

# Birds as disseminators of ixodid ticks and tick-borne pathogens: note on the relevance to migratory routes

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**Összefoglalás** A madarak gyakran kullancsfertőzöttek, így szerepük – különösen vonulásuk során – a kullancs közvetítette kórokozók terjesztésében és az ezek által okozott betegségek járványtanában régóta ismert és kutatott terület. A hazánkban végzett első ilyen molekuláris epidemiológiai felmérés kapcsán azonban érdemes kitérni az ilyen és hasonló vizsgálatok egy új, ornitológiai jelentőségű aspektusára. A közép- és hosszútávú vonuló madarokról eltávolított kullancsok és a bennük található kórokozók molekuláris szintű azonosítása (azaz egyes génjeik nukleotid sorrendjének meghatározása) lehetőséget nyújt azok nemzetközi (génbanki adatokkal való) összehasonlítására. Ez alapján valószínűsíthető lehet a kullancsral való fertőződés hozzávetőleges helyét, tehát a vonulás hozzávetőleges útvonalát is.

Kulcsszavak: madárvonulás, *Hyalomma*, *Rickettsia*, *Francisella*, szekvenálás

**Abstract** It has been a long studied issue, that birds are frequently infested with ixodid ticks, and consequently play a significant role in disseminating tick-borne pathogens (especially during their seasonal migration) and influence the epidemiology of relevant diseases. In connection with the first Hungarian molecular epidemiological survey on this topic the authors would like to note, that a new, ornithological aspect of similar researches may deserve future attention. Ticks removed from mid- and long-distance migratory birds and the tick-borne pathogens they may contain can be molecularly identified (i.e. with sequencing certain genes), and their sequences could be compared with others internationally available (deposited in the GenBank). This may provide clues for determining the place or country where the bird most likely acquired its tick-infestation, and thus for the probable route of seasonal migration.

Keywords: bird migration, *Hyalomma*, *Rickettsia*, *Francisella*, sequencing

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Birds are the most mobile animals taking into account the large distance they can cover in the course of a few days, particularly during their seasonal migration. Additionally, birds are long known for their epidemiological role as carriers of ticks (Hoogstraal *et al.* 1963), implying that ticks attached to them – as well as the tick-borne pathogens – can also be transported by them to places far away from the original habitats. This is a well studied issue from the point of view of ticks and tick-borne pathogens. However, in most (if not all) of the reports concerned about the import of exotic tick species and tick-borne pathogens by birds into regions formerly exempt of them focus on epidemiological implications. Therefore in this note the authors would like to highlight that some findings in the first molecular study on ticks and tick-borne pathogens associated with migratory birds in Hungary (Hornok *et al.* 2013) show that tracking the possible geographical origin of DNA sequences from ticks or tick-borne pathogens carried by birds may be relevant to their migratory routes (and *vica versa*).

Ticks (Acari: Ixodidae) were removed from birds mist-netted at the Ócsa Bird Ringing Station in 2011. From 1.786 birds caught in the spring 108 subadult ticks were collected (Hornok *et al.* 2013). The majority (96.3%) of them was *Ixodes ricinus*, but three *Hyalomma* immatures (two moulting larvae and one nymph) were also collected from a Robin (*Erithacus rubecula*). Molecular analysis of these revealed 100% sequence homology only to an isolate of *H. marginatum* from Morocco (accession number AF150034 for the 12S rRNA gene).

This tick species occurs in most of the Mediterranean basin and is not indigenous in Hungary, thus the infestation probably originated from the Mediterranean. Robins ringed

in Hungary have mostly been recaptured while wintering in south-western Europe, some of them have even crossed the Mediterranean to winter along the northern shores of Algeria (Gyurácz & Csörgő 2009). Although until now recaptures of Robins did not link Morocco to Hungary, the present data may indicate that the relevant bird arrived from the region of Morocco (*Figure 1*).

*Hyalomma marginatum* is a two-host tick (i.e. its larva moults to the nymph stage without detachment from the host) and therefore the immature stages remain for a prolonged period (12–26 days) on the host (Farkas *et al.* 2013). The average migration speed of Robins is 65 km/day, however, this may show considerable daily variations; some birds may fly even hundreds of kilometers daily (Remisiewicz *et al.* 1997). This means that ticks carried by them (or by similar mid-distance or even long distance migrants) may arrive from 2–3.000 kilometers away.

Although we can not exclude that the Moroccan genotype of *H. marginatum* can be found in other parts of the Mediterranean basin in Europe, the possible African origin of these ticks is supported by yet another finding. In all three specimens of these ticks *Rickettsia aeschlimannii* was identified, also for the first time in Hungary (Hornok *et al.* 2013). This bacterial pathogen is responsible for spotted fever in humans and is endemic to the Mediterranean countries. This *Rickettsia* genotype showed 100% sequence similarity to an isolate from Egypt (HQ335153). Considering that Hungarian Robins overwinter in the Western Mediterranean prompts the question whether this genotype may also occur in North-Western Africa.

Additionally, from an *I. ricinus* larva also obtained from a Robin the sequence of a

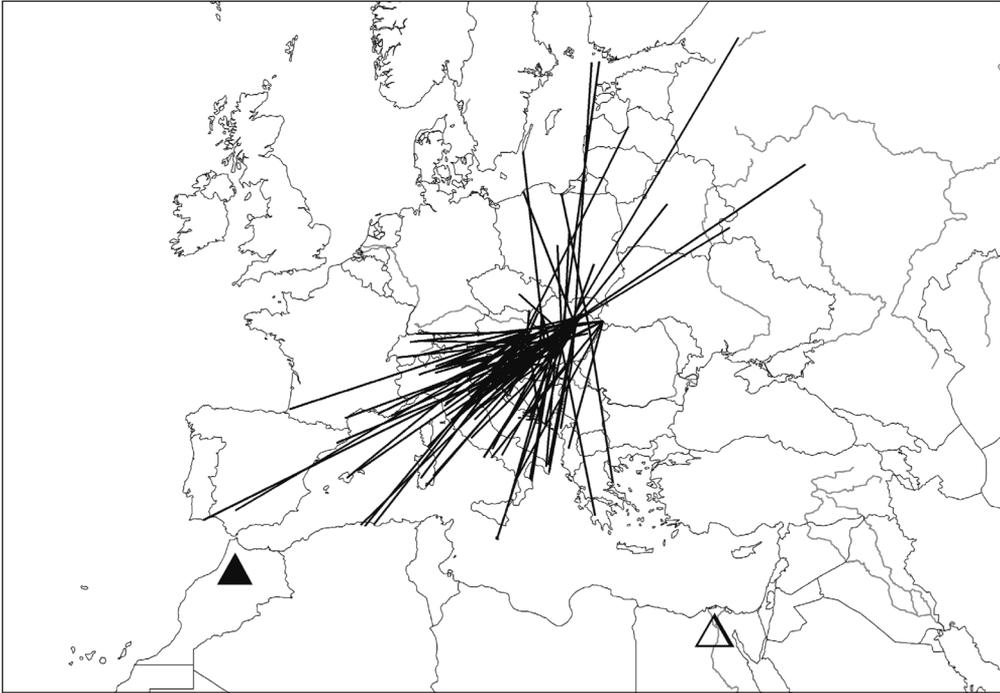


Figure 1. Recaptures of Robins ringed in Hungary.

Triangles show the likely origin of *H. marginatum* ticks collected from a Robin in 2011 in Hungary (▲) and the likely origin of *Rickettsia aeschlimannii* carried by these ticks (△) as judged by comparisons of genetic sequences

1. ábra A magyarországi vonatkozású vörösbegy visszafogások eloszlása.

Egy hazai vörösbegyőről 2011-ben gyűjtött *H. marginatum* kullancsokhoz (▲) és az általuk hordozott *Rickettsia aeschlimannii* (△) baktériumokhoz genetikailag hasonló kullancsok, illetve baktériumok ismert előfordulása a Mediterráneumban

novel *Francisella*-like genotype was identified (Hornok *et al.* 2013). This endosymbiont is taxonomically close to the causative agent of tularemia in mammals. The new genotype showed the closest (99%) similarity to endosymbionts detected in *Derma-centor reticulatus* in Central-Europe. Accordingly, although the geographical range of *I. ricinus* extends to southern Europe, the relevant tick most likely attached to its avian host in Central-Europe shortly before capturing.

In conclusion, bird ticks and associated pathogens may be used as tracers (indica-

tors) of migratory routes because their molecular analysis provides a basis for genetic comparison with internationally available data. However, the unfolding of this new approach to track bird migration depends on and necessitates the availability of target sequences from many or most countries of possible places of departure/destination.

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