

Influence of hosts migration between woodland and pasture on tick population dynamics: a modelling approach



T. Hoch, Y. Monnet, A. Agoulon



UMR 1300, Veterinary School, INRA, BP 40706, 44307 Nantes cedex 03, France Ph. +33 240 687 855; Fax +33 240 687 768; Email hoch@vet-nantes.fr

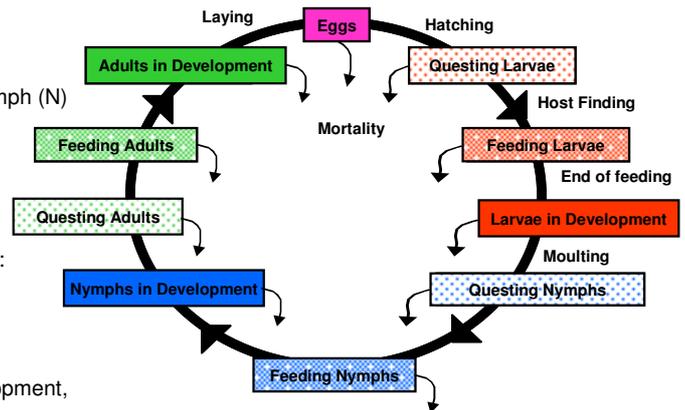
INTRODUCTION

Ticks are vectors of numerous pathogens that can affect both animals (e.g. *Babesia divergens* for cattle) or humans (*Borrelia burgdorferi*). Vector-borne diseases strongly depend on the vector population dynamics which determines the evolution of vector densities. A population dynamics model is therefore required to simulate these densities, to be further used in epidemiological models representing the spread of a pathogen. This work deals with a tick (*Ixodes ricinus*) population dynamics model. Furthermore, this model is applied to different habitats between which hosts migrate, in order to study the influence of these migrations on tick densities.

MODEL DESCRIPTION

Model structure

The model takes into account the following stages: Egg (E), Larvae (L), Nymph (N) and Adult (A). For the stages L, N and A, three phases were considered: Questing (Q), Feeding (F) and in Development (D). This model is discrete-time and deterministic.



Equations of the model

The equations governing the evolution of nymphs densities are the following:

$$N_Q(t+1) - N_Q(t) = L_{D \rightarrow Q}(t) - N_Q(t) \cdot (HF_N + \mu_{ND})$$

$$N_F(t+1) - N_F(t) = N_Q(t) \cdot HF_N - N_F(t) \cdot (\mu_{NF} + \mu_{ND})$$

$$N_D(t+1) - N_D(t) = N_F(t) \cdot \mu_{NF} - N_D(t) \cdot (\mu_{ND} + N_{D \rightarrow Q}(t))$$

$L_{D \rightarrow Q}(t)$ represents the number of larvae that have accomplished their development, $N_E(t)$ the number of engorged nymphs that come off from their host. HF is the host finding rate and μ the mortality rate.

The hosts considered are either small mammals (rodents,...) for L and N, or large mammals (deer, cattle) for L, N and A.

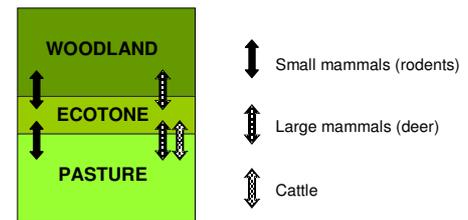
The model is applied to habitats representing a typical cattle farm (woodland, ecotone and pasture) between which the mortality rates and host densities vary.

Hosts migration between the different habitats modifies tick densities in the following way:

$$N_{Dw}(t+1) - N_{Dw}(t) = N_{Ew}(t) - N_{Dw}(t) \cdot \mu_{ND} - N_{Dw \rightarrow Ec}(t) + m_{we} \cdot (N_{Ee}(t) - N_{Ew}(t))$$

where m_{we} represents the migration rate between woodland and ecotone.

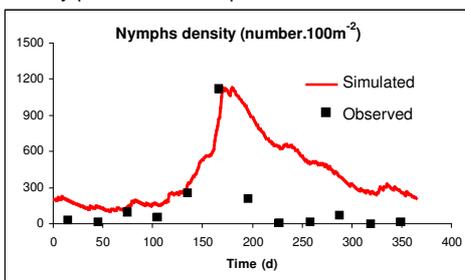
Engorged individuals coming off from bovine are distributed homogeneously between woodland and pasture.



RESULTS

Comparison with data

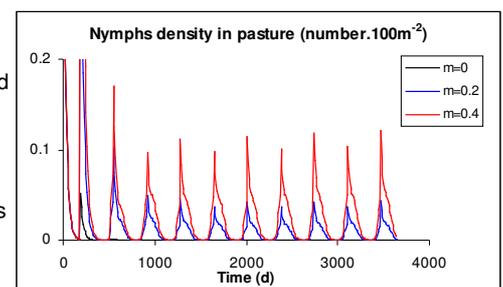
Simulated nymphs densities are compared with data from L'Hostis (1994) in a temperate area. Parameters used correspond to those applied to an ecotone, as data from this study were collected near the hedges of pastures in cattle farms. The timing and the intensity of the spring density peak are well reproduced.



Multi-habitat model

Influence of migration

Without any migration between woodland (where tick densities are high), ecotone and pastures, tick densities become extinct in pastures, on account of less favourable conditions for survival in this habitat. On the contrary, migration allows the presence of ticks in the pasture, and this effect increases with the migration rate. However, tick densities remain low.



Influence of cattle

With or without cattle, the maximal yearly tick density does not vary much in the woodland. Including cattle in the model generates a decrease in ecotone tick densities and an increase in the pasture, where densities remain low.

Maximal nymph density (number.100m⁻²)

	Woodland	Ecotone	Pasture
Without cattle	434.38	95.34	0.044
With cattle	432.38	75.91	0.082

CONCLUSIONS

This modelling study underlines the importance of hosts migration between the different habitats on pasture tick densities. Ticks densities in pasture remain however at low levels, unlike densities in ecotone. The risk of being bitten by a tick should therefore not be neglected in the intermediate zone between pasture and woodland.

This model simulates realistically the timing and the intensity of the spring peak in nymph density. It is to be coupled with an epidemiological model representing the spread of pathogen, for instance in a dairy herd infected by *B. divergens*.