

# Modelling Coxiella burnetii spread within and between dairy herds





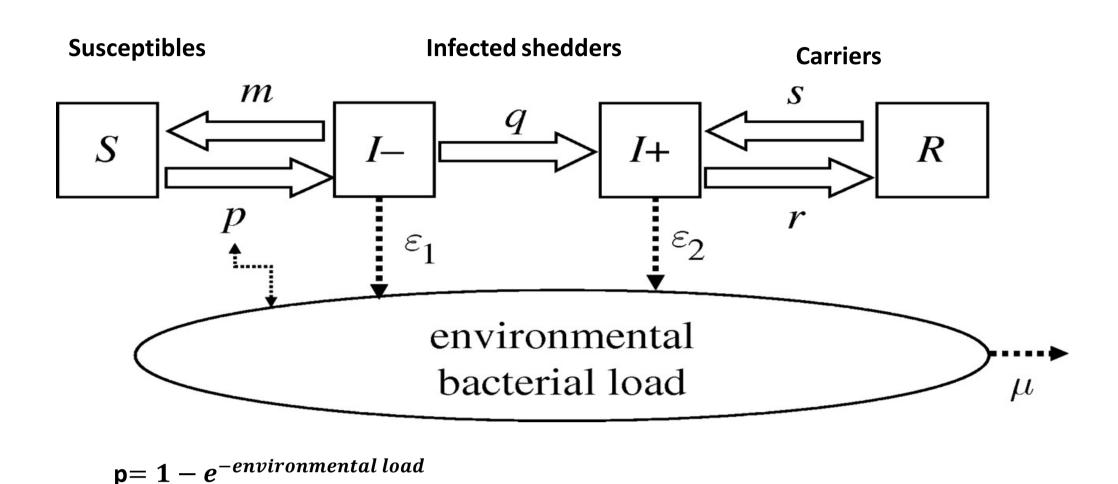
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Q fever is one of the most important zoonotic diseases in Europe caused by the bacterium Coxiella burnetii. Previous modeling studies described the disease dynamics in a dairy cattle herd. In order to simulate transmission between herds, we extend this model by including airborne dispersion modeling to understand the spread of the disease on a regional scale.

#### **INTRA-HERD MODEL**



- Compartmental deterministic model in discrete-time
- Four health states: S: susceptible, I-: shedder without antibodies, I+: shedder with antibodies, C: non-shedder with antibodies, E: environment
- Intra-herd dynamics as described in previously.
- Animals infected by inhalation of the contaminated aerosols

### **DISPERSION MODEL**

- One dimensional Gaussian Dispersion model
- Ground level dispersion of the particles

Courcoul A et al. Proc. R. Soc. B 2010;277:2857-2865

- Bacterial plume reaching= $C_{(x,y,0,t)}=rac{Q_{(t-x/u)}}{2\pi\sigma_x(x)\sigma_y(x)}e^{[-rac{y^2}{2\sigma^2y(x)}]}$
- Flat terrain with no geographical wind barriers
- No settling of infectious particles during the transport

Where,

**Q** = Concentration of bacteria at source  $\sigma_{v}^{2}$  &  $\sigma_{x}^{2}$  = standard deviations of diffusion *u*= wind velocity

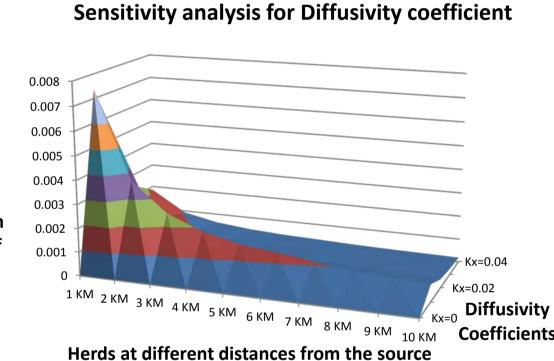
Standard deviation of lateral diffusion is calculated as below  $\sigma^2_y = \frac{2K_y(x)}{y} \qquad \sigma^2_x = \frac{2K_x(x)}{y}$ 

Where,  $K_{\nu}(x) \& K_{x}(x)$  are coefficients of eddy

diffusivity

**SIMULATIONS** 

0.005 0.004 0.003 Concentration 0.002 (at the end of 0.001 simulation)



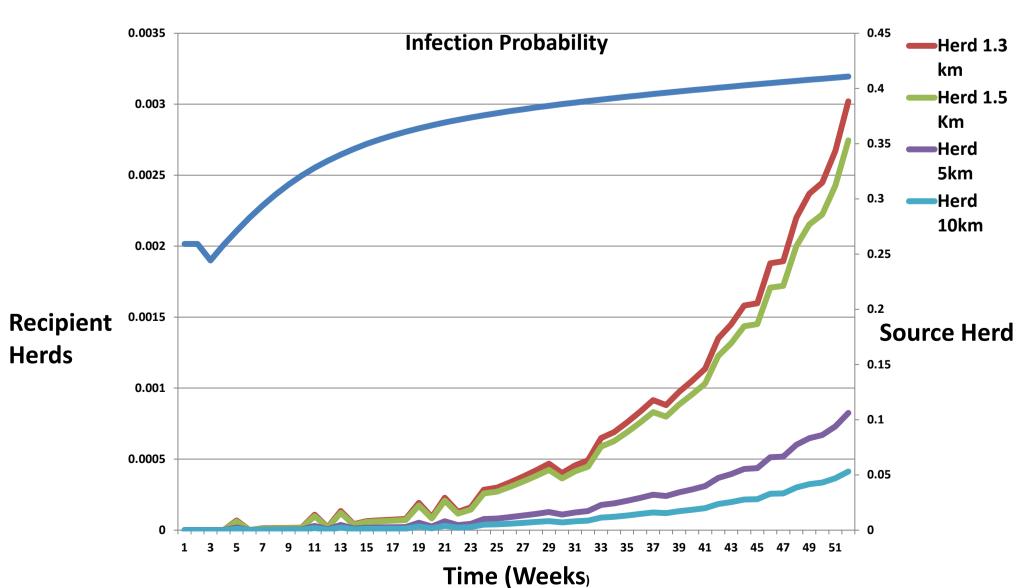
The bacterial plume generated was found to be highly sensitive to lower values of diffusivity coefficients at smaller distances from the source

 $K_y(x) = K_x(x) = 0.03$  were used in current simulations Ssematimba A et al. Plos ONE 2012; 7(2): e31114.

**Bacterial** 

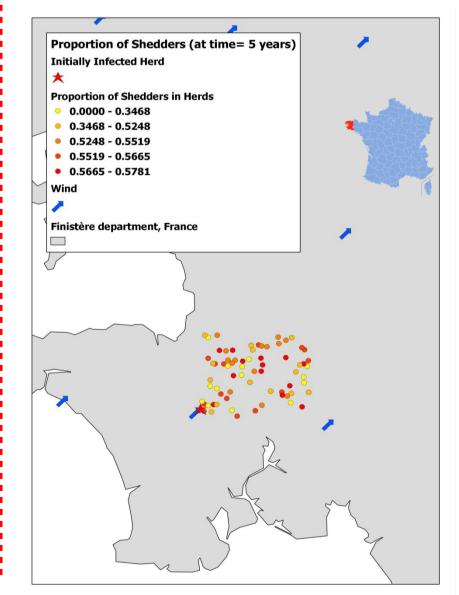
## **Modeling Scenario 'A'**

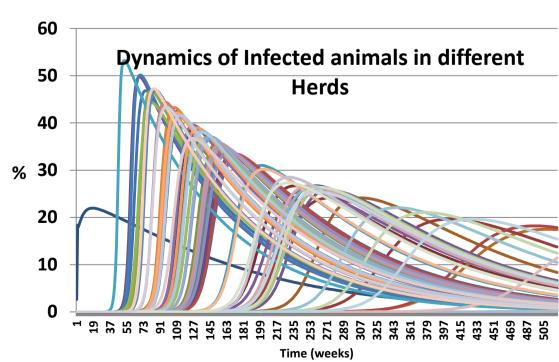
- 5 cattle dairy herds, 1 source herd and 4 completely susceptible herds
- Situated at 1.3, 1.5, 5 and 10 kms from the source herd
- Source herd is endemically infected herd, steady state as in [1].
- All herds can produce plume once they are infected
- All herds are on the same latitude



## **Modeling Scenario 'B'**

- 70 dairy cattle herds in a single meteorological grid located in the department of Finistère in France.
- 1 source herd at the beginning of the simulation
- Simulation of the windborne spread over one year and varying wind velocities





**Analysis for possible parameters** influencing transmission such as distance, wind velocities, direction and herd size will be done

#### **DISCUSSION**

- Inclusion of wind-borne dispersion of bacteria allows simulation of plausible patterns of disease spread at the regional level
- The proposed framework will be used to quantify the relative role of wind borne and animal movements related infections and to assess different local controls and preventive strategies (ongoing work)