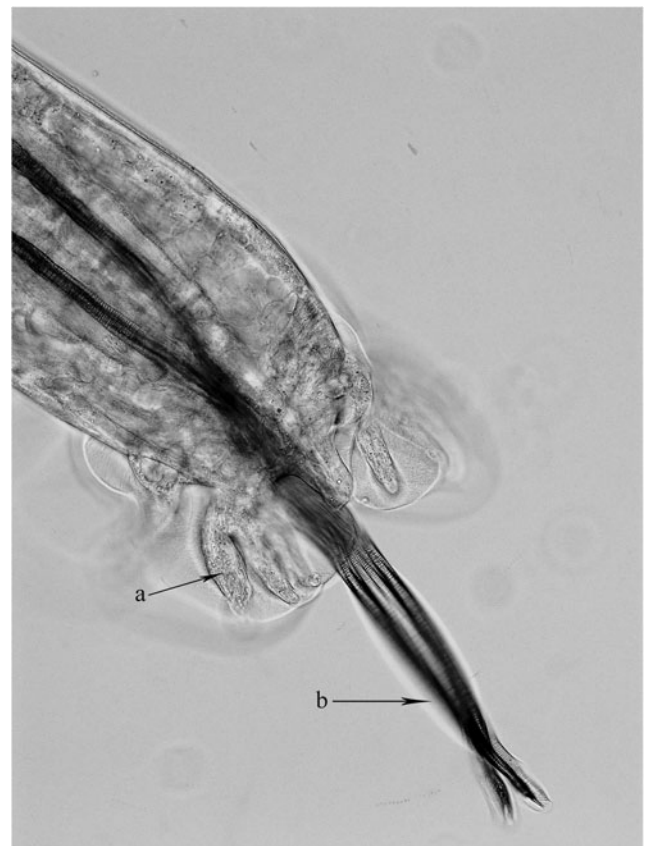
The females had a specific barber-pole appearance due to their brownish (blood-filled) intestinal tract that is entwined around the pale uterus. Their size ranged from 18.9- to 23.8-mm length and 0.249- to 0.293-mm width in the mid body. The distance between the nerve ring and cephalic end varied between 265.2 and 297.8 µm. The excretory pore was localized at 396.1–450.9-µm distance from the anterior end. The rhabditiform esophagus was composed of an elongated posterior bulb, followed by an isthmus and a cylindrical corpus, delimitation between these three esophageal components being weakly noticeable. Its size ranged from 313.7 to 355.1 µm. The distances between different posterior structures specific to females, namely from the vulva to the anus, vulva to the caudal end, and anus to the caudal end, ranged as follows: 138.7 to 148.5 µm, 200.3 to 222.9 µm, and 58.6 to 71.7 µm, respectively.

The males had a uniformly colored body with sizes ranging between 14.8- and 15.2-mm length and 0.197 and 0.219-mm width. The distances between the nerve ring and cephalic end varied from 149.2 to 178.8 µm, while the excretory pore was located at 305.1–344.5 µm from the anterior end. The esophagus length ranged between 313.7 and 355.1 µm. The copulatory bursa was small, with two symmetrical lateral lobes and an underdeveloped dorsal lobe. Lateral rays showed a common base, the externolateral being thicker and distant from the mediolateral and posterolateral which are thinner and closer (Fig. 3). The spicules were thin and had unequal lengths; the shorter ranged between 500.2 and 551.0 µm and the longer

**Fig. 1** Location of *A. chabaudi* in the pulmonary arteries (black arrow)



**Fig. 2** Anterior end of *A. chabaudi*: (a) small cephalic vesicle; (b) esophagus



**Fig. 3** Copulatory bursa of *A. chabaudi*: (a) lateral rays; (b) spicules

from 502.35 to 595.74  $\mu\text{m}$ . The spicules showed transverse striations and the tip was corrugated, ending with a yellowish hyaline apex.

The larvae isolated from the feces measured 307.0–419.7  $\mu\text{m}$  in length and 15.3–17.2  $\mu\text{m}$  in width and had a typical metastrongyloid posterior end with a wavy tail and a subterminal spine separated by a notch (Fig. 4).

The morphometry of the isolated parasites was similar to that of *A. chabaudi* recorded in the original description and was compared to the measurements provided by Biocca (1957), Varcasia et al. (2014), Traversa et al. (2015), and Diakou et al. (2015) (Table 1—*A. chabaudi* min/max represent the limits recorded in all reports).

### Molecular analysis

The BLAST analysis of ITS2 sequence (accession number KU521522) revealed a 100 % nucleotide similarity to an *Angiostrongylus* sp. recovered from a wildcat from Germany (accession number KM216825) and was 99 % similar to an *A. chabaudi* sequence (accession number KM009115) originated from a domestic cat from Italy. The *cox 1* gene sequence (accession number KU521521) was 99 % similar to the same *Angiostrongylus* sp. from Germany (accession number KM409651) and showed similarities of 88–90 % to other species of *Angiostrongylus* (e.g., *A. vasorum*—GQ982844; *A. cantonensis*—LK950095; *A. costaricensis*—KR827449).

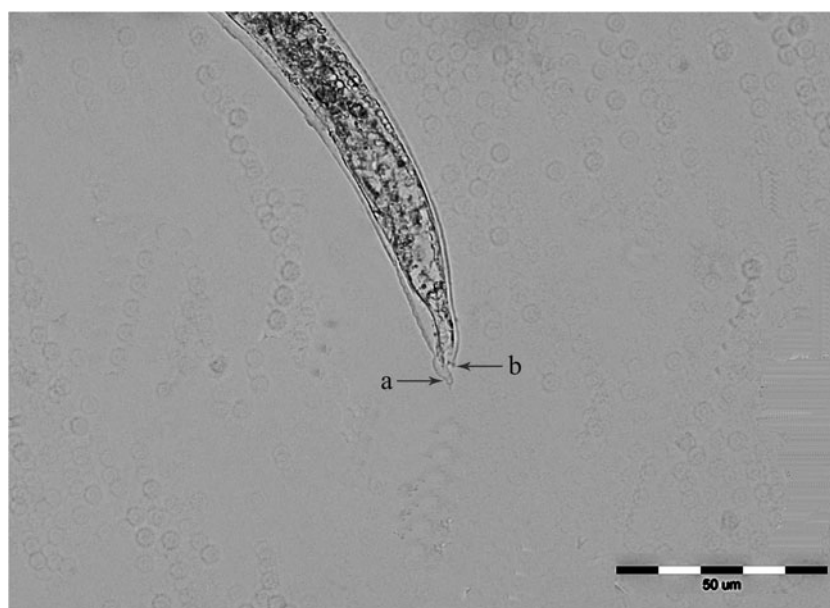
### Discussion

Cardio-pulmonary nematodes of carnivores have been considered for a long time of minor importance, being *A. vasorum*

the most common species of the genus, which is diagnosed in domestic and wild canids throughout Europe. Scientific data on the distribution and host range of *A. chabaudi* are minimal, and since its first report in wildcats from Roma and Grosseto provinces in Italy (Biocca 1957), it was diagnosed three times, in a road-killed domestic cat (Varcasia et al. 2014), in a stray cat from Italy (Traversa et al. 2015), and in a road-killed wildcat from Greece (Diakou et al. 2015). Another report of *Angiostrongylus* sp., showing a 99 to 100 % molecular similarity to *A. chabaudi* from Greece and Italy, was recorded in a wildcat from Germany, but this nematode had an undefined morphological similarity to *Angiostrongylus gubernaculatus*, a parasite of mustelids, originally described in North America (Steeb et al. 2014; Dougherty 1946).

The molecular analysis clustered the nematode into the genus *Angiostrongylus*. Indeed, in the present case, both the *cox 1* and ITS2 sequences were mostly similar to the ones registered in Germany while morphometric data fully supports its conspecificity with *A. chabaudi*. However, the small number of *A. chabaudi* sequences recorded in the GenBank (*cox 1*: accession KM068059; ITS2: accession KM009115) and their relatively short length prevent a thorough molecular analysis. Under these circumstances, only morphometric data can provide the basis for certain species differentiation among the *Angiostrongylus* genus. Morphological parameters of angiostrongylid species reported in carnivores, in Europe, have been herein compared (Table 1). In addition, *A. gubernaculatus*, identified in American badger (*Taxidea taxus*) and striped skunk (*Mephitis mephitis*) in North America, was also considered due to its likely occurrence in wildcat collected from Germany (Steeb et al. 2014). However, a large variability in body length and width (Table 1) was found in adult *Angiostrongylus* species, therefore indicating

**Fig. 4** Posterior end of *A. chabaudi* L1 larva: (a) wavy tail; (b) subterminal spine



**Table 1** Comparative morphometry of adult *Angiostrongylus* species

Species	Present specimens	<i>A. chabaudi</i> (Biocca 1957)	<i>A. chabaudi</i> (Yarcasia et al. 2014)	<i>A. chabaudi</i> (Traversa et al. 2015)	<i>A. chabaudi</i> (Diakou et al. 2015)	<i>A. chabaudi</i> min/max	<i>A. vasorum</i> (Costa et al. 2003)	<i>Angiostrongylus</i> sp. – fox (Gerrikagoitia et al. 2010)	<i>Angiostrongylus</i> sp. – badger (Gerrikagoitia et al. 2010)	<i>A. daskalovi</i> (Janchev and Genov 1988)	<i>A. gubernaculatus</i> (Dougherty 1946)
Parameters/sex											
Body length (mm)	♂ (n = 3) 14.8–15.2	14.6–16.3		9.0	14–18	9.0–18	12.40	13.90 ± 4.75	19.36 ± 7.69	13.36–21.31	18.0–19.5
Body width (µm)	197–219	185.0–225.0		79	193–200	79–225.0	243	221.40 ± 12.13	243.20 ± 19.63	254–306	300
Distance from the nerve ring to the cephalic end (µm)	149.2–178.8	185–230					191				
Distance from the excretory pore to the cephalic end (µm)	305.1–344.5	335.0–405.0			370	305.1–405.0	373	356.5 ± 34.68	409.5 ± 25.50	386–463	
Esophagus length (µm)	313.7–355.1	300.0–345.0		275.0	330	275.0–355.1	220–275	255.33 ± 13.60	333.30 ± 18.24	336–366	300–355
Spicules length (µm)	500.2–551.0	510.0–555.0		503.3–512.1	576–610	500.2–610.0	410–485	411.06 ± 17.71	345.57 ± 23.95	336–409	510–560
Parameters/sex											
Body length (mm)	♀ (n = 9) 18.9–23.8	19.8–24.1	16.9	19.0	21–22	16.9–24.1	15.57	18.97 ± 10.21	24.76 ± 13.66	14.39–31.12	22.0–24.0
Body width (µm)	249–293	245.0–298.0	195.8	103.7	260–270	103.7–298.0	268	304.14 ± 14.84	344.52 ± 17.95	340–511	350
Distance from the nerve ring to the cephalic end (µm)	265.1–297.8	210–240					215				
Distance from the excretory pore to the cephalic end (µm)	396.1–450.9	395.0–470.0	361.5	370.0	410–430	361.5–470.0	403	391.86 ± 21.44	447.40 ± 101.72	379–636	
Esophagus length (µm)	323.9–375.1	345.0–380.0	276.6	338.0	360	276.6–380.0	240–280	279.88 ± 20.27	368.45 ± 17.00	356–556	335–350
Distance from the vulva to the anus (µm)	138.7–148.5				135–142	135.0–148.5	141	233.63 ± 32.41	295.15 ± 46.25		
Distance from the vulva to the caudal end (µm)	200.3–222.9	170.0–210.0	160.6	264.1	204–210	160.6–222.9	205	275.66 ± 30.75	366.25 ± 44.17	269–412	205–250
Distance from the anus to the caudal end (µm)	58.6–71.7		43.4	64.9	67.0–72.0	43.4–72.0	67	69.70 ± 2.87	78.82 ± 3.45	76–115	75–90

that they cannot be considered as a criterion for a definitive identification.

The length of the spicules discriminated among species of *Angiostrongylus* identified in carnivores in Europe. It ranges between 503.3 and 610.0  $\mu\text{m}$  in *A. chabaudi*, differentiating this species from *A. vasorum*, *A. daskalovi*, and *Angiostrongylus* sp. isolated from a fox and badger in Spain, whose spicules are significantly smaller (410–485  $\mu\text{m}$ , 336–409  $\mu\text{m}$ ,  $411.06 \pm 17.71 \mu\text{m}$ , and  $345.57 \pm 23.95 \mu\text{m}$ ). This data confirms early observation by Biocca (1957), on that *A. chabaudi* can be differentiated from *A. vasorum* due to the length of spicules. Nonetheless, the morphology and morphometry of any nematode are affected by the method of preservation (Boag 1984; Naem et al. 2010).

Even though *A. chabaudi* was first collected from wildcats which, in turn, were considered as the primary host for the parasite (Biocca 1957), recent reports indicated the presence of this species equally in domestic and wildcats (Varcasia et al. 2014; Traversa et al. 2015; Diakou et al. 2015; Veronesi et al. 2016).

The paucity of clinical reports of *A. chabaudi* infection depends on the accuracy of the necropsy and coprological exam. For example, the location of the parasite in the right heart and lung vessels requires their careful examination. Regarding the coprological examination, in spite of its correctness, the lack of a thorough diagnosis of *A. chabaudi* L1 and the similarity with other metastrongyloid L1 (a transparent body and sigmoid tail) have created difficulties in species identification (e.g., the morphological description of *A. chabaudi* L1 has been only recently provided (Diakou et al. 2015). The geographical distribution is also affected by the occurrence of intermediate hosts. Though the life cycle of *A. chabaudi* is not known, it is considered that terrestrial mollusks are involved in the parasite transmission, by the similarity with other cardio-pulmonary nematodes of carnivores (Spratt 2015). However, there are numerous cases in which species belonging to the same genus, parasitizing the same host, with the same location, have completely different life cycles.

Temperature and humidity may represent major drivers for the spread of *A. chabaudi*. For example, survival of *A. vasorum* L1 is reduced to 18 % after 66 h in outdoor conditions (Ferdushy and Hasan 2010), therefore needing to rapidly find an intermediate host soon after their shedding with feces. Therefore, the south European distribution of *A. chabaudi* may be related to favorable environmental temperature and humidity values, which ensure a longer survival of the L1 larvae.

Similarly, the survival of L3 larvae in the intermediate hosts may also be important for the spreading of *A. chabaudi*. For instance, in the case of *A. vasorum*, experimental studies have shown that the survival rate and activity of larvae were greater at lower temperatures, having an optimum value of 15 °C in

Iberian slugs *Arion lusitanicus* (Dias and Dos Santos Lima 2012; Ferdushy et al. 2010).

The present study confirms the occurrence of *A. chabaudi* in the wildcat in southeastern Europe and provides an exhaustive analysis of certain morphometric criteria, which allows the identification of *A. chabaudi* under the conditions of uncertain results in molecular identification.

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**Competing interests** The authors declare that they have no competing interests.

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RESEARCH

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# A rare cardiopulmonary parasite of the European badger, *Meles meles*: first description of the larvae, ultrastructure, pathological changes and molecular identification of *Angiostrongylus daskalovi* Janchev & Genov 1988

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## Abstract

**Background:** *Angiostrongylus daskalovi* is a rare cardiopulmonary nematode infecting badgers. The parasite was described in 1988 and, since then, found only once in mustelids in Europe. The present study aims to report new cases of patent *A. daskalovi* infection in badgers from northern Romania and to provide new information on its ultrastructure, molecular diagnosis, and pathology.

**Methods:** Eight road-killed or hunted badgers originating from Maramureș and Alba counties in Romania were collected and necropsied. Adults and larvae of cardio-pulmonary nematodes were collected and examined by light and scanning electron microscopy (SEM). Genomic DNA was extracted from adults and first-stage larvae (L1). PCR amplification of the internal transcribed spacer 2 (ITS2, ~500 bp) of the rRNA gene was performed. Amplicons were purified, sequenced, and compared to those available in the GenBank database. Histopathological examination of the lungs was performed and lesions described.

**Results:** The necropsy revealed the presence of nematodes in the pulmonary arteries of three animals. All parasites were mature adults and the coproscopic examination showed the presence of eggs and L1 larvae in all three positive animals. Light microscopy examination confirmed the morphological and morphometric similarity of parasites to *Angiostrongylus daskalovi*. SEM highlighted the typical angiostrongylid structure of the rays of the copulatory bursa and the anterior extremity, with the presence of six sensory papillae surrounding the mouth opening in which a triangular tooth was visible. The first-stage larva (L1) of *A. daskalovi* is described here for the first time. Histopathological examination of the lungs showed chronic interstitial verminous pneumonia due to the presence of adult parasites. Molecular analysis showed 100 % nucleotide similarity to an *Angiostrongylus* sp. isolate originating from a badger from Spain, tentatively identified as *A. daskalovi*.

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**Conclusions:** Our study unequivocally demonstrates the presence of *A. daskalovi* in European badgers from Romania, provides the first description of the larvae and reveals new data about the ultrastructure of adult parasites and their pathological impact, contributing to the understanding of the phylogenetic relationships with other congeneric species.

**Keywords:** *Angiostrongylus daskalovi*, Badger, *Meles meles*, Romania, SEM, Histopathology, Molecular analysis

## Background

The family Mustelidae is the richest group within the order Carnivora, comprising five subfamilies: Lutrinae (otters), Melinae (European badgers), Mellivorinae (honey badgers), Taxidiinae (American badgers) and Mustelinae (weasels, tayra, wolverines, martens, polecats) [1]. According to recent multigene phylogenetic analysis, the family is split into four major clades and three monotypic lineages [2]. Among all these mustelids, the European badger (*Meles meles*) is spread throughout Europe and in some parts of the Middle East. It is an opportunistic omnivorous species; its diet includes a broad range of animals and plants. This varied diet exposes the badger to the risk of contamination by a wide variety of cysts, eggs, larvae or intermediate hosts of certain parasites. Of these, cardiopulmonary nematodes represent a particular group, several species being reported in mustelids. The genus *Aelurostrongylus* Cameron, 1927 contains two species that are rarely reported in badgers in Europe: *A. falciformis* Schlegel, 1933 in Italy, Germany, Norway and Great Britain [3–6] and *A. pridhami* Anderson, 1962 in Spain. Two other metastrongyloid species belonging to the genus *Angiostrongylus* Kamensky, 1905 have been recorded in badgers. *Angiostrongylus daskalovi* Janchev & Genov, 1988 was described from the pulmonary arteries of the European badger (*M. meles*) in the north-central region of Bulgaria [7] and more recently in Spain [8]. Additionally, *Angiostrongylus vasorum* (Baillet, 1866) was identified in the cardiopulmonary system of badgers in Switzerland, Italy and Spain [9–12]. Another species, *Angiostrongylus gubernaculatus* Dougherty, 1946, was described from the right ventricle of the Californian badger, *Taxidea taxus neglecta* in California and the California Channel Islands, the United States [13, 14].

Apart from these two genera, other lung nematodes have been reported in European badgers including *Crenosoma* sp., *C. vulpis* (Dujardin, 1845) and *C. melesi* Janchev & Genov, 1988, as well as the trichuroid nematode *Capillaria aerophila* Creplin, 1839 [3, 4, 12, 15, 16]. Cardiopulmonary nematodes have also been reported in other mustelids like the stoat (*Mustela erminea*) and weasel (*Mustela nivalis*) infected with *A. vasorum* [17, 18] and the European pine marten (*Martes martes*) and the beech marten (*Martes foina*) infected with *A. daskalovi* [7].

The European badger is considered the typical host for *A. daskalovi* [7]. This nematode has a poorly known geographical distribution, so far being recorded only in Bulgaria and Spain. Moreover, the life-cycle and the host spectrum are incompletely known; the larvae are unknown and the pathological aspects have never been described. Due to these shortcomings, it is important to add new data regarding the infection caused by this nematode species. In this context, the present paper reports the first cases of patent *A. daskalovi* infection in badgers in Romania, emphasizing the ultrastructure of adult parasites and morphology of the L1 larval stage, molecular characterization, and pathological changes.

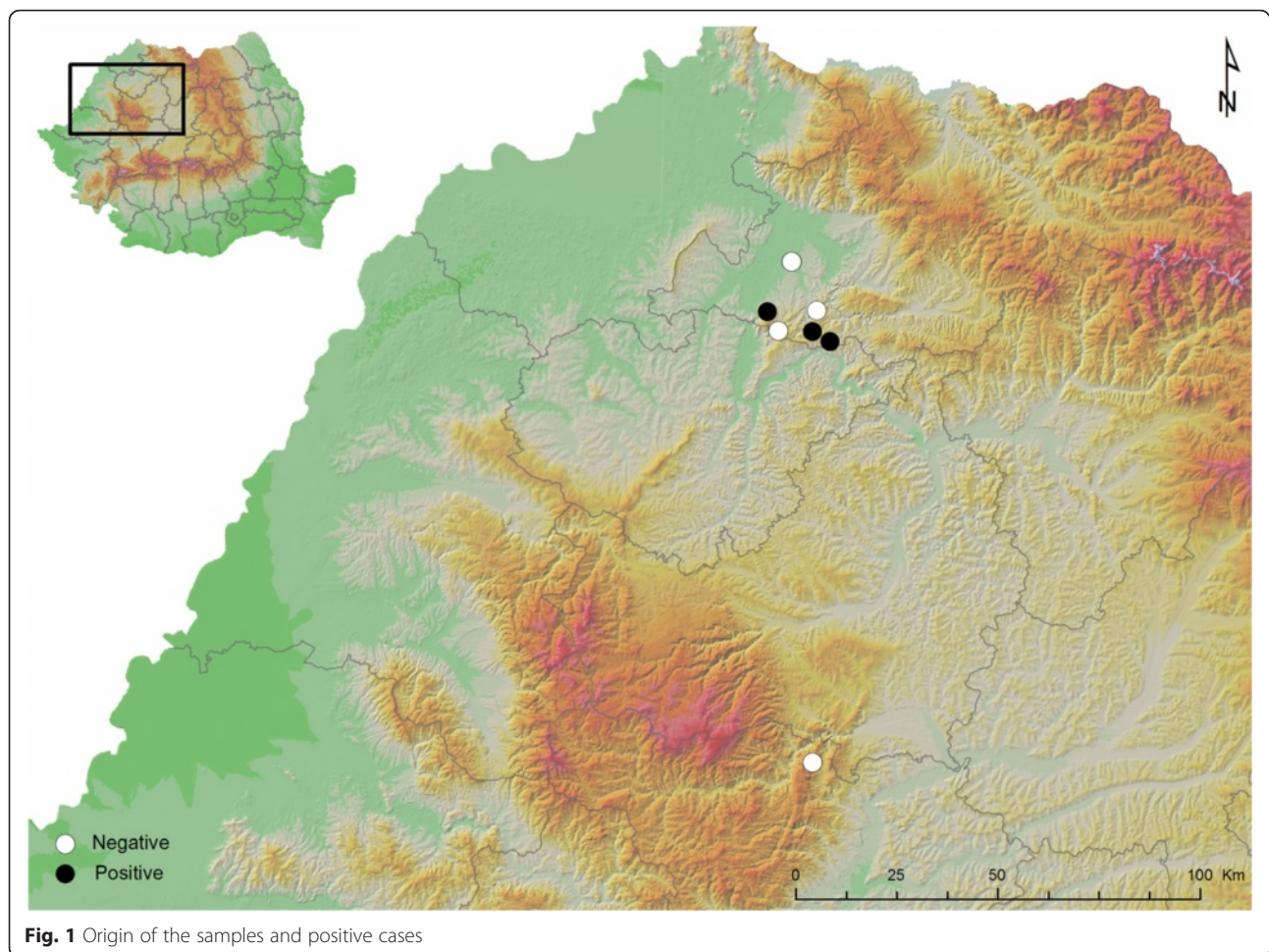
## Methods

### Sample origin and collection

Between February 2015 and April 2016, eight European badgers (*Meles meles* L.) were collected in the counties of Maramureş and Alba, in northern and central Romania (Fig. 1). The animals were either road-killed or hunted. Their carcasses were submitted for pathological and parasitological examination within a few hours after the death of the animals and examined immediately. During the necropsy, all nematodes found in the pulmonary arteries were collected in formalin (for morphological examination) and absolute ethanol (for molecular analysis). The classical Baermann method [19] was performed on the lung tissue and faeces, and the metastrongyloid first-stage larvae (L1) were collected. The morphology and morphometry under light microscopy of adults and larvae and SEM characteristics of adults were analysed, ten parameters being compared to other reports of angiostrongylid parasites in mustelids (Table 1).

### Pathology

Full necropsy and histological examination were carried out on all badgers included in this study. Selected samples from the right atrium, pulmonary arteries, pulmonary parenchyma and tracheobronchial lymph nodes were collected for histological analysis. Samples were fixed in 10 % phosphate-buffered formalin for 24 h, routinely processed, embedded in paraffin wax, cut into 4 µm sections, and stained with hematoxylin and eosin (H&E).



**Fig. 1** Origin of the samples and positive cases

### Scanning electron and light microscopy

All adult worms were washed in saline, preserved for 24 h in 0.5 % formalin, dehydrated, cleared in lactophenol, mounted in Canada balsam and analyzed by light microscopy using an Olympus BX 61 microscope (Japan). For scanning electron microscopy, some adult parasites were fixed for 2 h at 4 °C in 2.7 % glutaraldehyde in 0.1 M sodium cacodylate buffer (pH 7.2) and washed in PBS. Samples were post-fixed for 1 h with 1 % OsO<sub>4</sub>. The parasites were dehydrated in an ethanol series (30–100 %), and infiltrated with hexamethyldisilazane, dried, mounted on aluminum stubs coated with a 10 nm gold layer, and examined with a Hitachi SU8230 Scanning Electron Microscope (Japan).

### Molecular analyses and species identification

Genomic DNA was extracted from three adult nematodes (one from each positive animal) and 30 L1 stages (a pool of ten from each positive animal) using a commercial kit (Isolate II Genomic DNA Kit, Bioline, London, UK) as stated in the manufacturer's instructions. PCR amplification

of the internal transcribed spacer 2 (ITS2, ~500 bp) of the rRNA gene was performed using the NC1/NC2 primer pair as previously described [20]. Amplicons were purified using silica membrane spin columns (QIAquick PCR Purification Kit, Qiagen, Hilden, Germany) and externally sequenced by Macrogen Europe (Amsterdam). Sequences were compared to those available in the GenBank database by Basic Local Alignment Search Tool (BLAST) analysis. Phylogenetic analyses were conducted using MEGA6 software [21]. The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model [22]. Species identification was based on morphological characteristics, associated with molecular analysis [7, 8].

### Results

#### Morphology and morphometry of *Angiostrongylus daskalovi*

Seven males and 16 females were collected from the pulmonary vessels of the infected badgers (Fig. 2a). Of these, 9 specimens (3 males and 6 females) originated from the first infected badger, two females from the

**Table 1** Morphometric features of *A. daskalovi* and comparative data for other *Angiostrongylus* spp. identified in mustelids

Feature/Species	<i>A. daskalovi</i>	<i>A. daskalovi</i>	<i>Angiostrongylus</i> sp. (badger)	<i>A. vasorum</i>	<i>A. gubernaculatus</i>
Source	Present study	Janchev & Genov [7]	Gerrikagoitia et al. [8]	Costa et al. [23]	Dougherty [13]
Male	(n = 7)				
Body length (mm)	15.8–20.5	13.4–21.3	19.4 ± 7.7	12.4	18.0–19.5
Body width (µm)	253–331	254–306	243 ± 20	243	300
Distance from excretory pore to cephalic end (µm)	227–526	386–463	409 ± 25	373	
Oesophagus length (µm)	312–335	336–366	333 ± 18	220–275	300–355
Spicule length (µm)	shorter 322–352 longer 337–380	336–409	346 ± 24	410–485	510–560
Female	(n = 16)				
Body length (mm)	24.0–34.0	14.4–31.1	25.0 ± 14.0	15.6	22.0–24.0
Body width (µm)	366–852	340–511	345 ± 18	268	350
Distance from excretory pore to cephalic end (µm)	454–618	379–636	447 ± 102	403	
Oesophagus length (µm)	305–456	356–556	368 ± 17	240–280	335–350
Distance from vulva to anus (µm)	203–515		295 ± 46	141	
Distance from vulva to caudal end (µm)	286–612	269–412	366 ± 44	205	205–250
Distance from anus to caudal end (µm)	60–193	76–115	79 ± 3	67	75–90
Vulvar opening (length/width, µm)	38–40/4–5				
Anus (length/width, µm)	8–10/2–3				

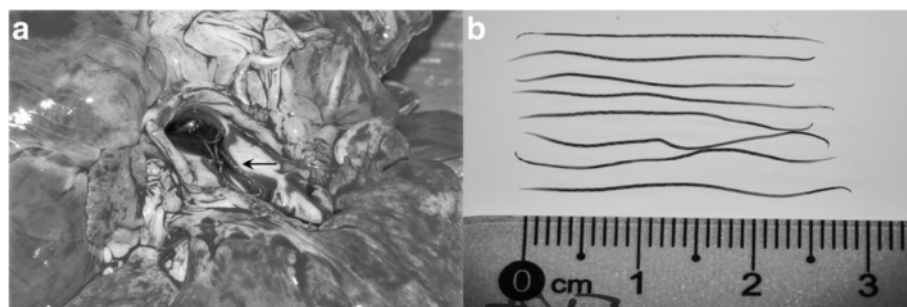
second and 12 (4 males and 8 females) were collected from the third animal. Adult worms exhibited a pronounced sexual dimorphism, females being larger than males, see Table 1 for detailed morphometric data for the adult worms.

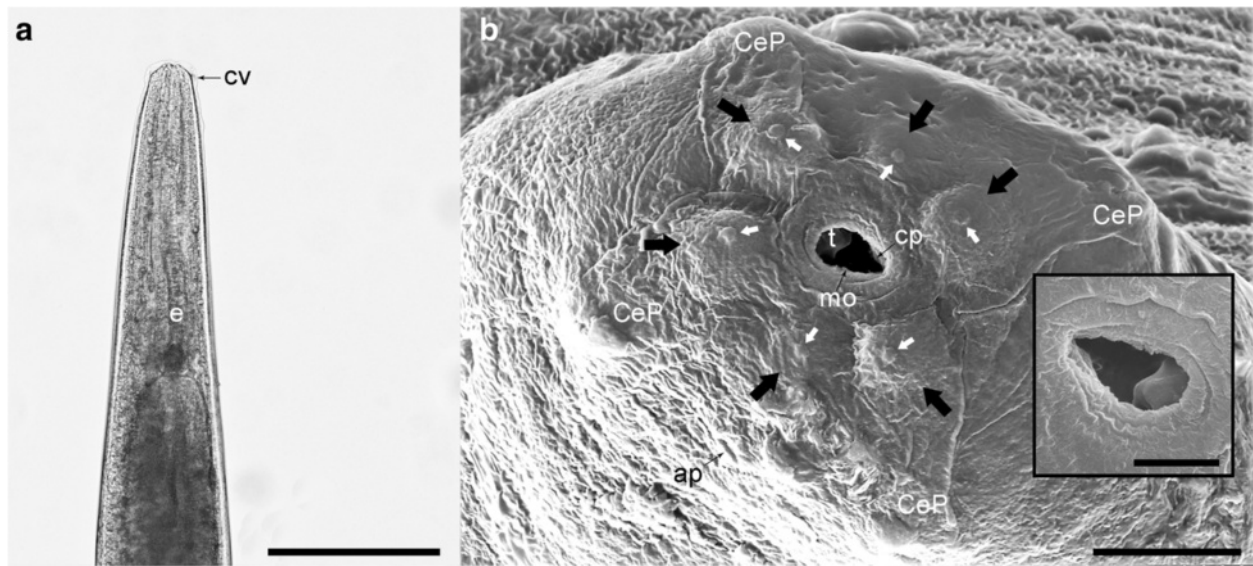
Both sexes have elongated, cylindrical and slender bodies, slightly tapered at both, anterior and posterior ends (Fig. 2b). The cuticle at the anterior extremity is smooth, more or less dilated, appearing as a small cephalic vesicle (Fig. 3a). Mouth opening, in both sexes, is terminally placed, slightly triangular, being surrounded by six labial papillae each of them having a small protuberance at the top. At the level of the amphids, there are four cephalic papillae. A single rudimentary triangular tooth is visible in the buccal cavity and a small cutting

plate in opposite position. Two amphidial pores are present at the anterior extremity (Fig. 3b). The buccal cavity leads into an oesophagus composed of a cylindrical corpus, slightly widened at its posterior part where it forms a bulb (Fig. 3a).

The females have a “barber pole” appearance due to their discolored uterus coiled with the brownish intestinal tract (Fig. 4a), and a slightly curved posterior extremity (Fig. 4b) showing the vulvar and anal openings on the lower curvature (Fig. 4c). The vulvar opening appears as a transverse slit (Fig. 4c). The anus is oval, transversely elongated and smaller than the vulva.

The males had a uniformly coloured body, a small bilobated copulatory bursa, and two unequal spicules. The copulatory bursa had two symmetrical, transparent,

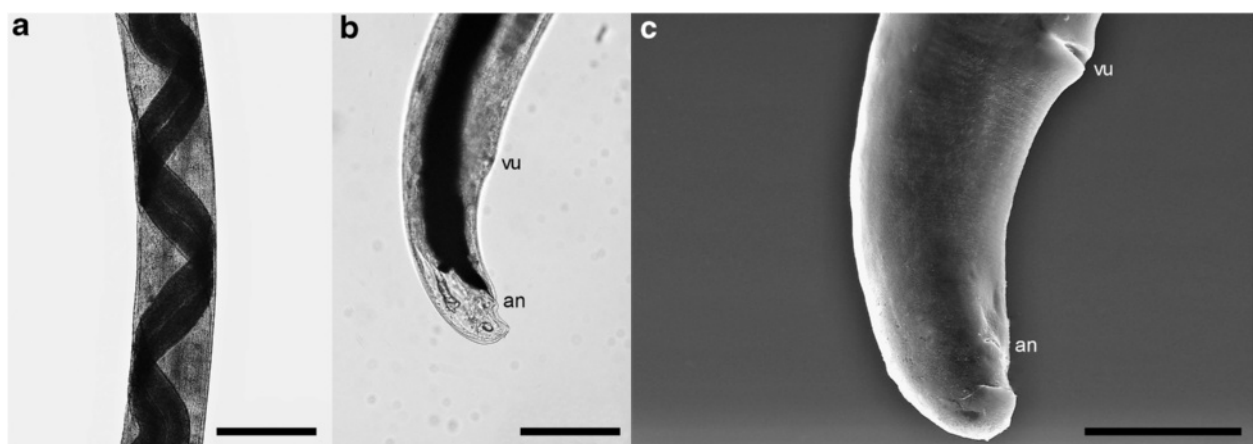
**Fig. 2** a Location of *Angiostrongylus daskalovi* in the pulmonary arteries (arrow). b Size of *A. daskalovi* females



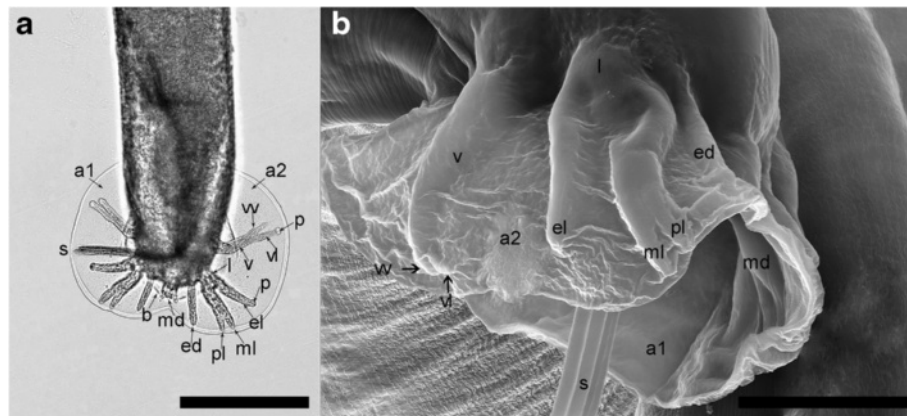
**Fig. 3** Light microscopy (**a**) and SEM photomicrographs (**b**) of the anterior extremity of *A. daskalovi*: The tooth and the cutting plate are clearly visible in the inset. Six labial papillae (black arrows) and six small protuberances (white arrows) are indicated. Abbreviations: ap, amphidial pore; CeP, four cephalic papillae; cp, cutting plate; cv, small cephalic vesicle; e, oesophagus; mo, mouth opening; t, tooth. Scale-bars: a, 500 µm; b, 10 µm; inset 5 µm

ventro-lateral lobes (Fig. 5), the latter supported by rays with a variable layout and different origin: ventral, lateral, externo-dorsal and median lateral. The ventral ray is distally divided into two branches, ventro-ventral and ventro-lateral, the former being slightly shorter than the latter; ventro-lateral branch ends with a protuberance at the top. The lateral ray is split into three branches: externo-lateral, showing a protuberance at the top, medio-lateral and postero-lateral, the last two being thinner and separated towards the terminal end. The externo-dorsal ray is straight, undivided, and

smaller than the previous two. The median dorsal ray is short, thick, strong and rectangular and has two digitations. The spicules are slender, thin, brownish and unequal, with striated alae. They protrude through the cloacal opening, two papillae (papillae 7) being present behind this orifice; several papillary structures, with a presumptive sensorial role, surround the cloacal opening (Fig. 6a). The spicules show transverse striations and the distal ends are corrugated. When the spicules are joined, they form a channel probably used for semen disposal during fertilization (Fig. 6b).



**Fig. 4** Light microscopy (**a**, **b**) and SEM photomicrographs (**c**) of *A. daskalovi* female. **a** "Barber-pole" appearance of the body. **b** Slightly curved posterior extremity. **c** Ventral view of the posterior extremity showing the vulva (vu) and the anus (an). Scale-bars: a, 500 µm; b, 500 µm; c, 100 µm



**Fig. 5** Light microscopy (a) and SEM photomicrographs (b) of copulatory bursa of *A. daskalovi*: left ventro-lateral lobe (a1); right ventro-lateral lobe (a2); dorsal lobe (b); ventral ray (v); ventro-ventral branch of ventral ray (vv); ventro-lateral branch of ventral ray (vl); protuberances (p); lateral ray (l); externo-lateral part of lateral ray (el); medio-lateral branch of lateral ray (ml); postero-lateral branch of lateral ray (pl); externo-dorsal ray (ed); median dorsal ray (md); spicules (s). Scale-bars: a, 200  $\mu$ m; b, 50  $\mu$ m

The measurements of eggs (mean  $101 \times 79 \mu$ m) and larvae (mean  $379 \times 17 \mu$ m) isolated from the lung tissue and faeces are given in Table 2. Stage-two larvae possess the typical metastrongyloid posterior end with a wavy tail, one dorsal spine, and a subterminal notch (Fig. 7a).

Microscopic examination of the Baermann sediment also revealed the presence of some eggs of *A. daskalovi*. These were embryonated, oval, with thin shells (Table 2, Fig. 7b).

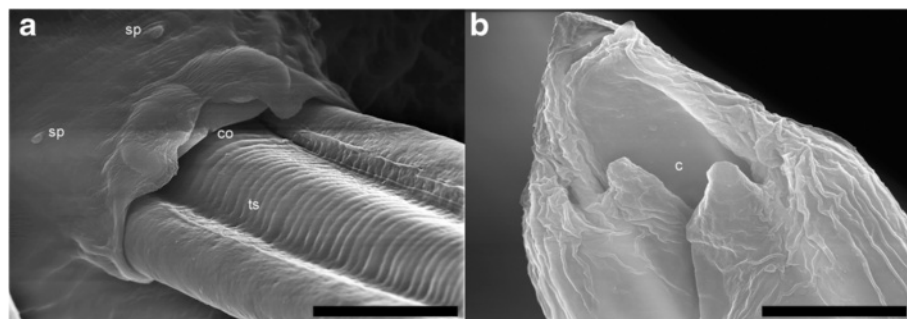
### Pathology

At necropsy, numerous adult worms were present in the pulmonary arteries and the right atrium, without visible gross morphological changes. The lungs showed diffuse congestion and contained several, variably-sized, firm, gray-red and slightly raised nodules that were randomly distributed within all lung lobes. The tracheobronchial lymph nodes were markedly and diffusely enlarged up to 2–3 times the normal size, irregular in shape, and gray

to red on the cross section. The histological findings were consistent with chronic interstitial verminous pneumonia. The fibrous tissue and granulomatous reaction consisting of reactive macrophages, multinucleated giant cells, and fewer neutrophils, eosinophils and plasma cells, occasionally surround the larvae (Fig. 8a).

Larvae were composed of numerous round, basophilic nuclei with scant eosinophilic cytoplasm and a thin amphophilic cuticle (Fig. 8b). Scattered hemorrhagic areas associated with hemosiderin deposits, hemosiderin-laden macrophages (Fig. 8b), and coagulative necrosis were found in the affected parenchyma.

Less affected areas of the lung presented mild congestion, edema, pulmonary atelectasis and alveolar emphysema. The pulmonary arteries exhibited moderate smooth muscle hypertrophy and hyperplasia of the arterial tunica media with mild vacuolar degeneration of the endothelial cells and intimal fibrosis. Multifocal and mild subendocardial fibrosis and minimal mononuclear infiltrates were observed in the right atrium.



**Fig. 6** SEM micrograph of adult male of *A. daskalovi*. a Details of the cloacal opening (co) with two papillae (papillae 7) (p), sensory papillae (sp) and transverse striations (ts) of the spicules. b Detail of the adjoining arrangement of spicules forming a channel (c). Scale-bars: a, 10  $\mu$ m; b, 5  $\mu$ m

**Table 2** Morphometric data for the eggs and first-stage larvae (L1) of *A. daskalovi*

Species	Stage	Range (µm)		Reference
		Length	Width	
<i>A. daskalovi</i>	Eggs (n = 10) <sup>a</sup>	98–105	74–90	Present study
	L1 (n = 150)	336–412	14–20	Present study
<i>A. chabaudi</i>	L1	307–420	15–17	[25]
	L1	362–400	15–18	[31]
<i>A. vasorum</i>	L1	310–399	14–16	[24, 32]

<sup>a</sup>Eggs measured in feces. No comparative data for eggs are provided, as the existing data in the literature for *A. chabaudi* and *A. vasorum* refer to measurements of eggs *in utero*

The tracheobronchial lymph nodes showed diffuse reactive hyperplasia, multifocal granulomatous reaction centered on parasitic organisms and numerous aggregates of hemosiderin-laden macrophages (Fig. 8c, d). There were no microscopic lesions in the area of pulmonary arteries where adult parasites were located.

### Molecular analysis

All sequences ( $n = 6$ ) obtained from adults and larvae (GenBank accession number KX242346) were identical and showed a 100 % homology to an *Angiostrongylus* sp. recovered from a badger from Spain (accession number GU323341). Phylogenetic analysis clustered *A. daskalovi* within the clade including all other European species *Angiostrongylus* with sequences available in the GenBank database (Fig. 9).

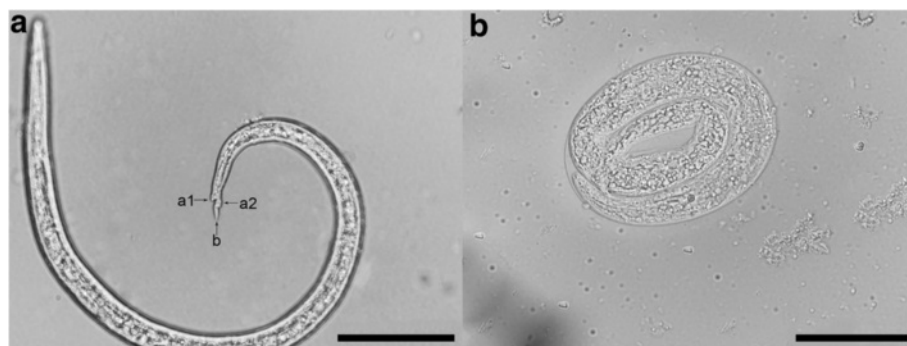
### Discussion

This report represents the first comprehensive study of *A. daskalovi* infection in European badgers. The study identified this species based on morphological, morphometric and molecular analyses. Three species of *Angiostrongylus* are described in different badger species across the world, namely *A. vasorum*, *A. daskalovi* and *A. gubernaculatus*. Morphometrically, *A. vasorum* is the

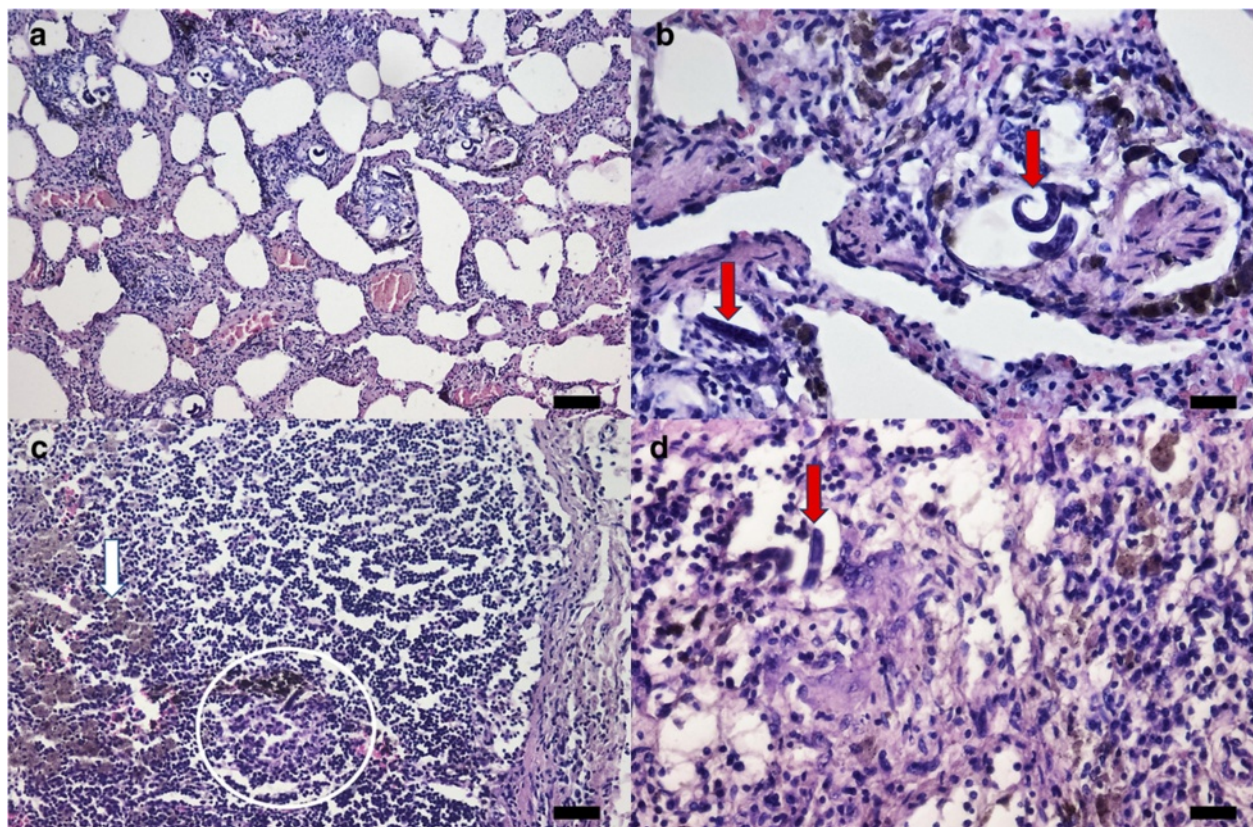
smallest species, the length of females ranging between 14.17–17.69 mm and that of males between 11.21–13.91 mm [23]. These values overlap the lower limits of the ranges for length of *A. daskalovi*: 14.39–31.12 mm in females and 13.36–21.31 mm in males [7]. Our data correspond to specific dimensions of *A. daskalovi*, and may differentiate these two species even if the recorded variations could be related to the intervals after infection [24]. The third species, *A. gubernaculatus* is morphometrically very similar to *A. daskalovi*, but host specificity and geographical range differ amongst the two species. Additionally, another congeneric species, *A. chabaudi* was recently found and redescribed in wildcats in the same geographical area from Romania, providing a detailed comparison of the morphometric features [25].

Scanning electron microscopy revealed similar structures of the anterior and posterior ends as described in adult *A. vasorum* [23], but also identified particular structures. At the anterior extremity, the mouth opening is surrounded by six papillae and two amphidal pores, but the small tooth observed in the mouth cavity of *A. daskalovi* is not known in *A. vasorum*. Comparison of the copulatory bursa of *A. vasorum* with that of *A. daskalovi* reveals only a slight difference in the median dorsal ray whose digitations are sometimes separated by a papilla, but none of the males of *A. daskalovi* exhibited this structure.

Despite the morphometric differences, these three species may have a common origin. *Angiostrongylus gubernaculatus* which resembles *Angiostrongylus* sp., currently accepted as a synonym [26], may represent a common ancestor for the Brazilian and European populations of *A. vasorum*. Some authors consider that *A. vasorum* is the ancestral species that subsequently spread globally with its carnivore hosts, and evolved into genetically distinct populations in various host species [27]. The phylogenetic analysis performed herein is also supportive of this hypothesis, as *A. daskalovi* clustered with *A. vasorum*.



**Fig. 7** Light microscopy photomicrographs of *A. daskalovi*. L1 larva. **a** Posterior extremity of L1 larva: dorsal spine (a1); subterminal notch (a2); wavy tail (b). **b** Egg. Scale-bars: a, 50 µm; b, 50 µm



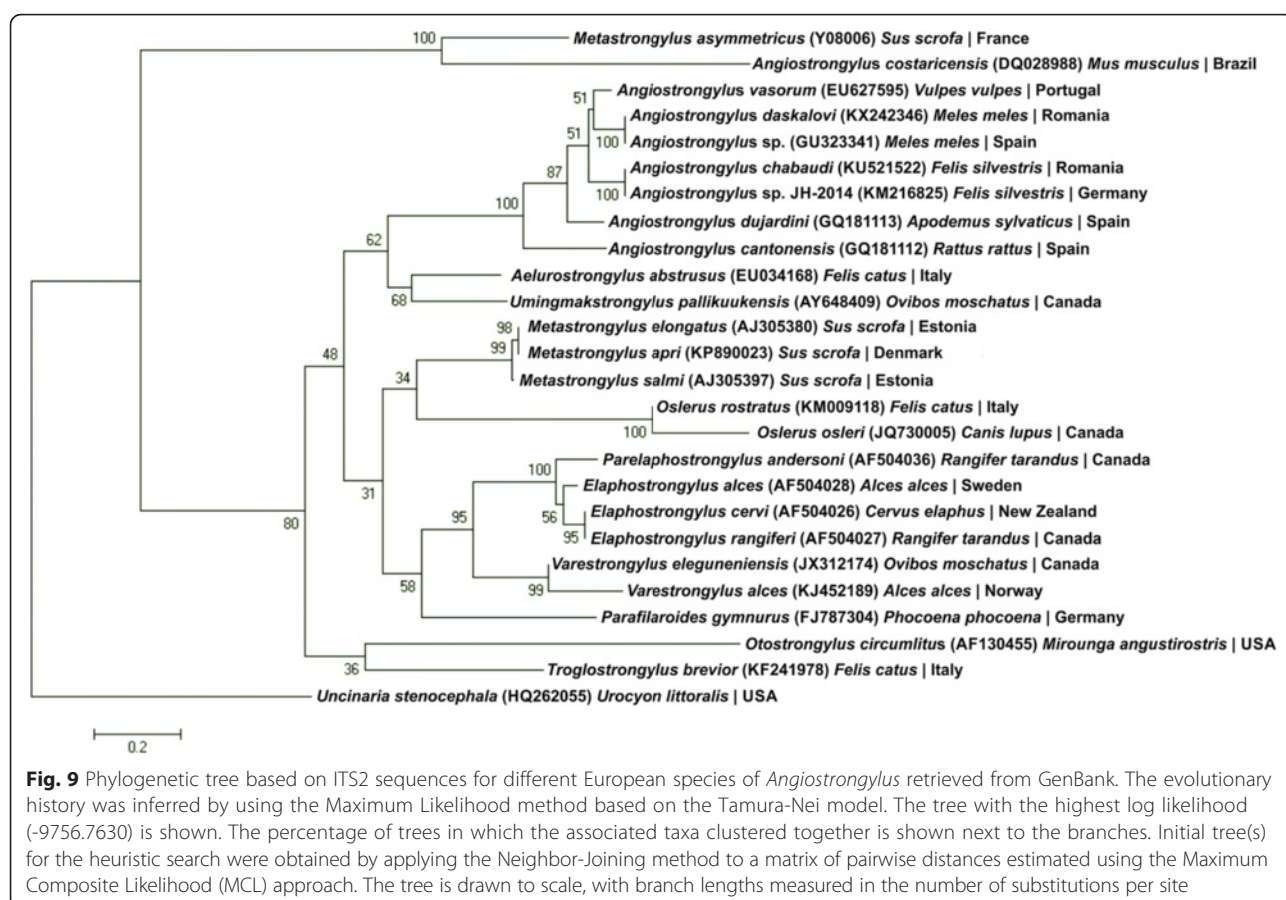
**Fig. 8** Histological sections (haematoxylin-eosin staining) of the lung and tracheobronchial lymph nodes of badgers infected with *A. daskalovi*. **a** Diffuse hyperemia, fibrosis and granulomatous reaction of the pulmonary interstitium. **b** Coiled larvae in the bronchial tree and interstitium (red arrows). **c** Hemosiderin deposits (white arrow) and granulomatous reaction surrounding fragments of parasites (white circle) in the tracheobronchial lymph node. **d** Detail of granulomatous reaction centered on larvae (red arrow) in the tracheobronchial lymph node. Scale-bars: a, 100 µm; b, 20 µm; c, 50 µm; d, 20 µm

To our knowledge, this is the first description of the first-stage larva (L1) of *A. daskalovi*. The differentiation of first-stage larvae of different *Angiostrongylus* species is difficult due to several common characters such as the transparent body, sigmoid tail, the presence of a dorsal spine and a visible notch. Their lengths partly overlap from one species to another: 310–400 µm for *A. vasorum* and 336–412 µm for *A. daskalovi* in the present study (L1s of *A. gubernaculatus* are not described). This does not allow a clear differentiation based on morphological and morphometric criteria. However, the adults and larvae of *A. daskalovi* identified in this study were 100 % similar to adults of *Angiostrongylus* sp. recovered from a badger in Spain and tentatively identified, based on morphology and morphometry, as *A. daskalovi* [8].

The presence of molting larvae in tracheobronchial lymph nodes and eggs in the lung parenchyma provides evidence that the life-cycle of *A. daskalovi* is probably similar to that of *A. vasorum*, following the type II of the known development in the definitive hosts [28]. During their migration, larvae may exert a significant pathogenic

action. Hypertrophy and hyperplasia of the arterial tunica media are explainable by pulmonary hypertension due to the presence of nematodes in the lung arteries, being similar to those lesions recorded in dogs naturally infected with *A. vasorum* [29]. The presence of hemosiderin deposits and hemosiderin-laden macrophages, edema, pulmonary atelectasis, alveolar emphysema, diffuse congestion of the lungs and the presence of the nodules randomly distributed within all lung lobes are similar to those produced by *A. vasorum* in dogs [30]. All these pathological alterations of the lungs and the pulmonary arteries confirm that *A. daskalovi* might play an important pathogenic role in infected badgers.

Although the species of *Angiostrongylus* infecting carnivores seem to show a relatively well-defined host specificity, some studies report certain overlaps. As badgers can occasionally be infected with *A. vasorum*, dogs might also be infected occasionally with *A. daskalovi*. Our new molecular data and larval morphology can partly solve possible misdiagnosis problems in European carnivores. Still to be solved is the life-cycle of *A. daskalovi*.



## Conclusions

The current study confirms the existence of *A. daskalovi* patent infection in badgers from Romania and provides the first description of the larvae, its pathological effect, and its phylogenetic relationships with other congeneric species.

## Abbreviations

BLAST, Basic local alignment search tool analysis; DNA, deoxyribonucleic acid; H&E, Hematoxylin and eosin; L1, First larval stage; PCR, polymerase chain reaction; SEM, Scanning electron microscopy

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## Availability of data and materials

The data supporting the conclusions of this article are included within the article.

## Authors' contributions

CMG, ADM and VC conceived and designed the study. GD and GD'A performed the necropsy. IAM and AMI performed molecular analysis of the parasites. MT conducted the histopathological study. LBT conducted the SEM analysis. AS collected the carcasses of the badgers. CMG wrote the paper. All authors contributed to improve the manuscript and read and approved the final version.

## Competing interests

The authors declare that they have no competing interests.

## Consent for publication

Not applicable.

## Ethics approval and consent to participate

Not applicable.

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# CO<sub>2</sub> flagging - an improved method for the collection of questing ticks

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## Abstract

**Background:** Most epidemiological studies on tick-borne pathogens involve collection of ticks from the environment. An efficient collection method is essential for large sample pools. Our main aim was to evaluate the efficacy of a new method, where traditional flagging was enhanced by the use of CO<sub>2</sub> dispersed into the white flannel. The CO<sub>2</sub> was spread through a rubber hose network inserted into the flag blanket. The research was conducted in spring, in March-April 2011 in two locations from Cluj County, Romania.

**Methods:** The research was conducted in March-April 2011 in two locations from Cluj County, Romania. The flag to be tested contained a fine silicone rubber hose network which dispersed the CO<sub>2</sub> in the shaft. On each collection site n=30 samplings were performed. Each sampling consisted in the simultaneous use of both flags (with and without CO<sub>2</sub>) by two persons. The CO<sub>2</sub> concentration level on the flag canvas surface was measured. The efficacy of the method was determined by counting comparatively the total number of ticks and separate developmental stage count.

**Results:** Using the CO<sub>2</sub> improved flag, 2411 (59%) *Ixodes ricinus* and 100 (53.8%) *Dermacentor marginatus* ticks were captured, while the CO<sub>2</sub>-free flag accounted for the collection of 1670 *I. ricinus* (41%) and 86 (46.2%) *D. marginatus* ticks. The addition of CO<sub>2</sub> prompted a concentration difference on the surface of the flag ranging between 756.5 and 1135.0 ppm with a mean value of 848.9 ppm.

**Conclusion:** The study showed that the CO<sub>2</sub> enhanced sweep flag increased the ability of *I. ricinus* ( $p < 0001$ ) but not of *D. marginatus* to be attracted to the flag blanket.

**Keywords:** Flagging, Carbon dioxide, Questing ticks, *Ixodes ricinus*

## Background

Ticks (suborder Ixodida) are obligate blood-sucking acarines attacking a wide variety of hosts from all tetrapod vertebrate classes [1,2]. Around 700 species of hard ticks are currently recognized as valid species [1]. Most of these species are three-host ticks (i.e. each stage detaches after engorgement) [3,4]. Regardless of the number of hosts, each tick must find a suitable host. In three-host ticks, most of their multiannual life is not spent attached to the host but as free-living organisms. Thus, newly hatched larvae, unfed nymphs and unfed

adults are in a permanent host finding state. Host detection and attachment in Ixodidae is achieved through three main alternative behavioral patterns: questing, hunting and tick-host cohabitation (nidicolous ticks) [4].

Most epidemiological studies on tick-borne pathogens involve collection of ticks from the environment [5]. Thus, an efficient collection method is essential for large datasets. Tick collection methods had been reviewed by Gray [6]. He divided these methods into four major categories: (1) flagging or dragging methods; (2) trapping using carbon dioxide baits; (3) collecting from hosts and (4) walking (i.e. on the clothes of the collectors). Despite all these methods are relative and do not estimate density (number per unit area) or absolute size (total number as measured in mark-release-recapture methods) [7], each of these has a variable efficacy depending on several

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factors (i.e. habitat type, tick species, developmental stage etc.). Nevertheless, all methods have been improved over the time in order to increase their efficacy [8].

One of the most important ticks species (regarding its range, abundance, and vectorial importance) in the Palearctic region, with tendency to expand its spread in Northern Europe [9,10], is *Ixodes ricinus* [11]. The host seeking strategy of all developmental stages in *I. ricinus* is questing, when ticks are typically positioned on the vegetation with their legs extended, waiting for a moving host to which they attach [12]. Though, questing is a complex behavioral process, which involves responses to stimuli like host movement, concentration of environmental carbon dioxide and increase of temperature [4]. The most commonly used method for collection of questing ticks is flagging. However, flagging stimulates only the tick sensor for movement, and leaves the other two sensorial components of questing (i.e. carbon dioxide and temperature) unexploited.

The vast majority of ecological and epidemiological studies of tick-borne pathogens involve collection of unfed ticks from the environment. In this view, our main aim was to evaluate the efficacy of a new method, where traditional flagging was enhanced by the use of dispersed CO<sub>2</sub> into the white flannel.

## Methods

### Sweep and flag design

The sweep consists of a shaft and a flag. The shaft is constructed from a hollow aluminum tube, and the flag from white technical flannel. A JBL 500 g CO<sub>2</sub> bottle with a CO<sub>2</sub> solenoid regulator attached (both aquarium use, JBL Aquarium<sup>®</sup>, Germany) were fixed with plastic lock seals on the shaft. A silicone rubber hose was attached to the CO<sub>2</sub> solenoid regulator; the hose was introduced through the aluminum shaft and connected to the flag. The rubber hose was pierced (to release CO<sub>2</sub>) and attached to the flag by sewing forming a network structure (Figure 1). The hose was made of bending-resistant silicone rubber with the inner diameter of 1 mm and the outer diameter of 2 mm with a wall thickness of 0.5 mm.

The flag surface area was 0.48 m<sup>2</sup> (80 x 60 cm) to allow unrestricted passage across all types of vegetation. Two identical flags were made; one of them with CO<sub>2</sub> and the other without CO<sub>2</sub> (control).

### Study area

Two hilly areas were chosen: Vultureni and Faget, both in Cluj county (Figure 2), according to preliminary results of sampling for the evaluation of the presence of tick-borne pathogens in Romania (manuscript under preparation). The habitats consisted in herbaceous

vegetation alternating with small shrubs, located at the edge of woods, specific areas for ticks. The climate is moderate continental, influenced by the vicinity of the Apuseni Mountains and Atlantic influences from west of the country, in autumn and winter [13]. The study was conducted in spring, between the end of March and the end of April 2011, as tick abundance is higher in North-western Romania in this season [14]. The GPS was used to measure the distance.

### Sampling procedure

On each collection site n = 30 samplings were performed (total 60 samplings in the two sites). Each sampling consisted in the simultaneous use of both flags, (with and without CO<sub>2</sub>), on 2 m wide adjacent areas, by two persons who had interchanged the sweep every fifty meters for the homogeneity of results. After each 5 m the flags were checked for ticks. All ticks were collected regardless their species and fixed in pure ethanol. Specific identification was performed using morphological keys [15] under a binocular microscope.

### Determination of carbon dioxide

The CO<sub>2</sub> concentration level on the flag canvas surface was measured using a portable CIRAS-2 Photosynthesis System equipped with a SRC-1 Soil Respiration Chamber (PP Systems International Inc<sup>®</sup>, USA). CO<sub>2</sub> level was determined at a single time, but from several points of the flag (n = 20) according to instruction manual and recommendations [16]. The results were expressed in ppm as compared to the standard CO<sub>2</sub> concentration of 393.71 ppm (reference data for 24.04.2011) [16].

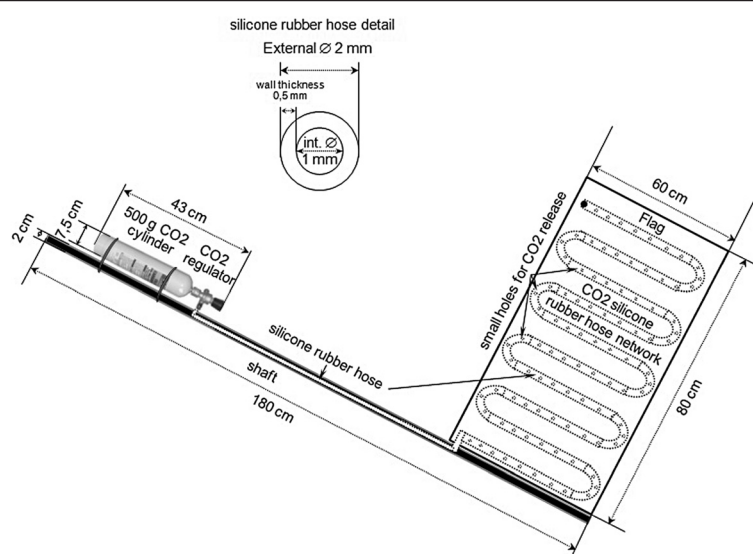
### Statistical analysis

The efficacy of the method was determined by counting the total number of ticks and separate developmental stage count, attached to the CO<sub>2</sub> flag compared with the control (CO<sub>2</sub>-free flag). For statistical analysis, the values were compared in CHI-SQUARE TEST [17]. A p value of <0.05 was considered statistically significant. The relative risk (RR) is a ratio of the probability of the event occurring in the exposed group versus a non-exposed group [18].

## Results

A total number of 4267 of ticks belonging to two species were collected in the 60 samplings: *I. ricinus* (n = 4081) and *Dermacentor marginatus* (n = 186).

*I. ricinus* accounted for 4081 tick captures (adults, nymphs and larvae) were collected in the 60 samplings (Table 1). Of these, 2617 (64.1%) were adults, 1422 (34.9%) nymphs and 42 (1%) larvae. Using CO<sub>2</sub> improved flag were captured 2411 (59%) ticks and 1670 (41%) without CO<sub>2</sub>.



**Figure 1** Sweep CO<sub>2</sub> flag diagram.

The statistical analysis revealed highly statistically significant ( $p < 0001$ ) difference between the two variables in adults and nymphs, in both locations and overall; for larvae, the recorded statistical differences were not significant (Table 2). Carbon dioxide flagging was more effective than CO<sub>2</sub>-free flagging, with average values of RR ranging between 1.4 and 1.6 for adults and nymphs.

The addition of CO<sub>2</sub> prompted a difference on the surface of the flag ranging between 756.5 and 1135.0 ppm with a mean value of 848.9 ppm.

## Discussion

Flagging is the most widespread tick collection method. Over time, several improvements to this method were



**Figure 2** Field studies location (shaded area shows the flagging surface).

**Table 1 Number of questing *Ixodes ricinus* ticks collected by flagging with and without CO<sub>2</sub>**

Location/stage/method		Faget		Vultureni		Total (both locations)	
		IR	DM	IR	DM	IR	DM
<b>Males</b>	CO <sub>2</sub> +	456	27	211	22	667	49
	CO <sub>2</sub> -	325	21	160	20	485	41
<b>Females</b>	CO <sub>2</sub> +	587	26	281	25	868	51
	CO <sub>2</sub> -	407	23	190	22	597	45
<b>Nymphs</b>	CO <sub>2</sub> +	547	0	304	0	851	0
	CO <sub>2</sub> -	353	0	218	0	571	0
<b>Larvae</b>	CO <sub>2</sub> +	22	0	3	0	25	0
	CO <sub>2</sub> -	16	0	1	0	17	0
<b>TOTAL</b>	CO <sub>2</sub> +	1612	53	799	47	2411	100
	CO <sub>2</sub> -	1101	44	569	42	1670	86
Per location		2713	97	1368	89	4081	186

proposed [8] and now there is many types used: double walking flagging and double walking with baited flagging [19], walking flagging with a loose-fitting and white cotton flannel garment worn [20] and strip-flag method [21].

The successful hosts attack in *Ixodes* species expressed as the ability to adhere to a flannel flag is influenced by many factors: light and/or shadow, radiation heat (temperature), mechanical vibration of questing substrate, host odor, and CO<sub>2</sub> concentration [22].

Chemical mediators also known as semiochemicals are as well important for behavioral patterns in ticks. These information-bearing compounds are secreted by animals into the external environment, and when recognized they trigger a specific behavioral response such as food location, sexual partner location or escape [23]. Semiochemicals are categorized into four major categories: (1) pheromones; (2) allomones; (3) kairomones; and (4) synomones [24].

Carbon dioxide acts like an attractant kairomone for ticks [25]. Experimentally, it acted as an attracting agent causing almost immediate activation in the soft ticks *Ornithodoros coriaceus* quiescent ticks [25]. Adults of *Dermacentor andersoni* respond also very well to stimulation with carbon dioxide. Garcia, 1965, described a system based on release of CO<sub>2</sub> for the collection of *D. andersoni*. The system involved a piece of dry ice placed on a wire mesh platform in the desired area. The results indicate that the CO<sub>2</sub> method is more sensitive for detection of adult ticks than is the conventional flagging technique [26]. Carbon dioxide (dry ice) trapping method was demonstrated to be effective in the collection of some tick species: *I. ricinus* [5], *Amblyomma americanum* [27-29] and *A. hebraeum* [30]. Our method is important in Europe as it enhances the capture of *I. ricinus*, the main vector of *Borrelia burgdorferi* s.l. and the tick-borne encephalitis (TBE) virus [31].

Our results are consistent with those cited above. The number of adults and nymphs of *I. ricinus* collected was significantly increased using CO<sub>2</sub> enhanced blanket comparing with flagging without CO<sub>2</sub>. The lower number of larvae collected can be explained by the months of sampling, March-April, when larvae may be not fully active and by the quality of blanket, made by technical flannel, material which may not have reached the lower levels of the vegetation where larvae sit to quest.

These data show that the responsiveness to CO<sub>2</sub> is enhanced during host-seeking periods of the life cycle and reduced at other times [32]. However, others [29] did not establish significant differences between flagging method with a strip blanket and CO<sub>2</sub> traps or rabbits scent baits. The response time of ticks to host attachment was shown to be dependent on the tick species and CO<sub>2</sub> concentration in the environment [33]. In *Amblyomma maculatum*, *A. americanum* and *Dermacentor variabilis*,

**Table 2 Statistical significance of tick collection efficacy using flagging with and without CO<sub>2</sub>**

Location		Faget		Vultureni		Total	
Statistical parameter		<i>I. ricinus</i>	<i>D. marginatus</i>	<i>I. ricinus</i>	<i>D. marginatus</i>	<i>I. ricinus</i>	<i>D. marginatus</i>
		P	P	P	P	P	P
		RR	RR	RR	RR	RR	RR
<b>Males</b>	CO <sub>2</sub> +	0.0001	0.31	0.0002	0.83	0.0001	0.30
	CO <sub>2</sub> -	1.40 (1.27-1.56)	1.29 (0.86-1.91)	1.32 (1.14-1.53)	1.1 (0.72-1.69)	1.38 (1.27-1.50)	1.20 (0.89-1.61)
<b>Females</b>	CO <sub>2</sub> +	0.0001	0.69	0.0001	0.68	0.0001	0.47
	CO <sub>2</sub> -	1.44 (1.32-1.58)	1.13(0.76-1.68)	1.48(1.30-1.67)	1.14(0.76-1.71)	1.45(1.35-1.57)	1.13(0.85-1.51)
<b>Nymphs</b>	CO <sub>2</sub> +	0.0001		0.0001		0.0001	
	CO <sub>2</sub> -	1.6 (1.4-1.7)		1.4 (1.2-1.6)		1.5 (1.4-1.6)	
<b>Larvae</b>	CO <sub>2</sub> +	0.25		0.48		0.13	
	CO <sub>2</sub> -	1.4 (0.9-2.2)		3 (0.5-18)		1.5 (0.9-2.3)	

the groups preconditioned with low ambient CO<sub>2</sub> (422 ppm) always produced response times of longer duration than ticks preconditioned to high ambient CO<sub>2</sub> (956 ppm) [34].

The lack of statistical significance for *D. marginatus* between the two collecting methods compared in the present study might be caused by the major differences in the sample size. The small total number of *D. marginatus* collected (regardless the method used) can be explained by the typical area of this species which prefers biotopes characterized by xerophilic plant communities: dry pasture shrub communities, grazing black locust forests (*Robinietum*), forest-steppe or grikes (*Quercetum pubescentis* and *Cometo-Quercetum*), margins of oak forests and bushy ridges between the fields and field paths [35]. Our study area is characterized by deforested hills and covered with low vegetation; predominant species in forest areas are hornbeam, birch, poplar, hazel, elm, ash and maple. Although *D. marginatus* is almost as widespread in Romania as *I. ricinus*, [36], the population density is significantly lower in most of the sampled localities [37]. Regarding seasonality, in Eastern Europe, *D. marginatus* is most numerous in February and March [38] and most of our sampling was done in April.

Flagging technique seems to work better for other species: *Ixodes dammini* [27], *I. pacificus*, *D. occidentalis* and *D. variabilis* [32], *I. rubicundus* [39] or *I. ricinus* [40]. Four different methods of surveying were tested for *D. variabilis* and *I. banksi* and it was shown that the most successful was flagging, compared with carbon dioxide trapping, nest boxes and collection from hosts [41].

Concerning the temperature, *I. persulcatus* is a more cold-resistant tick than *I. ricinus* and it is more successful both in adhering to the flag and in remaining attached to it at two ranges: 6–10°C and 17–22°C [42]. In general a greater percentage of *I. rubicundus* displayed an appetite response at lower (12, 17 and 21°C) than at high (30°C) temperatures [39]. It is known that all life stages of *I. ricinus* are equipped to sense shifts in light intensity. This allows *I. ricinus* to use onset of darkness to trigger mobility when desiccation risk is reduced in nature [43]. The nymphs are stimulated to walk horizontally by humidity and host scent. When the atmosphere is sufficiently wet they are likely to walk towards odor secreted by host skin [44,45]. The larvae of *I. hirsti* seem to be more sensitive to shade and heat, while they were unresponsive to CO<sub>2</sub> concentration and host odor [46]. Radiation heat and shadowing caused the greatest percentage of *I. rubicundus* to display an appetite response; shadowing and radiation heat had the least effect on *R. punctatus* [22]. A single mechanical perturbation of the substratum caused a mean of 50% of *I. rubicundus*

to display an appetite response. Constant mechanical perturbation resulted in a progressive decrease in the proportion of ticks reacting [22]. Host scent is known to initiate questing behavior in *I. persulcatus*, *I. ricinus* and *I. crenulatus*. Both *I. ricinus* and *I. crenulatus* respond strongly to sheep wool [47,48].

Entire-blanket flagging is a better sampling method for *I. ricinus* comparing with others variants of flagging or dragging. Significantly more nymphs and adults were caught by the entire-blanket versus strip-blanket flagging [49]. Flagging was 1.5–1.7 times as effective as dragging; impregnation of the cloths with different substances, like host odor, increased the efficacy by 2.4 (dragging) to 2.8 (flagging) times [39]. From several types of material used (i.e. cotton, woolen flannel, “molleton” - soft thick cotton, and toweling - spongecloth), the last was the best cloth type to optimize the number of ticks collected [36]. However, dry-ice-baited tick-traps is more effective for ticks with increased mobility, like *A. americanum* [27].

Our enhanced technique that combines, for the first time, classical flagging and carbon dioxide trapping methods improved significantly the ability of *I. ricinus* to adhere to flag blanket. By introducing CO<sub>2</sub> in the white blanket we tried to simulate the time approach of a host to the tick. Sudden increase of the CO<sub>2</sub> concentration in the air stimulates its vivacity and questing position, increasing the chance of attachment of ticks to the flag.

## Conclusion

The study showed that the CO<sub>2</sub> enhanced sweep flag increased the ability of *I. ricinus* ( $p < 0001$ ) but not of *D. marginatus* to be attracted to the flag blanket.

## Competing interests

The authors declare that they have no competing interests.

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## Authors' contributions

GCM wrote the manuscript, performed flagging. MAD concept idea, performed the flagging. DMO identified the ticks. GA statistical analysis. OI measurement of CO<sub>2</sub>. SM measurement of CO<sub>2</sub>. CV team coordinator. All authors read and approved the final manuscript.

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**CASE REPORT**

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# First report of *Borrelia burgdorferi* sensu lato in two threatened carnivores: the Marbled polecat, *Vormela peregusna* and the European mink, *Mustela lutreola* (Mammalia: Mustelidae)

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## Abstract

**Background:** Lyme disease is a widespread cosmopolitan zoonosis caused by species belonging to the genus *Borrelia*. It is transmitted from animal reservoir hosts to humans through hard - ticks of genus *Ixodes* which are vectors of the disease.

**Case presentation:** *Borrelia burgdorferi* sensu lato infection was identified in a marbled polecat, *Vormela peregusna*, and two European minks, *Mustela lutreola*, from Romania, by PCR. RFLP revealed the presence of a single genospecies, *Borrelia burgdorferi* sensu stricto.

**Conclusions:** This is the first report of the Lyme disease spirochetes in the two mentioned hosts.

**Keywords:** *Borrelia burgdorferi* s.s, First report, *Mustela lutreola*, *Vormela peregusna*, Romania

## Background

*Borrelia burgdorferi* sensu lato is the causative agent of Lyme borreliosis, the most widespread vector-borne disease in the cool-temperate regions of the Northern hemisphere. The medical importance of this pathogen is generally restricted to humans and few domestic species. However, as for many vector-borne diseases, the key to the understanding of the epidemiology of Lyme borreliosis consists in revealing the ecological relationships that exist between pathogens, vectors and wildlife hosts [1]. All 18 currently recognized genotypes [2] circulate in nature between vectors (several ticks of genus *Ixodes*) and reservoir hosts (various vertebrates) which are able to maintain and transmit the spirochetes [3].

## Case presentation

Between 2009 and 2011, 5 specimens belonging to two species of threatened mustelids were brought to the Laboratory of Parasitology and Parasitic Diseases in deep frozen state (Table 1). The dead animals were collected either as road kills (*Vormela peregusna*) or as accidental casualties of live-trapping during field studies (*Mustela lutreola*). The trapping was performed as part of biodiversity and ecology studies in the central part of the Danube Delta using box traps [4]. The accidental death of animals in live traps was caused by extreme morning frost or poor overall health status caused by floods (Kiss JB personal communication). Examination of the fur and skin did not reveal the presence of external parasites.

During the necropsy of these animals, tissue samples (myocardium) were collected and processed for DNA extraction (Qiagen, DNeasy Blood & Tissue Kit). An extraction blank was included in each extraction procedures to control the cross-contamination between extracts. The crude DNA was analyzed by a PCR protocol according to Priem et al. (1997) [5] using primers (Generi Biotech) for *Borrelia burgdorferi* sensu lato (5'-GGGAATAGGTCTAATTTAGCC-3', 5'-CACTAA

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**Table 1 The collection localities of threatened Mustelidae specimens used in this study**

Sample	Species	Locality (County*)	Coordinates	Date
ML1	European mink ( <i>Mustela lutreola</i> )	Canal Litcov (TL)	45°08'N 29°19'E	05.03.2010
ML2	European mink ( <i>Mustela lutreola</i> )	Canal Litcov (TL)	45°08'N 29°18'E	06.03.2010
ML3	European mink ( <i>Mustela lutreola</i> )	Canal Litcov (TL)	45°08'N 29°18'E	06.03.2010
VP1	Marbled polecat ( <i>Vormela peregusna</i> )	Sinoe (CT)	44°37'N 28°43'E	30.11.2009
VP2	Marbled polecat ( <i>Vormela peregusna</i> )	Agighiol (TL)	45°02'N 28°53'E	10.06.2011

\* CT: Constanța; TL: Tulcea.

TTGTTAAAGTGGAAAGT-3') targeting the OspA gene [6]. Each time the PCR was performed including negative control samples. The positive PCR products were further analyzed by RFLP using two restriction enzymes *AlwI* (BsPI) and *MseI* (TruI I) (Fermentas), according to the manufacturers protocol. PCR analysis revealed positivity to *Borrelia burgdorferi* sensu lato in three samples (ML2, ML3 and VP1) belonging to the two host species: *M. lutreola* and *V. peregusna*.

Analysis of the RFLP pattern of the amplified OspA gene cut, showed bands at 183/134/74 base pairs (bp) for *MseI* (TruI I) (Figure 1A) restriction enzyme and a second pattern at 227/164 bp for *AlwI* (BsPI), which is indicative of *Borrelia burgdorferi* sensu stricto (s.s.) in all three positive samples (Figure 1B).

## Discussion

*Borrelia burgdorferi* is maintained in natural cycles of infection by vector ticks and reservoir hosts. In Western and Central Europe, *Ixodes ricinus* is particularly important in the transmission of the Lyme spirochete. Moreover, *I. hexagonus* has been experimentally confirmed as a vector [7], but was also shown to be important in secondary cycles of *B. burgdorferi* transmission [1,8]. Both of them, together with other congeneric ticks, are well represented in mustelids (Table 2). Although ticks are commonly found on mustelids, *B.*

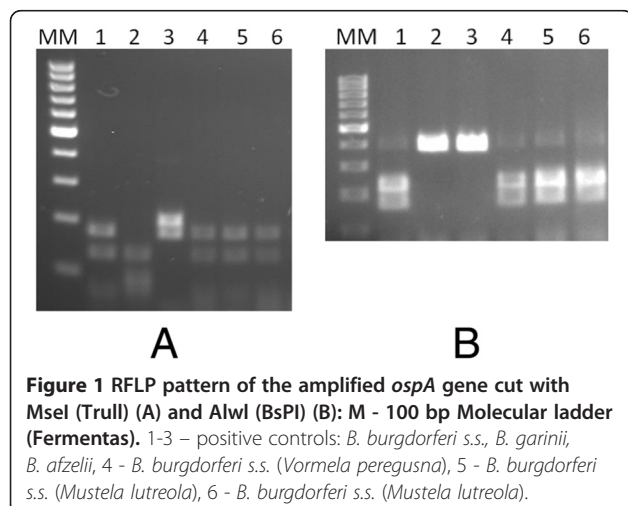
*burgdorferi* s.l. infection is rarely reported. The scarcity of reports can be explained either by the fact that the infection is rare or, most probably by the lack of studies on this topic.

Several authors have previously reported the presence of *Borrelia burgdorferi* s.l. in *Ixodes* ticks removed from mustelids: European badger (*Meles meles*) [9], American mink (*Mustela vison*) [10], weasel (*Mustela nivalis*) [11], beach marten (*Martes foina*), European polecat (*Mustela putorius*), and stoat (*Mustela erminea*) [12]. In Italy, none of the *I. hexagonus* and *I. ricinus* collected from beech marten was positive by PCR for *B. burgdorferi* s.l. [13].

An interesting study from Switzerland, where questing ticks were analyzed for the host of the previous feeding stage by Reverse Line Blotting revealed the presence of *Borrelia burgdorferi* s.l. DNA in specimens positive for *Meles meles* and *Mustela putorius* probes. The authors suggest the role of mustelids as reservoir hosts for *Borrelia burgdorferi* [14].

Other authors examined mustelids for the presence of anti-*Borrelia burgdorferi* s.l. antibodies. One least weasel caught in forests of the western part of France was seropositive for *B. burgdorferi* at 1/50 antibody titer [15], however stoats from Canada infested with *I. Scapularis* (the most important vector of Lyme disease in North America) were seronegative [16].

To our knowledge, there is a single study showing the presence of *B. burgdorferi* s.l. DNA in tissues of mustelids. McDonald and Lariviere (2001) [17] found the infection in 10 of 45 stoats from Great Britain. However, no information was provided on the tissues examined or the genospecies identified. Here we report the first identification of *B. burgdorferi* s.l. from the myocardium of a marbled polecat and two European minks. The Marbled polecat, *Vormela peregusna* is widespread from South-eastern Europe to Russia, China and northern Africa [18]. It is listed by IUCN as vulnerable. The European mink, *Mustela lutreola* is a semi-aquatic species of mustelid native to Europe and it is listed by IUCN as Critically Endangered. Its current distribution includes small isolated populations in northern Spain, western France and Eastern Europe (Latvia, Estonia, Belarus, Ukraine, central regions of European Russia, the Danube Delta in Romania and northwestern Bulgaria) [19]. In Romania,



**Table 2 Check-list of Ixodid tick species associated with mustelids**

Ticks species	Mustelid hosts
<i>I. acuminatus</i>	<i>Mustela nivalis</i> [22], <i>Mustela putorius</i> [22], <i>Mustela vison</i> [23]
<i>I. angustus</i>	<i>Mustela erminea</i> [24]
<i>I. cookei</i>	<i>Mustela frenata</i> [25], <i>Mustela nivalis</i> [26], <i>Mustela vison</i> [26,27]
<i>I. crenulatus</i>	<i>Martes foina</i> [28], <i>Meles meles</i> [24], <i>Mustela erminea</i> [29], <b><i>Mustela lutreola</i></b> [30], <i>Mustela nivalis</i> [28], <i>Mustela putorius</i> [31], <i>Mustela vison</i> [23],
<i>I. gregsoni</i>	<i>Martes americana</i> [32], <i>Martes pennanti</i> [33], <i>Mustela</i> sp. [32], <i>Mustela vison</i> [32,33]
<i>I. hexagonus</i>	<i>Martes foina</i> [13,31,34-36], <i>Mustela putorius</i> [31,35,36], <i>Mustela erminea</i> [29,31,35-37], <i>Mustela nivalis</i> [31,38], <i>M. putorius furo</i> [31,39], <i>Meles meles</i> [34-36], <i>Mustela vison</i> [23]
<i>I. muris</i>	<i>Mustela vison</i> [40]
<i>I. nipponensis</i>	<i>Mustela sibirica</i> [41]
<i>I. pacificus</i>	<i>Mustela frenata</i> [42], <i>Taxidea taxus</i> [42]
<i>I. persulcatus</i>	<i>Martes flavigula</i> [37], <i>Martes martes</i> [37], <i>Meles meles</i> [37], <i>Mustela erminea</i> [37], <i>Mustela nivalis</i> [37], <i>Mustela putorius</i> [37], <i>Mustela sibirica</i> [37]
<i>I. ricinus</i>	<i>Martes foina</i> [13,22,35,37], <i>Martes martes</i> [37], <i>Meles meles</i> [14,35,37], <i>Mustela erminea</i> [14,29], <b><i>Mustela lutreola</i></b> [37], <i>Mustela nivalis</i> [37], <i>Mustela putorius</i> [14,37], <i>Mustela vison</i> [23]
<i>I. rugicollis</i>	<i>Martes</i> sp. [43]
<i>I. scapularis</i>	<i>Mustela erminea</i> [16], <i>Mustela frenata</i> [25]
<i>I. tanuki</i>	<i>Martes flavigula</i> [44]
<i>I. texanus</i>	<i>Mustela frenata</i> [25]
<i>I. ventralloi</i>	<i>Mustela nivalis</i> [38]

both species are present in the Southeastern part of the country, Dobrogea [20,21].

## Conclusions

Detection of Lyme spirochete is relatively rare in mustelids, suggesting the limited role of these hosts in natural foci. The detection of pathogens in tissues or in ticks feeding on various vertebrates does not confer to these hosts the status of reservoir host, but rather carrier hosts. Hence, although it has been suggested that mustelids are reservoir hosts for *B. burgdorferi* s.l., experimental transmission is required to clarify this aspect.

## Competing interests

All authors have seen and approved the manuscript and declare that they have no competing interest.

## Authors' contributions

CMG conceived the study and drafted the manuscript. ADS made major contribution to the study design, identified the mustelid species and

contributed to the writing of the manuscript. JK performed PCR and RFLP. MM had trapped the mustelids. ADM contributed to the writing of the manuscript. All authors read and approved the final manuscript.

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# Tick parasites of rodents in Romania: host preferences, community structure and geographical distribution

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## Abstract

**Background:** Ticks are among the most important vectors of zoonotic diseases in temperate regions of Europe, with widespread distribution and high densities, posing an important medical risk. Most ticks feed on a variety of progressively larger hosts, with a large number of small mammal species typically harbouring primarily the immature stages. However, there are certain Ixodidae that characteristically attack micromammals also during their adult stage. Rodents are widespread hosts of ticks, important vectors and competent reservoirs of tick-borne pathogens. Micromammal-tick associations have been poorly studied in Romania, and our manuscript shows the results of a large scale study on tick infestation epidemiology in rodents from Romania.

**Methods:** Rodents were caught using snap-traps in a variety of habitats in Romania, between May 2010 and November 2011. Ticks were individually collected from these rodents and identified to species and development stage. Frequency, mean intensity, prevalence and its 95% confidence intervals were calculated using the EpiInfo 2000 software. A *p* value of <0.05 was considered statistically significant.

**Results:** We examined 423 rodents (12 species) collected from six counties in Romania for the presence of ticks. Each collected tick was identified to species level and the following epidemiological parameters were calculated: prevalence, mean intensity and mean abundance. The total number of ticks collected from rodents was 483, with eight species identified: *Ixodes ricinus*, *I. redikorzevi*, *I. apronophorus*, *I. trianguliceps*, *I. laguri*, *Dermacentor marginatus*, *Rhipicephalus sanguineus* and *Haemaphysalis sulcata*. The overall prevalence of tick infestation was 29.55%, with a mean intensity of 3.86 and a mean abundance of 1.14. Only two polyspecific infestations were found: *I. ricinus* + *I. redikorzevi* and *I. ricinus* + *D. marginatus*.

**Conclusions:** Our study showed a relatively high diversity of ticks parasitizing rodents in Romania. The most common tick in rodents was *I. ricinus*, followed by *I. redikorzevi*. Certain rodents seem to host a significantly higher number of tick species than others, the most important within this view being *Apodemus flavicollis* and *Microtus arvalis*. The same applies for the overall prevalence of tick parasitism, with some species more commonly infected (*M. arvalis*, *A. uralensis*, *A. flavicollis* and *M. glareolus*) than others. Two rodent species (*Mus musculus*, *Rattus norvegicus*) did not harbour ticks at all. Based on our results we may assert that rodents generally can act as good indicators for assessing the distribution of certain tick species.

**Keywords:** Hard-ticks, Ixodidae, Rodents, Micromammals, Romania

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## Background

Rodents (Order Rodentia) are usually small-sized mammals with a worldwide distribution, accounting for over 40% of all mammal species. Rodents are both widespread and abundant, as are their associated ticks. Thus, mainly from a human health perspective, the rodent-tick associations have a huge importance in most ecosystems [1]. Besides their role as tick hosts, rodents serve as reservoirs of tick-borne pathogens, hence increasing their importance in the eco-epidemiology of diseases like Lyme borreliosis, rickettsiosis, babesiosis, ehrlichiosis or tularaemia [1-3].

Most of the hard ticks feeding on rodents follow a three-host life cycle (i.e. each of the active stages - larva, nymph and adult - feeds on a different host individual). Usually, these ticks feed on a variety of progressively larger hosts, meaning that a large number of small mammal species typically harbour the immature stages [1]. On the other hand, there are certain Ixodidae that characteristically attack micromammals also during their adult stage. One of the most comprehensive reviews on micromammal-tick associations [1] lists 14 species of adult Ixodidae parasitic on rodents (*Anomalohimalaya cricetuli*, *A. lama*, *A. lotoskyi*, *Haemaphysalis verticalis*, *Ixodes angustus*, *I. apronophorus*, *I. crenulatus*, *I. laguri*, *I. nipponensis*, *I. occultus*, *I. pomarantzevi*, *I. redikorzevi*, *I. trianguliceps*, *Rhipicephalus fulvus*). However, the variety of species parasitizing rodents as immature stages is much higher [1].

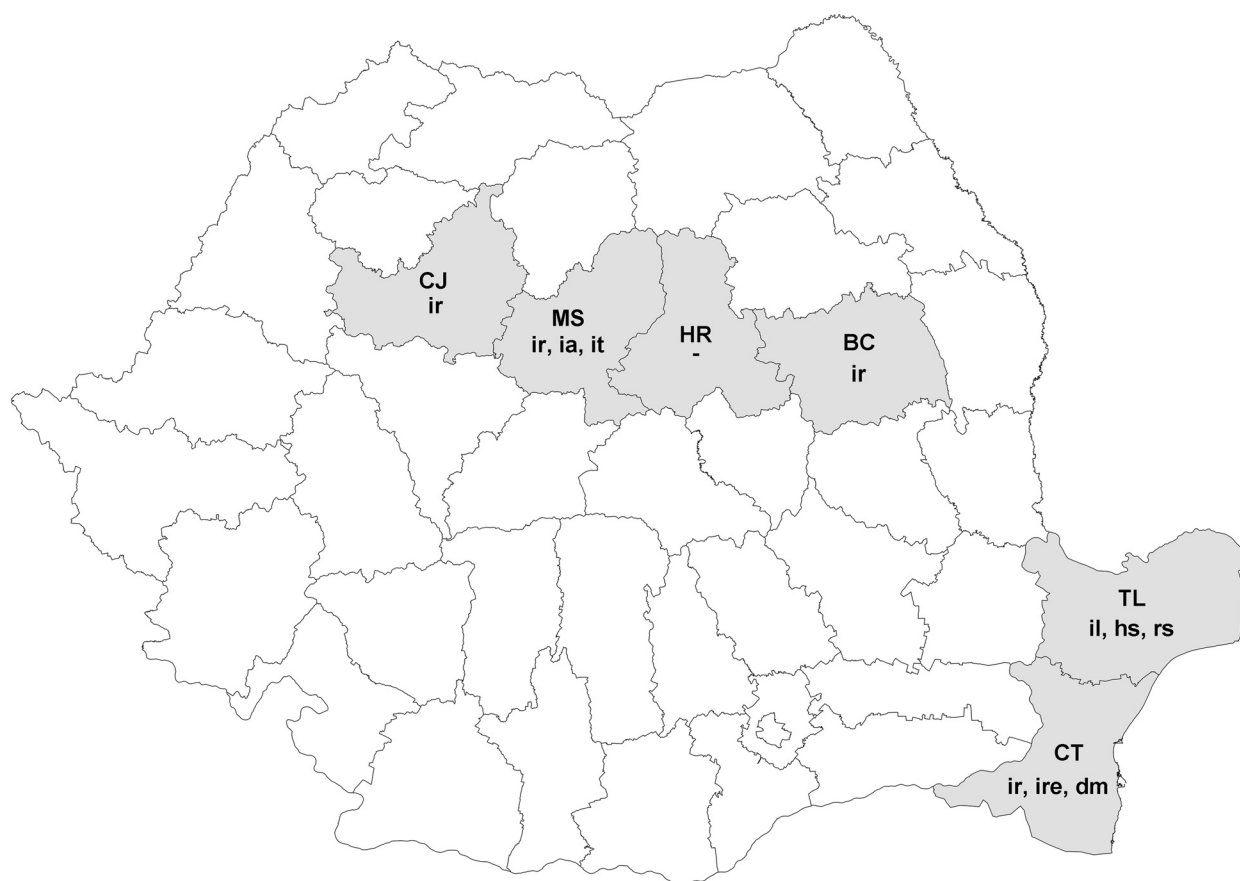
The importance of hard-ticks in the epidemiology of several human vector-borne infections has received

considerable attention in recent years and will certainly offer an opportunity for new studies in the years to come. The ecology of tick-borne infections is a popular field in parasitology and besides the research focused on the molecular epidemiology of tick-borne pathogens, studies on host preferences, seasonal variation and community structure are nevertheless important. From their reservoir-host perspective, rodents are known to act as key ecological links in the very complex transmission chains of tick-borne diseases as Lyme borreliosis or viral encephalitis [1,4].

Romania has an outstanding position in terms of biodiversity, being the only European country with five ecoregions on its territory [5]. This unique situation created a wide range of habitats and is mirrored by the number of mammal species present (112 species) [6]. Moreover, Romania not only holds this high biodiversity (especially among rodents [7]), but has nearly half of its human population living and working in rural areas and maintaining close contacts with nature [8], creating an interesting situation for epidemiological processes. Thirty-two species of wild rodents are known to occur in Romania [6]. Both this habitat variety and available host diversity [9] account for relatively high tick species diversity in Romania (25 species) [10], as compared to neighbouring countries [11]. However, micromammal-tick associations have been poorly studied in Romania despite the importance of each in the ecology of public pathogens. In this context, our manuscript shows the results of a study of tick infestation epidemiology in rodents from Romania.

**Table 1 Rodent species collected (total number, number by county and by month)**

Species	By County	By Month
<i>Apodemus agrarius</i> (n=94)	Buzău (n=2) Cluj (n=72) Constanța (n=3) Mureș (n=17)	April (n=5) May (n=4) August (n=3) September (n=27) October (n=47) December (n=8)
<i>Apodemus flavicollis</i> (n=51)	Bacău (n=1) Cluj (n=17) Mureș (n=28) Tulcea (n=5)	April (n=4) May (n=8) August (n=12) September (n=6) October (n=15)
<i>Apodemus sylvaticus</i> (n=22)	Cluj (n=8) Constanța (n=10) Mureș (n=3) Tulcea (n=1)	April (n=3) May (n=3) June (n=1) September (n=2) October (n=10) December (n=3)
<i>Apodemus uralensis</i> (n=24)	Constanța (n=18) Harghita (n=2) Mureș (n=2) Tulcea (n=2)	April (n=5) May (n=2) October (n=17)
<i>Myodes glareolus</i> (n=32)	Cluj (n=6) Mureș (n=26)	May (n=2) August (n=7) October (n=23)
<i>Micromys minutus</i> (n=11)	Cluj (n=7) Constanța (n=3) Tulcea (n=1)	April (n=1) July (n=1) October (n=8) December (n=1)
<i>Microtus arvalis</i> (n=54)	Cluj (n=5) Constanța (n=39) Mureș (n=10)	April (n=1) May (n=4) June (n=2) August (n=3) September (n=1) October (n=41) November (n=1) December (n=1)
<i>Microtus subterraneus</i> (n=49)	Cluj (n=44) Harghita (n=1) Mureș (n=4)	May (n=5) June (n=1) August (n=1) September (n=21) October (n=18) December (n=5)
<i>Mus musculus</i> (n=53)	Cluj (n=47) Harghita (n=5) Mureș (n=1)	April (n=3) May (n=2) June (n=1) August (n=2) September (n=25) October (n=15) November (n=5)
<i>Mus spicilegus</i> (n=8)	Bacău (n=1) Cluj (n=1) Constanța (n=1) Tulcea (n=5)	April (n=2) July (n=5) September (n=1)
<i>Rattus norvegicus</i> (n=12)	Cluj (n=10) Harghita (n=1) Mureș (n=1)	April (n=1) June (n=1) July (n=1) September (n=1) October (n=5) November (n=3)
<i>Spermophilus citellus</i> (n=13)	Constanța (n=1) Tulcea (n=12)	



**Figure 1** Geographical distribution of ticks collected from rodents (county names: BC - Bacău, CJ - Cluj, CT - Constanța, HR - Harghita, MS - Mureș, TL - Tulcea; tick species: dm - *Dermacentor marginatus*, hs - *Haemaphysalis sulcata*, ia - *Ixodes apronophorus*, il - *Ixodes laguri*, ire - *Ixodes redikorzevi*, ir - *Ixodes ricinus*, it - *Ixodes trianguliceps*, rs - *Rhipicephalus sanguineus*).

## Methods

423 rodents from 12 species (Table 1) were collected from a variety of habitats in Romania between May 2010 and November 2011 (Figure 1). Rodents were caught using overnight snap-traps with peanut butter or chocolate bait. The traps were controlled early in the morning and the captured animals were immediately transferred to individual plastic zip bags and frozen. Each individual rodent was carefully checked for the presence of ectoparasites under a dissection microscope in the laboratory. All collected ticks were fixed in 70% ethanol for subsequent examination. Identification to species level was done according to morphological keys [12,13]. Identification of rodent species was carried out according to Aulagner *et al.* 2009 [14]. Digital maps were created using ArcGis/ArcMap 9.2 (ESRI, © 1999–2006). The following epidemiological parameters were calculated: prevalence (per cent of infested animals from the total number of examined animals), mean intensity (total number of ticks collected per total number of infested animals) and mean abundance (total number of

ticks collected per total number of examined animals) [15]. Frequency, prevalence and its 95% confidence intervals were calculated using the EpiInfo 2000 software. A *p* value of <0.05 was considered statistically significant.

## Results

From the total of 423 examined animals, 125 (29.55%) harboured ticks with a mean intensity of 3.86 and a mean abundance of 1.14 (Table 2). The highest prevalence of tick infestation was found in *Microtus arvalis* (70.37%) while two species did not harbour ticks at all (*Mus musculus*, *Rattus norvegicus*). The highest intensity was found in *Apodemus agrarius* (7.10) and the highest mean abundance in *M. arvalis* (2.87).

The total number of ticks collected from rodents was 483, with eight species identified (Table 3). The dominant species was *I. ricinus* (71.01%), followed by *I. redikorzevi* (23.60%) and *I. apronophorus* (2.48%). The other 5 species accounted each for less than 1.5% from the total of the collected ticks. The majority of *I. ricinus* collected were

**Table 2 Prevalence, intensity and abundance of hard-tick parasitism in rodents by host species**

Host	Examined (n)	With ticks (n)	Prevalence (%)	Intensity (range; mean±sd)	Abundance (mean±sd)
<i>Apodemus agrarius</i>	94	21	22.34	1-67; 7.10±14.16	1.59±7.21
<i>Apodemus flavicollis</i>	51	26	50.98	1-12; 3.65±3.24	1.86±2.94
<i>Apodemus sylvaticus</i>	22	4	18.18	1-5; 2.50±1.91	0.45±1.22
<i>Apodemus uralensis</i>	24	13	54.17	1-6; 2.69±1.97	1.46±1.98
<i>Myodes glareolus</i>	32	16	50.00	1-4; 1.69±1.01	0.84±1.11
<i>Micromys minutus</i>	11	2	18.18	1; 1.00±0.00	0.18±0.40
<i>Microtus arvalis</i>	54	38	70.37	1-25; 4.08±4.25	2.87±4.01
<i>Microtus subterraneus</i>	49	2	4.08	2; 2.00±0.00	0.08±0.40
<i>Mus musculus</i>	53	0	0.00	-	-
<i>Mus spicilegus</i>	8	1	12.50	1; 1.00±0.00	0.13±0.35
<i>Rattus norvegicus</i>	12	0	0.00	-	-
<i>Spermophilus citellus</i>	13	2	15.38	1-4; 2.50±2.12	0.38±1.12
<b>Total</b>	<b>423</b>	<b>125</b>	<b>29.55</b>	<b>1-67; 3.86±6.58</b>	<b>1.14±3.98</b>

larvae (76.97%), while in case of *I. redikorzevi*, nymphs were predominant (82.46%).

The highest overall prevalence was recorded for *I. ricinus* (20.57% of rodents infested) followed by *I. redikorzevi* (7.09%). All other ticks species had prevalences below 0.5% (Table 4). Only two hosts had polyspecific parasitism, with *I. ricinus* + *I. redikorzevi* and *I. ricinus* + *Dermacentor marginatus* respectively.

The highest number of host species was recorded for *I. ricinus* (8 host species) followed by *I. redikorzevi* (3 host species) and *Rhipicephalus sanguineus* (2 host species). All the other tick species were found only on a single host species (Table 5). Adult ticks (regardless of the species) were found on 5 host species, nymphs on 6 host species and larvae on 7 species (Table 5).

**Table 3 Developmental stage distribution of ticks feeding on rodents in Romania (number and percentage of all collected)**

Tick species	Total number of ticks	Adults	Nymphs	Larvae
<i>Ixodes ricinus</i>	343 (71.01)	16 (4.66)	63 (18.37)	264 (76.97)
<i>Ixodes redikorzevi</i>	114 (23.60)	20 (17.54)	94 (82.46)	0 (0.00)
<i>Ixodes laguri</i>	1 (0.21)	1 (100)	0 (0.00)	0 (0.00)
<i>Ixodes apronophorus</i>	12 (2.48)	0 (0.00)	0 (0.00)	12 (100)
<i>Ixodes trianguliceps</i>	2 (0.41)	1 (50.00)	0 (0.00)	1 (50.00)
<i>Dermacentor marginatus</i>	1 (0.21)	1 (100)	0 (0.00)	0 (0.00)
<i>Rhipicephalus sanguineus</i>	6 (1.24)	0 (0.00)	2 (33.33)	4 (66.67)
<i>Haemaphysalis sulcata</i>	4 (0.83)	0 (0.00)	0 (0.00)	4 (100)
<b>Total</b>	<b>483 (100)</b>	<b>39 (8.07)</b>	<b>159 (32.92)</b>	<b>285 (59.01)</b>

The regional distribution of ticks parasitizing rodents shows that certain species were found in both examined regions (i.e. *I. ricinus* central and south-eastern Romania), while others were restricted to the central part (*I. apronophorus*, *I. trianguliceps*) or the south-eastern part (*I. laguri*, *Haemaphysalis sulcata*, *R. sanguineus*, *I. redikorzevi*) (Figure 1).

## Discussion

### Host preferences

In the case of Lyme borreliosis, small mammals are the vertebrate group that has been the most extensively investigated up to now, mainly because they can be easily captured in large numbers, handled and maintained

**Table 4 Prevalence of developmental stages by tick species (number and percentage of all collected)**

Tick species	Number of rodents infested	Host with adults	Host with nymphs	Host with larvae
<i>Ixodes ricinus</i>	87 (20.57)	6 (6.90)	28 (32.18)	64 (73.56)
<i>Ixodes redikorzevi</i>	30 (7.09)	12 (40.00)	23 (76.67)	0 (0.00)
<i>Ixodes laguri</i>	1 (0.24)	1 (100.0)	0 (0.00)	0 (0.00)
<i>Ixodes apronophorus</i>	2 (0.47)	0 (0.00)	0 (0.00)	2 (100)
<i>Ixodes trianguliceps</i>	1 (0.24)	1 (100)	0 (0.00)	1 (100)
<i>Dermacentor marginatus</i>	1 (0.24)	1 (100)	0 (0.00)	0 (0.00)
<i>Rhipicephalus sanguineus</i>	2 (0.47)	0 (0.00)	2 (100)	1 (50.00)
<i>Haemaphysalis sulcata</i>	1 (0.24)	0 (0.00)	0 (0.00)	1 (100)
<b>Total</b>	<b>125 (29.55)*</b>	<b>21 (16.80)</b>	<b>53 (42.40)</b>	<b>69 (55.20)</b>

\*2 animals with polyspecific infestation.

**Table 5 Tick-rodent associations in Romania**

Tick species	Hosts for adults	Hosts for nymphs	Hosts for larvae	Host species
<i>Ixodes ricinus</i>	Aa, Mm, Ma	Aa, Af, As, Au, Ma	Aa, Af, As, Au, Mg, Ma, Msu	Aa, Af, As, Au, Ma, Mg, Mm, Msu
<i>Ixodes redikorzevi</i>	Au, Ma, Mm	Au, Ma	-	Au, Ma, Mm
<i>Ixodes laguri</i>	Sc	-	-	Sc
<i>Ixodes apronophorus</i>	-	-	Af	Af
<i>Ixodes trianguliceps</i>	Msu	-	Msu	Msu
<i>Dermacentor marginatus</i>	Ma	-	-	Ma
<i>Rhipicephalus sanguineus</i>	-	Af, Msp	Af	Af, Msp
<i>Haemaphysalis sulcata</i>	-	-	Sc	Sc
<b>Total</b>	Aa, Mm, Ma, Msu, Sc	Aa, Af, As, Au, Ma, Msp	Aa, Af, As, Au, Mg, Ma, Msu	

Aa - *Apodemus agrarius*; Af - *Apodemus flavicollis*; As - *Apodemus sylvaticus*; Au - *Apodemus uralensis*; Mg - *Myodes glareolus*; Mm - *Micromys minutus*; Ma - *Microtus arvalis*; Msu - *Microtus subterraneus*; Msp - *Mus spicilegus*; Sc - *Spermophilus citellus*.

in the laboratory [2]. The main reservoir hosts for *Borrelia burgdorferi sensu lato* (s.l.) in Europe are *A. agrarius*, *A. flavicollis*, *A. sylvaticus* and *Myodes glareolus*. Moreover, certain genospecies of this pathogen (i.e. *Borrelia afzelii*) are cycled almost exclusively by rodents [2]. The ecological importance of reservoir hosts is greater if they are also common hosts to competent vector ticks. For instance, several vertebrate species were experimentally demonstrated to be competent reservoir hosts but their role as hosts to competent vector ticks is less important (i.e. *R. norvegicus*, *R. rattus*, *Sciurus vulgaris*, *Glis glis* [2]. Our study suggests that certain rodent species are more prone to be attacked by ticks than others. In species like *M. arvalis*, *A. uralensis*, *A. flavicollis* and *M. glareolus* the overall prevalence of parasitism with hard ticks was more than 50%. On the other hand, we found lower prevalence in *A. agrarius*, *A. sylvaticus*, *Micromys minutus*, *Mus spicilegus* and *Spermophilus citellus* even if sympatric with other infested hosts species. Interestingly, very abundant synanthropic rodent species like *M. musculus* and *R. norvegicus* were not harbouring ticks at all.

In a similar study from France, the overall prevalence of tick burden in micromammals was 25.19%, with *I. ricinus* being the dominant tick-parasite [16]. The authors found the highest prevalence in *M. arvalis* (31.58%), followed by *A. sylvaticus* (22.73%), *M. agrestis* (16.13%) and *M. glareolus* (14.16%). In the Netherlands [17], variable prevalences (19-56%) of tick parasitism in *A. sylvaticus* were reported during spring and summer and the only tick species found was *I. ricinus*. It seems also that the most important reservoir hosts for the Lyme borreliosis agent are usually infested with a higher number of ticks than other rodent species. Higher mean intensity and abundance were found in *A. agrarius*, *A. flavicollis*, *A. sylvaticus*, *A. uralensis* and *M. arvalis* while in other host species these parameters were lower (i.e. *Mus spicilegus*, *Micromys minutus*).

### Community and population structure

Another important aspect is the tick species diversity found in our study. Most published data on ticks of rodents from Europe report few species. A survey on 799 micromammals in France revealed the presence of only two tick species: *I. ricinus* and *I. trianguliceps* [16]. In the Netherlands, only *I. ricinus* was reported from rodents [16], while in rodents from Russia four tick species were found [18]. In a multinational study (Germany, Slovakia and Romania) on the epidemiology of TBE virus, the authors reported only *I. ricinus* on *A. flavicollis*, *A. sylvaticus*, *A. uralensis* and *M. glareolus* and *I. trianguliceps* on *Microtus subterraneus* [19]. In a study from Germany, out of 11,680 ticks collected from rodents (*A. flavicollis*, *A. sylvaticus* and *M. glareolus*), 97.9% were *I. ricinus*, while the rest were *I. trianguliceps* [20].

All these data, together with other nation-wide surveys [21] add new evidence that the principal tick infesting rodents in Europe is mainly *I. ricinus*. *Ixodes ricinus* is also the most common tick feeding on humans [22], which may confer to rodents an important status as reservoir hosts for human diseases [23].

The host sharing by different tick species is important mainly for the bridging of microbial pathogens through the reservoir hosts. Although ticks specifically feeding on rodents (i.e. *I. apronophorus*, *I. redikorzevi*, *I. trianguliceps*) are attacking humans only exceptionally [24], they may maintain the infection cycle of their rodent host with certain pathogens. Subsequently, a more generalist tick (usually *I. ricinus*) can bridge the pathogens from these rodents to humans. Examples include *B. burgdorferi* s.l. isolated from *I. trianguliceps* [25] and *I. redikorzevi* [26] or the Omsk virus isolated from *I. apronophorus* [27], all in Russia.

Assessing the age structure of tick populations infesting rodents, using the prevalence of each developmental stage showed a skewed age ratio towards immatures. In Germany, a study of the population structure of *I.*

*ricinus* on three rodent species showed that 97.9% of all ticks were larvae, 2.0% nymphs, and 0.1% females [20]. A multinational study focusing on rodents' ticks in Central Europe found only larvae and nymphs [19]. In the case of *I. ricinus*, our study confirmed other general observations [13], according to which rodents are important hosts mainly for the immature stages of this tick. Although in our study we found adults of *I. ricinus* on 1.4% of the examined animals, interestingly, the majority of them were collected from *M. arvalis*. From 54 examined animals, four (7.4%) harboured adults of *I. ricinus*. This suggests that certain rodent species can act also as more common hosts for *I. ricinus*.

### Geographical distribution

According to a recent review [10], a number of tick species found in the present study have a widespread distribution in Romania (*I. ricinus*, *D. marginatus*), while others are restricted to the southern regions (*I. laguri*, *H. sulcata*, *R. sanguineus*). The results of tick community structures from rodents analysed in accordance with general distribution maps [10] show that rodents are a good marker for assessing the distribution of certain tick species, but more heterogeneous seasonal collection campaigns are required to draw reliable conclusions.

### Conclusions

Our study showed a relatively high diversity of ticks parasitizing rodents in Romania. The most common tick in rodents was *I. ricinus*, followed by *I. redikorzevi*. Certain rodents seem to host a significantly higher number of tick species than others, the most important within this view being *Apodemus flavicollis* and *Microtus arvalis*. The same applies for the overall prevalence of tick parasitism, with some species more commonly infected (*M. arvalis*, *A. uralensis*, *A. flavicollis* and *M. glareolus*) than others. Two rodent species (*Mus musculus*, *Rattus norvegicus*) did not harbour ticks at all. Based on our results we may assert that rodents generally can act as good indicators for assessing the distribution of certain tick species.

### Competing interests

All authors have seen and approved the manuscript and declare that they have no competing interest.

### Authors' contributions

MAD conceived the study and drafted the manuscript. DMA and MC identified the ticks. SDA contributed to study design and identified the small mammals. OM, MIA and IA examined the rodents and collected the ticks. GA performed the data analysis. DG collected the samples in the field. CV is the team coordinator, while GCM designed the study and coordinated the research grant. All authors read and approved the final manuscript.

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