

Ehrlichia-Infected Ticks on Migrating Birds

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During the spring of 1996, an estimated 581,395 *Ehrlichia*-infected ticks were imported into Sweden by migrating birds. *Ehrlichia* gene sequences found in ticks collected from these migrating birds were identical to those of granulocytic ehrlichiosis found in domestic animals and humans in Sweden. These findings support the idea that birds may play a role in dispersing *Ehrlichia*.

The genus *Ehrlichia* contains several species of intracellular bacteria capable of causing clinical disease in humans and animals. Ehrlichiosis caused by *Ehrlichia* of the *Ehrlichia phagocytophila* genogroup has been diagnosed in horses, dogs, and cats in Sweden, as well as in cattle and sheep (1). Cases of ehrlichiosis have been reported among humans in Scandinavia (2), and in Sweden, *Ehrlichia* have been detected in the tick *Ixodes ricinus*(3).

A common behavior of migrating birds is to feed and rest at stopover sites along their routes (4,5). At these sites, ticks and other ectoparasites may attach, and later detach along the migration route or in breeding areas. New foci of tick-borne diseases can be established in this way (6,7). Several investigations in Europe and the Middle East have examined the role of birds as carriers of ticks infected with tick-associated arboviruses and the Lyme borreliosis agent, *Borrelia burgdorferi* sensu lato (7). However, the involvement of birds in the ecology and epidemiology of ehrlichiosis has not yet been studied.

The Study

Our investigation was designed to determine the frequency of *Ehrlichia*-infected ticks on migrating birds in Sweden and estimate the number of *Ehrlichia*-infected ticks being imported and exported by these birds. Ticks were collected from migratory passerine birds at a stopover site in southern Sweden (east coast of Öland), identified, and checked for the presence of *Ehrlichia* by polymerase chain reaction (PCR). To determine if different genomic species of *Ehrlichia* could be found in bird-borne ticks and indirectly in the birds, all *Ehrlichia*-positive PCR products were further subjected to DNA sequencing analysis.

A total of 3,054 birds (1,204 in the spring and 1,850 in the fall) of 56 species were caught and examined for ticks. One hundred sixty-five ticks, all *I. ricinus*, were collected from 73 birds of 18 species (Table), for a tick infestation frequency of 2.4% (73/3,054) and a relative density of 0.054 ticks per bird (165/3,054). Fifty-one larvae, 112 nymphs, and 2 adult females of *I. ricinus* were found (Table), suggesting

that nymphs are more common than larvae on birds and that adult *I. ricinus* rarely feed on birds.

Ehrlichia DNA was detected in none of the 51 larvae, in 8.0% (9/112) of the nymphs, and in none of the adult ticks. *Ehrlichia* DNA was detected in 8.9% (7/79) of the nymphs in the spring and 6.1% (2/33) in autumn.

Ehrlichia 16SrRNA gene sequences in the nine positive nymphs were analyzed by DNA sequencing. The gene sequences (base positions 20-570 corresponding to base numbering for the U.S. human granulocytic ehrlichiosis (HGE) agent 16S rDNA; GenBank Accession Number U02521) were identical to *E. phagocytophila* genogroup sequences found in clinical cases of granulocytic ehrlichiosis in horses, dogs, cats, and humans in Sweden (1).

Conclusions

Every spring, approximately 100 million birds migrate through Sweden, importing large numbers of potentially infectious ectoparasites. If the frequency of infected ticks is assumed to be similar to that in this study (7 *Ehrlichia*-infected ticks on 1,204 birds), 581,395 *Ehrlichia*-infected ticks were imported into Sweden by birds during the spring migration of 1996. The bird species we found carrying *Ehrlichia*-infected ticks (Table) breed in Fennoscandia and arrived from wintering grounds in continental Europe, North Africa, and sub-Saharan Africa. During the fall migration, the frequency was lower (2 *Ehrlichia*-infected ticks found on 1,850 birds). However, even if the same number of birds migrated in the fall as in the spring, an estimated 108,108 *Ehrlichia*-infected ticks were exported from Sweden that fall by the birds. These figures support previous studies indicating that migratory birds are an important component in the dispersal of ticks infected with medically important pathogens (8).

Only one species of tick (*I. ricinus*) was recorded in this study. This species is the main vector of *B. burgdorferi* sensu lato, *E. phagocytophila*, and tick-borne encephalitis virus, both in Sweden and the rest of western and central Europe. The facts that a large number of birds are infested with this tick and that the *Ehrlichia* 16S rRNA gene sequences found in these ticks are identical to the gene sequences found in HGE patients in Sweden, Slovenia, and the USA suggest that birds may play an important role in the dispersal of *I. ricinus* infected with *Ehrlichia* and may contribute to the distribution of granulocytic ehrlichiosis (9). We found no *I.*

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Dispatches

Table. Migrating birds carrying *Ixodes ricinus* ticks and the frequency of infection with *Ehrlichia* sp. in bird-borne ticks, Sweden, 1996

Bird species ^a	No. of birds infested/ no. examined (%)	No. of ticks	<i>Ehrlichia</i> DNA detected by PCR of ticks examined		
			Larvae	Nymphs	Adults
Starling (<i>Sturnus vulgaris</i>)	1/10 (10)	1			0/1
Dunnock (<i>Prunella modularis</i>)	1/33 (3)	1		0/1	
Reed Warbler (<i>Acrocephalus scirpaceus</i>)	1/5 (20)	1		0/1	
Icterine Warbler (<i>Hippolais icterina</i>)	1/12 (8)	1	0/1		
Garden Warbler (<i>Sylvia borin</i>)	2/79 (2.5)	2	0/1	0/1	
Blackcap (<i>S. atricapilla</i>)	3/26 (11.5)	3	0/1	1/2	
Whitethroat (<i>S. communis</i>)	1/29 (3.4)	1	0/1		
Greenish Warbler (<i>Phylloscopus trochiloides</i>)	1/1 (100)	1	0/1		
Willow Warbler (<i>P. trochilus</i>)	3/1,025 (2.9)	4	0/4		
Goldcrest (<i>Regulus regulus</i>)	1/892 (0.1)	1		0/1	
Pied Flycatcher (<i>Ficedula hypoleuca</i>)	1/22 (4.5)	1		0/1	
Collared Flycatcher (<i>F. albicollis</i>)	1/2 (50)	1		0/1	
Redstart (<i>Phoenicurus phoenicurus</i>)	7/76 (9.2)	28	0/11	1/17	
Robin (<i>Erithacus rubecula</i>)	33/655 (5)	54	0/14	3/40 ^b	
Thrush Nightingale (<i>Luscinia luscinia</i>)	5/27 (18.5)	22	0/8	2/14	
Blackbird (<i>Turdus merula</i>)	5/41 (12.2)	27	0/7	1/19 ^c	0/1
Song Thrush (<i>T. philomelus</i>)	4/24 (16.7)	14	0/2	1/12	
Bullfinch (<i>Pyrrhula pyrrhula</i>)	2/27 (7.4)	2		0/2	
Total	73/2,986 (2.4)	165	0/51	9/112	0/2

^aBird species sampled that did not carry ticks are not listed.

^bOne of these infected ticks was collected in the autumn.

^cThis infected tick was collected in the autumn.

ricinus larvae infected with *Ehrlichia*, which may suggest that birds are incompetent reservoirs of *Ehrlichia* but act as carriers of infected ticks. In this way, avian transport of *Ehrlichia* might differ from that of *B. burgdorferi* sensu lato. In the latter disease, birds not only carry infected ticks of all stages but can also carry latent infections of *Borrelia* that can be reactivated by the stress of migration (10). However, the potential of a vertebrate to function as a tick host and a reservoir for *Ehrlichia* depends on many factors, including the host's density in the tick habitat, the degree of contact between the potential tick vector and the host, and its infectivity. Therefore, the question of whether birds act as reservoirs of *Ehrlichia* has not yet been conclusively answered, and additional studies of various bird host species should be conducted over longer time spans than our study. Moreover, the reservoir competence of birds should be studied by isolation or detection of *Ehrlichia* after natural or experimental infection.

The apparent increase of granulocytic ehrlichiosis in animals and humans during the last few decades may be the result of several factors, such as increased awareness of this disease and the distribution of reservoirs, vectors, and host animals. Whether passerine birds have affected this increase has not yet been conclusively demonstrated. However, our data suggest that birds are important in the dispersal of *Ehrlichia*.

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