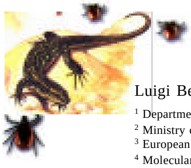

Dynamics of Borrelia burgdorferi sensu lato transmission between ticks and two different hosts: basic reproductive number estimation, in an Italian Natural Reserve

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Introduction

Lyme borreliosis (LB) is an emerging tick-borne zoonosis caused by spirochetes in the *Borrelia burgdorferi* sensu lato (s.l.) complex. In Europe, its transmission cycle involves *Ixodes ricinus* ticks as vectors and a wide variety of reservoir hosts species. Not all vertebrates are competent reservoirs for *B. burgdorferi* s.l., whose genospecies are associated with peculiar host species.

LB can be studied with mathematical models: basic reproduction number (R_0) permits to analyze pathogens maintenance conditions.

LB transmission dynamics was investigated in a 500-ha enclosed natural reserve in Le Cerbaie Hills, Tuscany, central Italy (Figure 1).

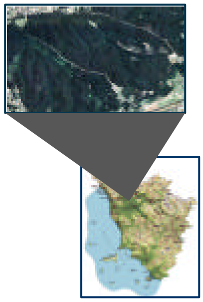

Figure 1. Study area

Our study area is characterized by:

- abundant *I. ricinus* population;
- two different *B. burgdorferi* s.l. genospecies (*B. lusitaniae* and *B. afzelii*) identified in host seeking and on-the-host *I. ricinus* ticks;
- presence of lizards (*Podarcis* spp.) and mice (*Apodemus* spp.) populations, that serve as hosts for immature ticks and are the reservoir hosts of *B. lusitaniae* and *B. afzelii* respectively (Figure 2).

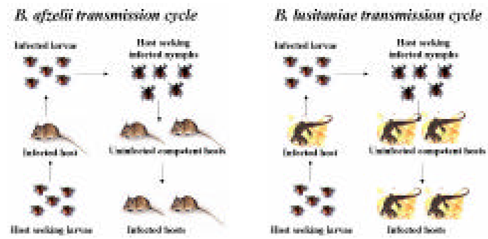

Figure 2. *B. afzelii* and *B. lusitaniae* transmission cycles

Research aims:

- to propose a formulation to qualitatively estimate R_0 for *B. lusitaniae* and *B. afzelii* in the study area, considering interactions among vectors, hosts and pathogens.
- to analyze the competition between mice and lizards to be preferential host for immature stages of *I. ricinus* ticks.
- to examine the coexistence of the two population hosts and specific factors associated to their dynamics, which affect *B. burgdorferi* s.l. R_0.
- to investigate thresholds in host abundance that determine maintenance ($R_0>1$) or extinction ($R_0<1$) of *B. afzelii*.

Model Formulation

Basic reproduction number (R_0) definitions:

1. The expected number of infected hosts when a single infected host has been inserted in a susceptible population of hosts and vectors
2. The expected number of infected vectors when a single infected vector has been inserted in a susceptible population of vectors and hosts.

Model Assumptions

- every infected nymph feeds on a different host ❸
- life span of a host is approximately the same as the cycle length of a vector ❽

According to the first R_0 definition:

$$R_0^{H?\ H} = F(L,H_c,a_{LH},D_H,t_L)\cdot b_{HL}\cdot s_N\cdot b_{LN}\cdot ?\,(N,H_c,H_{nc})\cdot b_{NH}$$

$F(L,H_c,a_{LH},D_H,t_L)$ number of susceptible larvae that feed on the infected host during the host's infectious time period

- L: number of larvae in the population of the vectors
- H_c: number of susceptible hosts
- a_{LH}: probability that a larva mounts and feeds on a host
- D_H: duration of the host infectious period, t_L: duration of the larvae feeding period

$?\,(N,H_c,H_{nc})$ proportion of competent hosts on which the infected nymphs feed

- N: expected number of nymphs on infested hosts
- H_c: competent hosts density
- H_{nc}: incompetent hosts density

b_{HL} transmission probability from an infected host to a susceptible larva
b_{NH} transmission probability from an infected nymph to a susceptible competent host
b_{LN} transmission probability for an infected larva through molting to a nymph
s_N survival probability from feeding larva to feeding nymph

$b_{HL}\,´\,b_{LN}$	0.50 for *B. lusitaniae* ❹
$b_{HL}\,´\,b_{LN}$	0.40 for *B. afzelii* ❷
b_{NH}	0.67 ❶
s_N	0.10 ❸❻❼

Model validation

Parameters influenced by habitat factors were derived from field data:

$F(L,H_c,a_{LH},D_H,t_L)$
(Expected number of larvae on the captured infested hosts) x (D_H = 122 days ❾) / (t_L = 2.5 ❸)

$?\,(N,H_c,H_{nc})$
(mean number of nymphs on captured competent infested hosts)/(number of nymphs on all hosts)
$(NH_c)\ /\ (NH_c + NH_n)$

Hosts captures

- *Apodemus* spp.: live traps set in a 9000 m² grid. Mice marked individually
- *Podarcis* spp.: captured by a noose, in the same sites of mice captures

Host Population Density

- *Apodemus* spp.: capture and recapture data (CAPTURE software, ❺)
- *Podarcis* spp.: mean number registered during observational sessions (2 grids of 200 m²/10')

Host tick infestation

- Mean number of larvae and nymphs per infested host and 95% confidence interval.
- Negative binomial distribution to take into account ticks aggregation on hosts

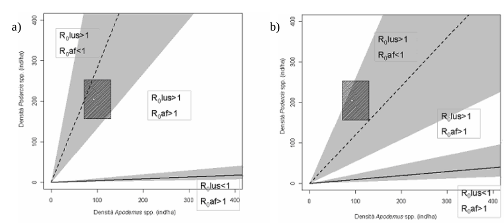

Figure 3. Estimation of the epidemic outbreak threshold (i.e. R_0 = 1) in Le Cerbaie; lus = *B. lusitaniae*, af = *B. afzelii*. a) absence of other incompetent hosts; b) presence of incompetent hosts harboring 1/2 of all feeding nymphs.

Solid line: R_0 = 1 for *B. lusitaniae*; dashed line: R_0 = 1 for *B. afzelii*
Light grey areas around the lines: range of negative binomial 95% CI of the mean nymphs infestation; area above the solid line: R_0 > 1 for *B. lusitaniae*; area beyond the dashed line: R_0 > 1 for *B. afzelii*;
White circle: mice and lizards population density estimations in the study area; dark grey rectangle: 95% CI of mice and lizards density estimations.

Results and Discussion

The model suggests a R_0 greater than 1 for *B. lusitaniae* and around the epidemic threshold for *B. afzelii* (Figure 3a):

- ✓coexistence of both spirochete genospecies in the study area, allowed by a right combination of the two host populations sizes
- ✓influence of either hosts density population or ticks infestation on *B. burgdorferi* s.l. genospecies R_0
- ✓ecological characteristics of reservoir host species (widespread and constant lizards population and its central host role for nymphs) for maintenance of *B. lusitaniae* transmission cycle
- ✓lizards abundance decreases the infection prevalence of genospecies other than *B. lusitaniae*
- ✓oscillations of *B. afzelii*'s R_0 due to mice population fluctuations and scarce nymphs infestation

Considering the presence of other hosts species, incompetent for *B. burgdorferi* s.l. (Figure 3b):

- ✓absence of an important influence on *B. lusitaniae* R_0
- ✓effect on the persistence of *B. afzelii*: R_0 results greater than one only with high mice population densities and/or low lizards abundance.

In conclusion, nymphs infestation, population density and diversity, and spirochetes host association are key factors for the maintenance of *B. burgdorferi* s.l. transmission cycle in the study area. *B. lusitaniae* and *B. afzelii* zoonotic role suggests a possible model implication for public health control.

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