

Quantifying the horizontal transmission of *Coxiella burnetii*, causative agent of Q fever, in dairy herds



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INTRODUCTION

- Q fever: a worldwide zoonosis caused by an obligate intracellular bacterium: *Coxiella burnetii* [1,2]
- Ruminants (Cattle, Sheep and Goats) are recognised as the most important source of human infection [1]
- Reliable detection of *Coxiella burnetii* infectious cows using real-time PCR technique for the different shedding routes: milk, faeces and vaginal mucus



- Need for a quantification of the horizontal transmission of *C. burnetii*, in order to:
 - evaluate and estimate the spread of the bacteria in dairy herds
 - be used further in models that allow the simulation of control measures scenario

Aim of this study:

Estimation of the horizontal transmission rate of *C. burnetii*, based on data collected over a longitudinal study

MATERIAL AND METHODS

Samples

- 280 dairy cows from 5 commercial herds, all sampled 3 months apart. At each time: concomitant sampling
 - Milk (according to NMC guideline)
 - Faeces (using sterile boxing glove)
 - Vaginal mucus (using sterile swab)
- At each time, a cow was considered as infectious when at least one sample out of the three collected was positive



The model

The transmission rate β was estimated by considering that the number of new infectious C depends on the respective numbers of Susceptible (S), Infectious (I) and total herd size (N), thanks to the following equation:

$$C(t+1) = S(t) \left(1 - \exp\left(-\beta \frac{I(t)}{N(t)} \right) \right)$$

We performed a Generalized Linear Mixed model (Macro GLIMMIX of SAS©) using a log link function and a Poisson error distribution. The herd was introduced in the model as a random variable. The response variable was $1 - \frac{C(t+1)}{S(t)}$.

The new cases were assumed to occur at half time-step (interval between two consecutive samplings), therefore corresponding to a value of 0.5 per new case. The same assumption was made for the susceptible or infectious cows that enter a herd between two time steps.

RESULTS AND DISCUSSION

From this study, we obtained a β value of $2.8 \cdot 10^{-3} \text{ d}^{-1}$ (standard error: $1.4 \cdot 10^{-3} \text{ d}^{-1}$). This means that, in a 50 cows herd with a prevalence of 10%, a bit less than 12 cows would be infected during a year.

Furthermore, considering a productive life span of 1000 days for a dairy cow and assuming a uniform probability of becoming infectious during this period, an infectious period of 500 days can be derived. Multiplying this value by the above transmission rate β leads to an estimation of the basic reproduction ratio (R_0) of 1.41. This value suggests a spread of the disease in the herds involved in the study.

The given estimation of the transmission rate could be fruitful when the simulation model of *C. burnetii* spread will be implemented.

REFERENCES

- [1]. Arricau-Bouvery et al., 2006. Vet Res, 36, 327-350.
- [2]. Berri et al., 2002. Vet Microbiol, 85, 55-60.