Spread of Q Fever within dairy cattle herd : key parameters inferred using a Bayesian approach

Aurélie Courcoul*[1], Elisabeta Vergu[2], Jean-Baptiste Denis[2], François Beaudeau[1]

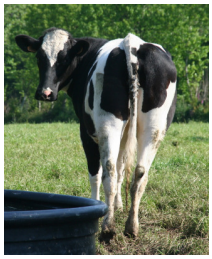
*aurelie.courcoul@oniris-nantes.fr, [1]Bioaggression, Epidemiology and Risk Analysis Research Unit, Oniris & INRA, Nantes, France
[2]Applied Mathematics and Informatics Research Unit, INRA, Jouy-en-Josas, France

Q Fever: a public health issue

Q Fever: worldwide zoonosis caused by *Coxiella burnetii*
Ruminants: main source of human infection

How does *C. burnetii* spread within cattle herds ?

- Probability of infection in a chronically infected herd?
- Frequency of intermittent shedding?
- Duration of shedding and non-shedding periods?
- Link between antibody status and shedding pattern?



Picture : A. Senkowski

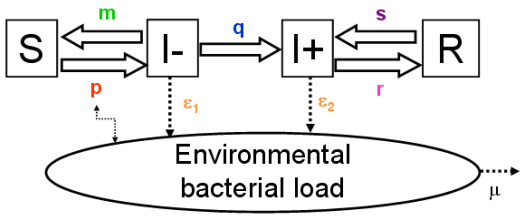
Objective: to quantify the key epidemiological parameters from field data

Modelling approach

DATA: **224 dairy cows from 5 infected herds** without clinical signs, sampled from 1 to 5 times over a one-month period

⇨ **Observed individual health states** are known for each cow at each sampling time point (**PCR** and **ELISA** tests)

EPIDEMIC MODEL:



S: non shedder without antibodies **I-:** shedder without antibodies
I+: shedder with antibodies **R:** non shedder with antibodies

Figure 1: Diagram flow describing the spread of *Coxiella burnetii* within a dairy cattle herd

Main modelling assumptions:

- ✓ **Contamination by inhalation of infected aerosols**: probability of infection *p* function of the environmental bacterial load *E*
- ✓ **Intermittence of shedding**: transitions I+ ⇔ R
- ✓ **Long-lasting antibodies:** no transition from R to S
- ✓ **Sojourn times in each state ≥ 1 week**
- ✓ **Markovian transitions**

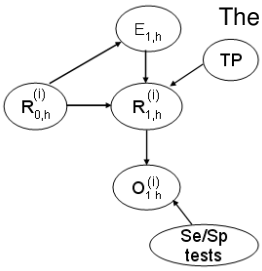
BAYESIAN FRAMEWORK:

Modelling of **individual trajectories** describing the **temporal dynamic** of **observed health states** for each cow

⇨ **Inference of transition and shedding parameters**

Picture : A. Senkowski

The **observed health state *O*** depends on:
- the **real health state *R*,**
- **Se and Sp of tests**

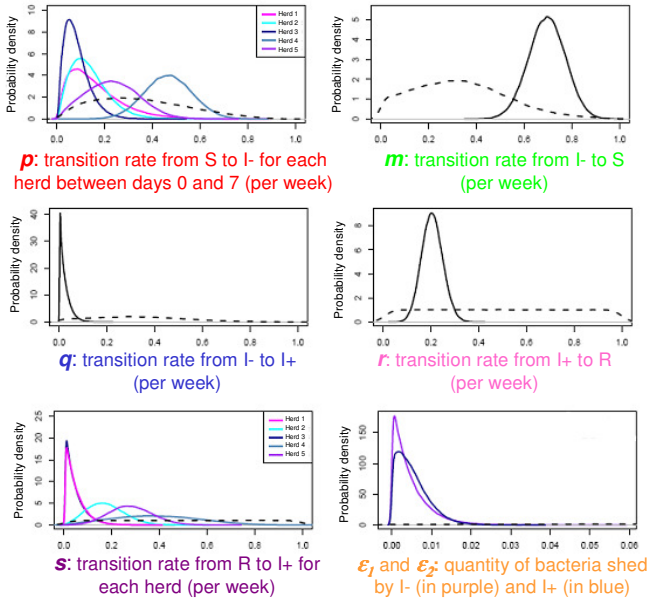


The **real health state *R* at time t** depends on:
- the **real health state *R* at time t-1,**
- the **environmental bacterial load *E* at time t**
- the **transition parameters (TP)**

Figure 2: Simplified Bayesian network for cow *i* from herd *h* at times 0 and 1

Prior distributions:
- consistent with expert knowledge for μ and initial real health states
- minimally informative priors for transition parameters and shedding parameters

Results and discussion



p: transition rate from S to I- for each herd between days 0 and 7 (per week)

m: transition rate from I- to S (per week)

q: transition rate from I- to I+ (per week)

r: transition rate from I+ to R (per week)

s: transition rate from R to I+ for each herd (per week)

ε1 and ***ε2***: quantity of bacteria shed by I- (in purple) and I+ (in blue)

Figure 3: Prior (dotted black line) and posterior (solid coloured lines) distributions of the model parameters

- ✓ Weekly **probability of infection: variable** between herds, attaining high values
- ✓ **Frequent clearance of the bacterium without seroconverting** (I- => S) but **rare seroconversions** (I- => I+)
- ✓ Frequency of **intermittent shedding** (R => I+): **variable** between herds, attaining high values
- ✓ **Shedders with antibodies (I+) shed for a longer time than shedders without antibodies (I-)**
  median time in I-: 1.4 weeks [CI 95%: 1.1-1.8]
  median time in I+: 4.9 weeks [CI 95%: 3.4-8.3]

Conclusion

This study provides the first quantitative assessment of *C. burnetii* spread within chronically infected dairy cattle herds

Perspectives:
- **use of the estimated parameter values to calibrate a simulation model**
- **assessment of the effectiveness of different infection control strategies**