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The role of migrating birds in transmission of arthropods and associated arthropod-borne diseases. The case of ticks and tick-borne pathogens

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Abstract

Geographic spread of parasites and pathogens poses a constant risk to animal health and welfare, particularly given that climate change is expected to potentially expand appropriate ranges for many key species. Anthropomorphic spread of deleterious organisms via trade routes and human travel is relatively closely controlled, though represents only one possible means of parasite/pathogen spread. Non-anthropomorphic spread, via natural parasite/pathogen movement between geographic locales, is far harder to manage. Though the extent of such movement may be limited by the relative inability of many parasites and pathogens to actively migrate, passive movement over long distances may still occur via migratory hosts. This paper reviews the potential role of migrating birds in the transfer of parasites and pathogens between geographic locales, focusing primarily on ticks. Bird-tick-pathogen relationships are considered, and evidence provided of long-range parasite/pathogen transfer from one location to another during bird migration events. As shown in this paper not only many different arthropod species are carried by migrating birds but consequently these pests carry many different pathogens species which can be transmitted to the migrating birds or to other animal species when those arthropods are dropping during these migrations highlighting the need to understand better dissemination paths and disease epidemiology.

Key words: migrating birds, arthropod pests, arthropod-borne diseases, vector capacity

Avian migration

Migrating birds can travel thousands of kilometres and carry with them ectoparasites such as mites, ticks, fleas and lice. Such arthropod pests can carry pathogens and potentially transmit them to indigenous fauna where migrating birds come into contact with local host populations. Sources and directions of movement of migratory bird species are often predictable, as our timings of migration events. A study on the migrating birds on the Western Africa-Western Europe flyway, for example, followed 34 migrating breeding birds arriving in Spain. A few species arrived in January, but the peak of migration intensity was between mid-April to Mid-May (Bosch et al., 2013).

Though certain elements of avian migration can be predicted, it is perhaps harder to quantify the risk that this presents in terms of movement of avian-associated parasites and the pathogens they may vector. The remainder of this review presents work from selected studies that support potentially significant movement of these organisms via migratory birds.

Birds as hosts for ectoparasites and associated pathogens

In domesticated settings, bird health and welfare is often threatened by parasitic infection and associated pathogen spread. Susceptibility of commercially-reared fowl, and especially egg-laying hens, to the poultry red mite, *Dermanyssus gallinae*, is perhaps the best known example, with these mites reportedly serving as potential vectors for a broad range of poultry pathogens (Sparagano et al., 2014). The success of *D. gallinae* as a parasite of poultry has been at least partially attributed to an inability of hens to develop resistance to these mites (Sparagano et al., 2014).

A similar host-parasite relationship seems to exist between wild birds and their major ectoparasites. Heylen et al. (2010), for example, investigated whether blue tits and great tits are able to acquire resistance after repeated infestation with *Ixodes ricinus* nymphs. As blue tits are less frequently exposed to *I. ricinus* in the wild than great tits, the authors expected *I. ricinus* to be less adapted to the blue tit’s resistance mechanisms. Over three infestation ‘events‘ the authors observed consistently high tick attachment rates and yields, high engorgement weights, and short engorgement and moulting durations, irrespective of host species, indicating that neither of these two birds is able to mount an effective immune response against *I. ricinus* nymphs, even after repeated infestations. As a consequence of their lack of resistance, birds were unable to prevent direct harm (acute blood depletion) caused by tick feeding, but did compensate for erythrocyte loss without reduction in general body condition (body mass corrected for tarsus length). The lack of resistance observed suggests that *I. ricinus* has a long co-evolutionary history with both species of tit, which enables the tick to avoid or suppress the host’s resistance responses.

The above in mind it is perhaps unsurprising that birds may harbour a large diversity of parasitic arthropods. Some species, such as *D. gallinae* (which also infests a broad range of wild birds), only reside on their hosts during short, relatively infrequent feeding bouts, minimising the possibility that an avian host could spread this species readily during migration. Others, however, may reside permanently on-host (i.e. lice), or, in the case of ticks such as *I. ricinus*, remain firmly attached to their host over relatively long feeding periods, facilitating ‘hitch-hiking‘ during avian migration. As key vectors of numerous significant pathogens, ticks represent a particular risk for disease spread from one geographic locale to another. Consequently, subsequent sections in this review focus almost exclusively on this group of ectoparasites.

Birds as reservoirs for ticks and associated pathogens

Several studies have investigated tick infestation of wild avian hosts, demonstrating that birds may harbour both diverse and simple infestations. Over the course of a year, between 2010 and 2011, Norte et al. (2012) captured 37 species of bird in two recreational forests in western Portugal: a suburban forest and an enclosed game area. Numerous tick species were found parasitizing sampled birds (*I. ricinus*, *Ixodes frontalis*, *Ixodes arboricola*, *Ixodes acuminatus*, *Haemaphysalis punctata*, *Hyalomma marginatum* and *Hyalomma lusitanicum*), with the highest prevalence of ticks recovered from Eurasian blackbirds, spotless starlings (though only two individuals of this species were captured) and European robins. Highest infestation intensities were registered on Eurasian blackbirds, Sardinian warblers and European robins. Conversely, in work by Marsot et al. (2012) only *I. ricinus* (larvae and nymphs) were recovered from 20 bird species captured in France between 2008 and 2009 during the breeding season. The most frequently sampled bird species were the European robin, the great tit, the Eurasian blackbird and the Eurasian blackcap, which accounted, respectively, for 22%, 21%, 12% and 9% of all birds examined. The five species with the highest average tick burden were blackbirds, song thrushes, robins, dunnock and winter wren. Excluding dunnock, these species hosted more than 90% of the ticks in the local bird community. Interestingly, Norte et al. (2012) noted that the importance of given bird species as hosts of larvae and nymphs of *I. ricinus* and *I. frontalis* differed, supporting that different bird species may contribute differently for tick population maintenance.

In many cases researchers have not only investigated bird-tick relationships, but also assessed whether one, the other, or both carry pathogens of concern (Hildebrandt et al,. 2010; Kartashov et al., 2014). Selected work in this area, undertaken throughout various regions in Europe, is summarised below.

The potential of ticks to travel long distances via migratory birds has been the subject of research for some time. *Hyalomma* ticks, mainly engorged nymphs, for example, were recorded as being transferred between regions by migrating birds in the 1960’s (Hoogstraal et al , 1961, 1963), with such ticks associated with the transmission of Crimean–Congo hemorrhagic fever (CCHF) virus and *Theileria* protozoans. More recent evidence of movement of ticks and tick-associated pathogens between regions in Europe is reported below.

Northern Europe

In 2007, *I. ricinus* ticks were collected from 11 species of bird on a conservation island in the Baltic Sea (Franke et al., 2010). DNA from *Borrelia* was detected in 14.1% of ticks, *Anaplasma phagocytophilum* in 2.6%, rickettsiae in 7.3% and *Babesia* spp. in 4.7%. Co-infections with different pathogens occurred in six ticks (3.1%). The fact that 11 ticks (five larvae and six nymphs) were infected with *Borrelia afzelii* suggests that birds may, contrary to current opinion, serve as reservoir hosts for this species. Further characterization of rickettsial infections revealed *Rickettsia monacensis* and *Rickettsia helvetica*; *Babesia* infections revealed *Babesia divergens* (in ticks from robins and blackbirds) and *Babesia microti* (in ticks from robins and great tits). The occurrence of *Babesia* spp. in a total of five tick larvae suggested that birds may be able to infect ticks, at least with *B. microti*, a species considered not to be transmitted transovarially in ticks.

Duneau et al. (2008) evaluated the potential role of seabirds in spreading Lyme Borelliosis (LB) spirochetes. They collected *Ixodes uriae* adults and nymphs from five colonial seabird species in the North Atlantic, Iceland and Northern Norway. The mean prevalence of *Borrelia burgdorferi* sensu lato (s.l.) across colonies was 26.0%. The majority of sequenced strains grouped with reference sequences of *Borrelia garinii*, *Borrelia lusitaniae* and *B. burgdorferi* sensu stricto (s.s.) were also identified.

During the spring and autumn migration periods in 2004, Pietzsch et al. (2008) determined whether ticks were being imported into the British Isles on migratory birds. Ticks were collected from ringed birds at 11 bird observatories and three inland sand martin colonies. A total of 38 ticks belonging to four species (*I. ricinus, I. frontalis, I. lividus* and *I. arboricola*) were collected from twelve species of bird. Ticks were tested for viruses in the *Flavivirus* and *Nairovirus* genera, though with no positive hits recorded.

Hasle et al. (2011b) examined 33 species of passerine birds at four bird observatories along the southern Norwegian coast during the spring migrations of 2003-2005. The presence of *Babesia* was detected in the nymphs (1%) of *I. ricinus* and identified as *Babesia venatorum* (EU1) collected from a European robin in Akerøya, a greenish warbler in Jomfruland and a bluethroat and a dunnock from Store Færder. In another study Hasle et al. (2011a) found *Borrelia* spp. in 13.6% of examined *I. ricinus* nymphs (19 *B. afzelii*, 38 *B. garinii*, two *B. turdi*, and 11 *B. valaisiana*) and in 8.1% of examined *I. ricinus* larvae (ten *B. garinii*, one *B. turdi*, and three *B. valaisiana*). Ticks collected from birds of the genus *Turdus* (blackbirds, song thrushes and redwings) had a higher prevalence of *Borrelia* spp. than ticks from the other passerine genera sampled.

A study in Latvia during an autumn migration recovered *Ixodes* ticks collected from nine species of passerine birds. In this work the authors recorded numerous pathogens being carried by ticks, including: *B. valaisiana*, *B. garinii*, *A. phagocytophilum*, *R. helvetica*, *B. divergens*, *B. microti* and *B. venatorum*. Mixed infections were found in 20% of the nymphal and 3% of the larval stages *Ixodes* ticks tested (Capligina et al., 2014).

Graham et al. (2010) investigated whether migratory birds could play a role in long-distance transportation of rickettsial agents. Authors characterized tick infestation in populations of migratory sand martins in northwest England in 2009. A total of 194 birds were sampled and female *I. lividus* ticks removed from infested birds. A single *Rickettsia* spp. was detected in 100% of the ticks and was designated *Rickettsia* sp~~p~~. IXLI1, which is fitted neatly into a group containing the strains *Rickettsia japonica*, *Rickettsia* spp. strain Davousti and *Rickettsia heilongjiangensis*.

In Sweden the role of migratory birds as long-distance vectors for multiple microorganisms was studied by Elfving et al. (2010). From migratory birds trapped in 2001 the authors collected *I. ricinus*, *I. lividus* and unspecified *Ixodes* spp. ticks. *Rickettsia* spp. were detected in 11.3% of ticks, with *R. helvetica* being the predominant species. In 0.8% of the ticks *R. monacensis* was identified. For 1.4% of the ticks, the 17kDa, ompB, gltA and ompA genes showed the greatest similarity to *Rickettsia* sp. strain Davousti, *R. japonica* and *R. heilongjiangensis.*

Eastern Europe

Špitalská et al. (2006) mist-netted birds in Slovakia in 2001 and 2003. Sixteen species of birds were infested with subadult *I. ricinus*. The highest intensity of parasitization was observed on Eurasian blackbirds, song thrushes and dunnocks. *Rickettsia* spp. was found in one nymph from a European robin, and the closely related *Ehrlichia*-like species “Schotti variant” was detected in another nymph removed from a song thrush. Samples were also screened for DNA of *Coxiella burnetii* and of Piroplasmida species, though neither was recovered.

In Slovakia and the Czech Republic individuals of 40 bird species were captured and found to be carrying larvae and nymphs of *I. ricinus.* Eurasian blackbirds and song thrushes were found to carry 95% of all spirochete infected tick larvae. More than 90% of the infections were typed as *B. garinii* and *B. valaisiana* (Tamara et al., 2008) . The authors concluded that thrushes are key players in the maintenance of these spirochete species in this region of Central Europe. At another study site in the Czech Republic, Dubská et al. (2009) collected subadult ticks from birds during the postbreeding period of 2005. *Borrelia garinii* was detected in 22.2% of ticks, *B. valaisiana* in 12.8%, *B. afzelii* in 1.6%, and *B. burgdorferi* (s.s.) in 0.3%. The authors concluded and confirmed that Eurasian blackbirds, song thrushes, and great tits are capable of transmitting *B. garinii.* The authors also reported that certain other passerine birds investigated play minor roles in transmitting *B. garinii*; and that the presence *B. afzelii* in ticks results from infection in a former stage.

Three tick species, namely *I. arboricola* (75.0%), *I. ricinus* (23.1%), and *H. concinna* (1.8%), were collected from 20 species of birds (Passeriformes) in the Czech Republic during 2003-2005 (Špitalská et al., 2011). Rickettsiae were detected in 44.0% larvae and 24.5% nymphs of *I. arboricola* collected from great tits, marsh tits and the Eurasian nuthatch. Rickettsiae-positive *I. ricinus* larvae (13.7%) were collected from great tits, Eurasian blue tits, and nuthatches, and 2.6% of nymphs from European robins and dunnocks. *Rickettsia helvetica* and other *Rickettsia* species were also identified. *Anaplasma phagocytophilum* was found only in two *I. ricinus* nymphs collected from robins and great tits. Infections with *B. burgdorferi* (s.l.) were recorded in 1.3% of larvae of *I. arboricola* acquired from marsh tits and great tits, and in 11.8% of larvae and 25.0% of nymphs of *I. ricinus* collected from great tits, marsh tits, blue tits, sedge warblers, Eurasian blackbirds, common rosefinches, Eurasian blackcaps, dunnocks and common chiffchaffs. *Borrelia garinii* and *B. valaisiana* were also identified. This study suggested that *I. arboricola*, with associated great tits and marsh tits, plays an important role in circulating of rickettsiae.

Between May and September of 2002, forest passerine birds and immature *I. ricinus* ticks infesting them were surveyed for infection with *B. burgdorferi* (s.l.) in a sylvatic habitat in west-central Poland (Michalik et al., 2008). The majority of ticks (65.7%) were collected from thrush species and blackbirds. *Borrelia burgdorferi* (s.l.) DNA was detected in 11% of the larval ticks and in 7.2% of nymphs. *Borrelia garinii* and *B. valaisiana* accounted for 88.5% and 11.5% of the infections detected in

Borrelia-positive ticks, respectively. Only one out of 53 blackbird blood samples were PCR-positive for *Borrelia* species, identified as *B. burgdorferi* (s.s.). Authors demonstrated that avian hosts were not reservoirs for *B. afzelii,* but reported that thrush species may support the circulation of *B. garinii* and *B. valaisiana* under natural conditions.

Hornok et al. (2013) mist-netted birds in Hungary during 2011 and removed *H. concinna*, *I. ricinus* and *H. marginatum* ticks from them. *Rickettsia helvetica* was identified in *I. ricinus* and *H. concinna* (17/72 samples) from the European robin, Eurasian blackbird, redwing, song thrush, great tit, common chiffchaff and Savi's warbler. *Rickettsia monacensis* was detected in *I. ricinus* (12/72 samples) and *Rickettsia aeschlimannii* in *H. marginatum* (3/72 samples) from European robins, Eurasian blackbirds and great tits*.* *Borrelia burgdorferi* (s.l.) was detected only in *I. ricinus* (8/72 samples) from robins, blackbirds, redwings, great tits, dunnocks and Savi’s warblers. In four samples simultaneous presence of *R. helvetica* and *B. burgdorferi* (s.l.) was reported and *A. phagocytophilum* was recovered from one pool of *I. ricinus* nymphs from the European robin, with simultaneous positivity to *R. monacensis*. In one *I. ricinus* larva, from the same host, a novel *Francisella*-like organism was identified. All samples were negative for *C. burnetii*.

Movila et al. (2008) studied the prevalence of *B. burgdorferi* (s.l.) in *I. ricinus* and *I. lividus* ticks collected from wild birds in the Republic of Moldova. *Borrelia burgdorferi* (s.l.) was detected in 14% of *I. ricinus* and 5.5% of *I. lividus*. *Borrelia* species were most prevalent in *I. ricinus* ticks collected from Eurasian blackbirds (17%). *Ixodes lividus* was infected with both *B. burgdorferi* (s.s.) and *B. garinii,* though *I. ricinus* was infected with *B. burgdorferi* (s.s.) only.

To study the role of wild birds in the transmission of tick borne encephalitis virus (TBEV), Mikryukova et al. (2014) sampled birds from 60 species captured in Tomsk city and its suburbs in Western Siberia, Russia. Between 2006 and 2011, *Ixodes* *pavlovskyi*, *Ixodes persulcatus* and *Ixodes plumbeus* were recovered. The highest average number of ticks per bird was found for the fieldfare and the tree pipit. TBEV RNA and antigen were found in 9.7% and 22.8% samples collected from wild birds, respectively. TBEV markers were also detected in 14.1% of *I. persulcatus* ticks, 5.2% of *I. pavlovskyi*, and 4.2% of *I. plumbeus* ticks collected. Sequencing of 5´-NCR of TBEV revealed that all TBEV isolates belonged to Far Eastern (dominate) and Siberian genotypes, supporting that wild birds are potential disseminators of TBEV, TBEV-infected ixodid ticks, and possibly other tick-borne infections.

Movila et al. (2011) revealed the prevalence of spotted fever group (SFG) rickettsiae and *Babesia* spp. in *I. ricinus* ticks from eight species of migratory Passeriformes collected at Curonian Spit in the Kaliningrad enclave of North-Western Russia during spring 2008. *Babesia* spp. were detected in 1.6% ticks from song thrushes and identified as *Babesia* spp. EU1. SFG rickettsiae were detected in 15.1% of ticks, *R. helvetica* in 10.3%, *R. monacensis* in 3.9%, and *R. japonica* in 0.8%. *Rickettsia helvetica* was detected in ticks detached from song thrushes, common chaffinches and great tits, whereas *R. monacensis* and *R. japonica* were identified in ticks taken from chaffinches and European starlings.

During the spring and autumn bird migrations of 2013, blood samples and ticks (*I. ricinus, H. concinna* and an unspecified *Hyalomma* specimen) were collected from birds belonging to 16 species in Hungary by Hornok et al. (2014). Birds were shown to be bacteraemic with *R. helvetica* (for European robins and dunnocks) and *A. phagocytophilum* (for redwing), but not with *Candidatus Neoehrlichia mikurensis*. The prevalence of rickettsiae was high (51.4%) in ticks, suggesting that some of them may have acquired their infection from their avian hosts. *Ixodes ricinus* ticks were infected with *R. helvetica, R. monacensis, A. phagocytophilum*. *Haemaphysalis concinna* were infected with *R. helvetica*.

Southern Europe

During April–October 2009, bird bandings were conducted in the protected area of Finca Ribavellosa in La Rioja, Spain. *Haemaphysalis punctata*, *I. frontalis*, *I. arboricola*, *I. ricinus*, and other *Ixodes* spp. were collected from birds. *Anaplasma phagocytophilum* was detected in a single larva of an *I. ricinus* tick (0.5%). *Borrelia burgdorferi* (s.l.) was detected in 13.1% samples; the most prevalent genospecies was *B. garinii*, which was detected in *I. ricinus*, *H. punctata*, *I. frontalis*, and *Ixodes* spp. *Borrelia valaisiana* was amplified in samples from *I. ricinus* and *Ixodes* spp. and *Borrelia turdi* was found in *I. frontalis*. *Rickettsia* infection was detected in 17.6% ticks. *Rickettsia monacensis*, *R. helvetica*, *Rickettsia sibirica sibirica*, and unspecified *Rickettsia* were detected in *I. ricinus* ticks. *Candidatus Rickettsia vini* was identified in *I. arboricola* and *I. ricinus* ticks. Two *I. ricinus* larvae showed co-infection with *B. garinii* and *Rickettsia* spp. and one nymph was co-infected with both *B. valaisiana* and *Rickettsia* spp. (Palomar et al., 2012).

Ioannou et al. (2009) collected blood samples into filter papers from 51 Cyprian bird species. Of the 131 pools prepared, four (3%) were positive for *Rickettsia* spp., 56 (43%) for *C. burnetii*, and 64 (49%) for *Anaplasma* spp. Fifteen ticks (all *Ixodes ventalloi* and all removed from the chukar partridge) and 18 lice were removed from the above birds. *Rickettsia* spp. and *C. burnetii* were detected in three *I. ventalloi* ticks, though all ectoparasites sampled were negative for *Anaplasma* spp.

Wallménius et al. (2014) collected ticks (*H. marginatum*, *I. frontalis*, *Amblyomma* spp., *Haemaphysalis* spp., *Rhipicephalus* spp. and unidentified ixodids) from birds during their seasonal migration northwards in spring 2009 and 2010 at bird observatories on two Mediterranean islands: Capri and Antikythira. Overall 48% of ticks were *Rickettsia*-positive. Of these, 96% were infected with *R. aeschlimannii* (in *H. marginatum*, *Hyalomma rufipes, I. frontalis* and *Haemaphysalis* spp.), and 4% with

Rickettsia africae (in *H. marginatum*) or unidentified *Rickettsia* species (in *H. marginatum*, *H. rufipes, I. frontalis* and *Haemaphysalis* spp.).

In Spain, Astobiza et al. (2011) investigated the distribution of *C. burnetii* in wild bird species. Samples were collected from 2001 to 2006, with wild birds from 23 families analyzed. Two individuals, one Eurasian griffon and one black kite, were positive for *C. burnetii*, though the same was note true of the three *I. frontalis* ticks removed from birds.

Western Europe

A 4-year study in Switzerland (considering more than 4,500 birds sampled during autumn migrations between August and October) found only *Ixodes* ticks to be carried by 71 bird species (breeding and migrating). Though diversity of the parasite was low, with *I. ricinus* constituting all but a single specimen, ticks were confirmed as carrying TBEV, *A. phagocytophilum, Borrelia spp., Rickettsia spp*. and *Candidatus Neoehrlichia mikurensis* (Lommano et al., 2014).

In 2010 Socolovschi et al. (2012) analyzed the presence of emerging zoonotic bacteria in ticks collected from passerine birds in the Camargue, in the south of France, which is a major rallying point for birds migrating from Eurasia and Africa. *Ixodes* spp. ticks (five larvae and six nymphs) were collected from the Eurasian blackcap, the European robin and the Eurasian blackbird. *Rhipicephalus sanguineus* group ticks (three adults) and a *Haemaphysalis* spp. tick (one adult) were collected from the house sparrow (a local resident). A single *Hyalomma* spp. tick (one nymph) was collected from a Eurasian reed warbler, and an *H. rufipes* (one nymph) was collected from a common nightingale. *Rickettsia massiliae* was detected in ticks from the house sparrow, *R. aeschlimannii* in ticks from the Eurasian weed warbler and the common nightingale, and *B. valaisiana* in one tick from a Eurasian blackbird.

Conclusions

This review represents only a selection of the available literature, but highlights the potential role that migrating birds can play in dispersion of ectoparasites and their associated pathogens, supporting that transmission of both may be commonplace. Though we have focused on ticks and tick-borne pathogens, it deserves note that research also confirms movement of other ectoparasites on migratory birds. A Slovakian study focusing on reed warblers and their nests, for example, found *Ceratophyllus garei* (a flea) to be carrying a rickettsia that was a 99.7% match to *R. africae* (Sekeyová et al., 2012). Also of note was that two *Wolbachia* sp. were detected in fleas sampled during the study.

By extrapolation for the Euro-centric data presented, it can be surmised that migratory birds represent a potential pest/disease threat the world over. Though detailed monitoring of migrating birds may not be feasible, knowledge of migratory routes, timings and ‘high risk’ species could be used to develop appropriate pest/disease monitoring approaches and management plans. These could be especially useful in ‘high risk’ areas, i.e. where influx of parasite-prone birds is commonplace, to promote optimal protection of local fauna from ‘migratory’ parasites and pathogens.

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Table 1 - Ticks and tick-borne pathogens found in ticks collected from wild bird (and/or in birds blood) from Europe.

	Geographical area	Number of Investigated wild birds species	Ticks	Pathogen detected in ticks	Birds species harbouring pathogens	References
Northern Europe	Baltic Sea Island	11 species	*Ixodes ricinus*	*Borrelia afzelii* *Anaplasma phagocytophilum* *Rickettsia monacensis* *Rickettsia helvetica* *Babesia divergens* *Babesia microti*	NR	Franke et al., 2010
	Northern Norway	unknown	*Ixodes uriae*	*Borrelia burgdorferi* (s.l.) *Borrelia garinii* *Borrelia lusitaniae* *B. burgdorferi* (s.s.)	NR	Duneau et al. 2008
	British Isles	unknown	*I. ricinus* *I. frontalis* *I. lividus* *I.arboricola*	none	NR	Pietzsch et al., 2008
	Norway	33 species	*I.ricinus*	*Babesia venatorum* (EU1)	European robin; greenish warbler bluethroat; dunnock	Hasle et al., 2011b
	Norway	unknown	*I.ricinus*	*B. afzelii* *B. garinii* *B. turdi* *B. valaisiana*	blackbirds, song thrushes; redwings	Hasle et al., 2011a
	Latvia	9 species of passerines	*Ixodes* spp.	*B. valaisiana* *B. garinii* *A. phagocytophilum* *R. helvetica* *B. divergens* *B. microti* *B. venatorum*	NR	Capligina et al., 2014
	England	194 birds	*Ixodes lividus*	*Rickettsia* sp. IXLI1	NR	Graham et al., 2010
	Sweden	unknown	*I. ricinus* *I. lividus* *Ixodes* spp.	*R. helvetica* *R. monacensis* *Rickettsia* sp.	NR	Elfving et al., 2010
Eastern Europe	Slovakia	16 species	*I.ricinus*	*Rickettsia* spp. (closely related *Ehrlichia*-like species "Schotti	NR	Špitalská et al., 2006

				variant”)		
	Slovakia and Czeck Rep.	40 species	*I.ricinus*	Spirochetes	NR	Tamara et al., 2008
				Borrelia garinii *B. valaisiana* *B. afzelii* *B. burgdorferi* (s.s.)	NR	Dubská et al. , 2009
	Czech Republic	20 species of passerines	*I. arboricola* *I. ricinus* *H. concinna*	*Rickettsia helvetica* *Rickettsia* spp. *A. phagocytophilum* *B. burgdorferi* (s.l.) *B. garinii* B. valaisiana	NR	Špitalská et al., 2011
		forest passerine birds	*I. ricinus*	*Borrelia burgdorferi* (s.l.) *Borrelia garinii* *B. valaisiana* *Borrelia* spp. *B. burgdorferi* (s.s.).	NR	Michalik et al., 2008
	Hungary	unknown	*H. concinna*	-	NR	Hornok et al., 2013
			I. ricinus	*Rickettsia monacensis* *Borrelia burgdorferi* (s.l.) *A.phagocytophilum* Novel *Francisella*-like	NR	
			H. marginatum	*Rickettsia aeschlimannii*	NR	
			I. ricinus	*Borrelia burgdorferi* (s.l.)		Movila et al., 2008
			I. lividus	*Borrelia burgdorferi* (s.s.)		
	Western Siberia, Russia	unknown	*Ixodes pavlovskyi*, *Ixodes persulcatus* *Ixodes plumbeus*	Tick borne encephalitis virus (TBV)		Mikryukova et al. (2014
	North-Western Russia	8 species	*I. ricinus*	*Babesia* spp. *Babesia* spp. EU1. SFG rickettsiae *R. helvetica* *R. monacensis* *R. japonica* *Rickettsia helvetica*	NR	Movila et al. (2011)
	Hungary	16 species	*I. ricinus*	*R. helvetica,* *R. monacensis,* *A. phagocytophilum*.	NR	Hornok et al., 2014
			H. concinna	*R. helvetica*		

Southern Europe	Spain	unknown	*I.ricinus*	*Anaplasma phagocytophilum* *Borrelia valaisiana* *Rickettsia monacensis, R. helvetica, Rickettsia sibirica sibirica,* *Rickettsia spp.*	NR	Palomar et al., 2012
			H. punctata	*B. garinii*		
			I. frontalis,	*Borrelia turdi*		
			Ixodes spp.	*Borrelia valaisiana*		
			I.arboricola	*Candidatus Rickettsia vini*		
	Cyprus	51 Cyprian bird species	*Ixodes ventalloi*	*Rickettsia* spp. and *C. burnetii*	NR	Ioannou et al., 2009
	Capri and Antikythira	unknown	*H. marginatum,* *Hyalomma rufipes,* *I. frontalis* *Haemaphysalis* spp.	*R. aeschlimannii* *Rickettsia* spp.	NR	Wallménius et al., 2014
			H. marginatum	*Rickettsia africae*		
	Spain	23 families	*I. frontalis*	*C. burnetii*	Eurasian griffon and one black kite	Astobiza et al., 2011
Western Europe	Switzerland	4,500 birds	*I. ricinus*	TBEV *A.phagocytophilum,* *Borrelia spp.,* *Rickettsia spp.* *Candidatus N. mikurensis*	NR	Lommano et al., 2014
	France	unknown	*Rhipicephalus sanguineus* group *Haemaphysalis* spp.	*Rickettsia massiliae* *R. aeschlimannii* *B. valaisiana*	NR	Socolovschi et al., 2012