

Dissemination of spotted Fever rickettsia agents in Europe by migrating birds

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Migratory birds are known to play a role as long-distance vectors for many microorganisms. To investigate whether this is true of rickettsial agents as well, we characterized tick infestation and gathered ticks from 13,260 migratory passerine birds in Sweden. A total of 1127 *Ixodes* spp. ticks were removed from these birds and the extracted DNA from 957 of them was available for analyses. The DNA was assayed for detection of *Rickettsia* spp. using real-time PCR, followed by DNA sequencing for species identification. *Rickettsia* spp. organisms were detected in 108 (11.3%) of the ticks. *Rickettsia helvetica*, a spotted fever rickettsia associated with human infections, was predominant among the PCR-positive samples. In 9 (0.8%) of the ticks, the partial sequences of 17kDa and *ompB* genes showed the greatest similarity to *Rickettsia monacensis*, an etiologic agent of Mediterranean spotted fever-like illness, previously described in southern Europe as well as to the *Rickettsia* sp. IrITA3 strain. For 15 (1.4%) of the ticks, the 17kDa, *ompB*, *gltA* and *ompA* genes showed the greatest similarity to *Rickettsia* spp. strain Davousti, *Rickettsia japonica* and *Rickettsia heilongjiangensis*, all closely phylogenetically related, the former previously found in *Amblyomma tholloni* ticks in Africa and previously not detected in *Ixodes* spp. ticks. The infestation prevalence of ticks infected with rickettsial organisms was four times higher among ground foraging birds than among other bird species, but the two groups were equally competent in transmitting *Rickettsia* species. The birds did not seem to serve as reservoir hosts for *Rickettsia* spp., but in one case it seems likely that the bird was rickettsiemic and that the ticks had acquired the bacteria from the blood of the bird. In conclusion, migratory passerine birds host epidemiologically important vector ticks and *Rickettsia* species and contribute to the geographic distribution of spotted fever rickettsial agents and their diseases.

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Rickettsial infections have been reported to represent the third most common vector-borne disease acquired during international travel (O'Brien et al. 2001). In North-Eastern Europe, local rickettsial infections caused by *R. helvetica* are also emerging and strictly correspond to the distribution range of *Ixodes ricinus*, its main tick vector in this region (Parola et al. 2005). While tick vectors are well identified for many Rickettsial agents, little information is available on natural vertebrate reservoirs and the existence of a "sylvatic" cycle. The present paper aims to elucidate the role of migratory birds in the epidemiology of *Rickettsia* spp. in Sweden through indirect examination in ticks infesting birds. Mean prevalence of infections in *Ixodes* ticks (11.3%) is similar to those classically reported in Europe (Nijhof et al. 2007). The results provide several evidences suggesting that birds may play an important role as disseminators of *Rickettsia* spp. infected tick vectors but not as competent reservoirs for *Rickettsia* spp. They confirm a previous survey published in 2006 by Santos-Silva from wild birds in Portugal. To better precise bird-pathogen interactions, it would have been interesting to have direct information on bird status instead of predictions based on tick status. However, experimental trials on captive birds seem too difficult and not representative of epidemiological processes in the nature. In addition, there was not any standardized and sufficiently sensitive PCR detection method to directly detect and identify *Rickettsia* spp. from wild birds or any other vertebrate host until recently (Boretti et al. 2009).

References:

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