



Arthropods and associated arthropod-borne diseases transmitted by migrating birds. 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. The spread of deleterious organisms via trade routes and human travelling is relatively closely controlled, though represents only one possible means of parasite/pathogen distribution. The transmission 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 ectoparasites 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. Data available from the literature are provided highlighting the need to understand better dissemination paths and disease epidemiology.

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1. 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. Geographic spread of ectoparasites and pathogens poses a constant risk to animal health and welfare, particularly due to the climate change and the expanded human travels/trades. Whereas spread via natural parasite/pathogen movement between geographic locales may be limited by the relative inability of many ectoparasites and pathogens to actively migrate, passive movement over long distances may still occur via migratory hosts. The remainder of this review presents work from selected studies that support potentially significant movement of these organisms via migratory birds.

2. Birds as hosts for ectoparasites and associated pathogens

In domesticated settings, bird health and welfare is often threatened by ectoparasitic 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

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servicing 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.

3. 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 common blackbird was an important host for nymphs and larvae of *I. ricinus*, and nymphs of *I. frontalis*, whereas *I. frontalis* larvae were more associated with the European robin. This suggests that ticks might switch hosts

between stages and, consequently, 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). In this view, a good example for the potential of ticks to travel long distances via migratory birds is given by *Hyalomma* ticks which were recorded as being transferred between regions by migrating birds in the 1960's (Hoogstraal et al., 1961, 1963) and strongly 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 and summarized in the Table 1.

3.1. 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 Jomfrulund 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

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