Ecology of infections and host-parasite interactions

- Population ecology of hosts and host-parasite interactions can explain spatial and temporal variation in the presence of an infection.

- Strong focus on microparasitic infections (viruses, bacteria) and mammals

- Some of them cause disease in humans (hantavirus disease, plague, arenaviruses,...)

\[
\begin{align*}
\frac{dS}{dt} &= b(S + I_n + I_c) - (m + k(S + I_n + I_c)) S \\
&\quad - \left( \beta_n I_n + \frac{\beta_c I_c}{P} \right) S - \varepsilon G S, \\
\frac{dI_n}{dt} &= \left( \beta_n I_n + \frac{\beta_c I_c}{P} \right) S + \varepsilon G S - \tau I_n \\
&\quad - (m + k(S + I_n + I_c)) I_n, \\
\frac{dI_c}{dt} &= \tau I_n - (m + k(S + I_n + I_c)) I_c.
\end{align*}
\]
Ecology of infections and host-parasite interactions

More recently: arthropod ectoparasites (as vectors, or as parasites in their own right) in songbirds.

Prof. E. Matthysen

Dr. D. Heylen
The role of birds and bird ticks in transmission of *Borrelia*: a community perspective

**Dieter Heylen¹, Hein Sprong² & Erik Matthysen¹**
Ixodidae – ‘hard ticks’

- Belgium > 15 species
- Vectors of many pathogens (TBE, rickettsiosis, LYME, ...)

- huge differences in habitat requirements and host specificity
*Ixodes* infestations of songbirds in Belgium

- **I. lividus**
  - bank swallow
  - nidicolous

- **I. arboricola**
  - hole-breeders
  - nidicolous

- **I. frontalis**
  - hole-breeders
  - open nesting
  - nonnidicolous

- **I. ricinus**
  - extreme generalist
  - nonnidicolous
Transmission dynamics of *Borrelia* bacteria in a bird tick community

*Ixodes ricinus*

Bird specific ticks
**Borrelia in bird-derived I. ricinus larvae (literature)**

Bird (# larvae screened; # birds; # studies)

- *Fringilla coelebs* (510; 148; 10)
- *Parus major* (413; 322; 17)
- *Troglodytes troglodytes* (248; 86; 11)
- *Turdus philomelos* (563; 262; 14)
- *Turdus merula* (1194; 473; 17)
- *Anthus trivialis* (299; 185; 4)

Prevalence in tested *Ixodes ricinus* larvae
**Borrelia in ticks from hole-breeding songbirds (own data)**

<table>
<thead>
<tr>
<th></th>
<th><em>I. ricinus</em></th>
<th><em>I. arboricola</em></th>
<th><em>I. frontalis</em></th>
</tr>
</thead>
<tbody>
<tr>
<td><em>B. turdi-like</em></td>
<td>0 (0 %)</td>
<td>0 (0 %)</td>
<td>5 (55.56 %)</td>
</tr>
<tr>
<td><em>B. afzelii</em></td>
<td>5 (10 %)</td>
<td>2 (18.18 %)</td>
<td>1 (11.11 %)</td>
</tr>
<tr>
<td><em>B. garinii</em></td>
<td>36 (72 %)</td>
<td>7 (63.64 %)</td>
<td>3 (33.33 %)</td>
</tr>
<tr>
<td><em>B. garinii bavariensis</em></td>
<td>1 (2 %)</td>
<td>0 (0 %)</td>
<td>0 (0 %)</td>
</tr>
<tr>
<td><em>B. sensu stricto</em></td>
<td>3 (6 %)</td>
<td>0 (0 %)</td>
<td>0 (0 %)</td>
</tr>
<tr>
<td><em>B. spielmanii</em></td>
<td>2 (4 %)</td>
<td>1 (9.09 %)</td>
<td>0 (0 %)</td>
</tr>
<tr>
<td><em>B. valaisiana</em></td>
<td>3 (6 %)</td>
<td>1 (9.09 %)</td>
<td>0 (0 %)</td>
</tr>
</tbody>
</table>

*Prevalence of Borrelia genospecies (above) and Venn diagrams of genotypes (below) found in three Ixodes tick species.*

**Borrelia** in ticks from hole-breeding songbirds (own data)

<table>
<thead>
<tr>
<th>Genospecies</th>
<th>I. ricinus</th>
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<th>I. frontalis</th>
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<tr>
<td>B. turdi-like</td>
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</tbody>
</table>

**VECTOR?**

Or just **CARRIER?**

Prevalence of *Borrelia* genospecies (above) and Venn diagrams of genotypes (below) found in three *Ixodes* tick species.

Vector competence bird-specific ticks

full ‘Koch’s postulates’ approach

**Phase 1: ISOLATE pathogen x vector**

I. arbo./front. larvae  |  Phase 1 (b)

**Phase 2: Expose naïve hosts**

I. ricin. larvae  |  Phase 2 (b)

Overview outcomes and conclusions

<table>
<thead>
<tr>
<th></th>
<th><em>I. ricinus</em></th>
<th><em>I. frontalis</em></th>
<th><em>I. arboricola</em></th>
</tr>
</thead>
<tbody>
<tr>
<td><em>B. garinii</em></td>
<td>V</td>
<td>C</td>
<td>C</td>
</tr>
<tr>
<td><em>B. valaisiana</em></td>
<td>V</td>
<td>C</td>
<td>C</td>
</tr>
<tr>
<td><em>B. turdi</em></td>
<td>V</td>
<td>V</td>
<td>I</td>
</tr>
<tr>
<td><em>B. burgdorferi s.s.</em></td>
<td>C*</td>
<td>C</td>
<td>?</td>
</tr>
</tbody>
</table>


- *B. garinii* cycles are **not** maintained by bird-specialized ticks (*I. arboricola* and *frontalis*), although they may carry the bacteria.

- Strong association between *Borrelia turdi* (*recently discovered in Europe*) and *I. frontalis*.

- *I. ricinus* could potentially act as a bridging vector for *Borrelia turdi*, but so far *B. turdi* has not been found in questing *I. ricinus*. 
The role of birds and bird ticks in transmission of *Borrelia*: a community perspective

Dieter Heylen¹, Hein Sprong² & Erik Matthyssen¹

¹ Department of Biology, University of Antwerp, Antwerp, Belgium
² National Institute of Public Health and Environment (RIVM), Bilthoven, The Netherlands

Introduction and general methods

Most human cases of Lyme borreliosis are transmitted by nymphs of the sheep tick *Ixodes ricinus*, a species with a broad host spectrum including humans, mammals, birds, and even reptiles. Some of these hosts are infected by other more specialized ticks capable of vectoring *Borrelia* bacteria. This capacity of vectoring *Borrelia* bacteria is mostly unknown. *Borrelia* shape is a complex organism of many genotypes, each with their own host specificity and immune systems. The complexity of the vectoring process and the immune response against the bacteria may act as a ‘bridge’ between different zoological cycles of *Borrelia*. Here we summarize recent findings on the prevalence of ticks and *Borrelia* in common birds. We also report on experimental data on the vector competence of bird-specialized ticks for *Borrelia* transmission.

Tick prevalence

Ticks were collected throughout the year from birds captured in two wooded areas: Reventure (Strassen) and Rozewie (Samborow). We found two species with strong differences in occurrence, seasonality, and host specificity. Below we report on their prevalence and summarize the ecology (GT = great tit, BT = blue tit).

*Zeus sanguineus* (sheep tick) (21% GT, 4% BT): generalist tick feeding on small and large vegetation, feeding on diverse animals; birds are infected by leaves and nymphs from spring to autumn.

*Zeus arboreus* (3% GT, 3% BT): highly specialized bird tick, feeds only on host-seeking ticks in all stages (mostly great tit and blue tit), found in nest-boxes and feeding on birds year-round.

*Zeus dorsalis* (2% GT, 1% BT): generalist bird tick, feeds on diverse bird species including great tits and blackbirds, weekly看见 known, found on birds year-round.

Borrelia prevalence

Overall, 20% and 17% of ticks collected from great and blue tits, respectively, were positive for *Borrelia*. *Borrelia* genotypes were identified by sequencing of the variable 55-255 (159-158) in IgG-specific region (205). As expected the ticks carried mostly *B. garinii*, known to be associated with birds, but also *B. afzelii* and *B. spielmanii*. Moreover, eight genotypes were shared between *I. ricinus* and the bird-specific ticks (Fig. 1).

Experiments on vector competence

We tested whether ticks are competent vectors, i.e. are able to carry and transmit *Borrelia* to new hosts. First, infected ticks were obtained by letting them feed on wild birds (great tits or blackbirds) from areas with endemic *Borrelia*. These ticks were then fed on uninfected young birds. We tested whether these birds were infected by *Borrelia*, e.g. exposing the birds to *Borrelia*-infected I. ricinus larvae, and screening these for presence of *Borrelia* (results are summarized below). While *I. ricinus* can vector most *Borrelia* genotypes, bird-specific ticks can carry but usually not transmit *Borrelia* with the exception of *I. dorsalis* and *I. turbellaris*.

CONCLUSIONS

Common songbirds are regularly infected with three different tick species, each with their own ecology and each carrying multiple *Borrelia* genotypes. We previously established that great tits are competent reservoirs for *Borrelia*, and can selectively amplify genotypes known to be human Lyme disease agents (*B. garinii*, *B. afzelii*). Further experiments show that cycles of these bacteria are not maintained by bird-specialized ticks, although they may carry the bacteria. A notable finding is the strong association between *Borrelia turbellaris* and J. montanum. This genospecies has only recently been discovered in Europe and its pathogenicity is unknown. Our results suggest that *I. ricinus* could potentially act as a bridging vector for this genospecies, but so far *B. spielmanii* has not been found in questing *I. rudius*.

Further reading:

Heylen et al., 2013, 2014a, 2014b, Environmental Microbiology

Department of Biology
Evolutionary Ecology Group
Universiteit Antwerpen
Genospecies level:

- Infection of host tissue by avian genospecies (B. garinii and B. valaisiana)
- Co-feeding transmission observed in B. garinii and B. afzelii
- Mammalian genospecies survived the exposure to bird blood (!)
- Trans-stadial transmission in all listed Borrelia genospecies