

# The Impact of Different Transmission Routes of Bovine Tuberculosis in British Cattle



Darren Green <sup>1</sup>★, Andrew Mitchell <sup>2</sup> & Rowland Kao <sup>1</sup>.

<sup>1</sup> Dept. of Zoology, University of Oxford, Oxford OX1 3PS, UK.

<sup>2</sup> Veterinary Laboratories Agency, Weybridge, Surrey KT15 3NB, UK.

\*darren.green@zoo.ox.ac.uk



## Introduction

Bovine tuberculosis (BTB) control in Great Britain (GB) cost over £90 million in 2005<sup>1</sup>. Spread is due to both cattle movements<sup>2</sup> and other factors, most controversially transmission from infected badgers<sup>3</sup>, and associated with 'high-risk' areas. There are two testing regimes:

- Herds are tested every one to four years on a parish-by-parish basis (Fig 1).
- Pre-movement testing for cattle aged over 6 weeks in frequent testing parishes.

We address the following questions:

- What proportion of transmission can be attributed to movements?
- Can current protocols for identifying testing areas and high-risk herds be improved?

Figure 1: Test frequencies

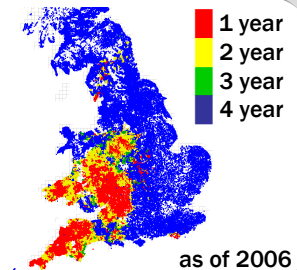
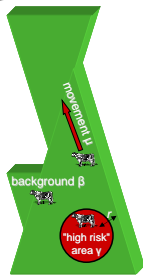


Figure 2: Model construction



**Three transmission routes:**  
movement  
background  
high-risk area

## Simulation model

Data used were Cattle Tracing System (CTS) data provided by RADAR, BTB breakdowns (cases) as reported to VetNet and the June Agricultural Survey for 2003.

We organised movements into groups of animals moving between two locations on a given day. For 2002-5, there were nearly three million such batches.

We model individual premises. Each maintains a simulated probability of infection, updated each model day. There are three modelled infection routes (Fig. 2):

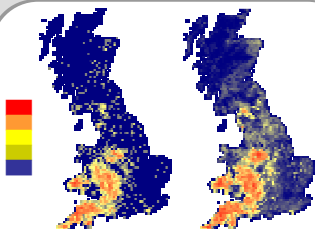
- Movements from infected premises are infectious at rate  $\mu$  per animal. Two cases:
  - 'high within-herd' transmission model' - all premises exposed to infected cattle are themselves a risk, and  $\mu$  applies to all cattle leaving exposed herds.
  - 'low within-herd' model, only cattle previously passed through high-risk areas are infectious.
- We assume areas of endemic BTB — 'high-risk (HR) areas' — with local spread including cattle-cattle transmission and spread from wildlife reservoirs. These farms are infected at rate  $\gamma$  (normalised by total premises in area). We model two types of HR area:
  - 'Parochial' areas: all premises in parishes with one- or two-year testing intervals.
  - 'Radial' areas: all premises within a radius  $r$  of an index case.
- Background infection through other causes at rate  $\beta$  per premises.

## Model parameterisation

We seed simulations in 2003 to predict forwards into 2004, using 2004 data to calculate model likelihood (Fig. 3).

Maximum likelihood models were obtained by fitting the four parameters, using both forms of transmission model and high-risk area type.

Figure 3: Model prevalence



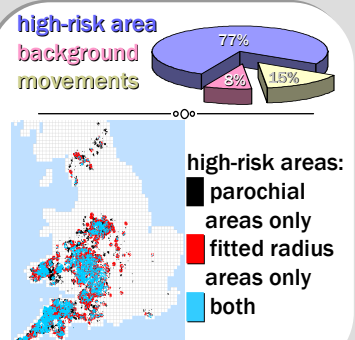
2004 observed      predicted

## Best-fit models

The best-fit model used radius-based high-risk areas ( $r \approx 5\text{km}$ ) and low within-herd transmission (only cattle having passed through HR areas potentially infectious). An estimated 23% of cases were due to known movements or unrelated to HR areas (Fig. 4). These proportions were similar whether or not confirmed cases only were used.

The fitted radii incorporated more farms than the contemporaneous parochial HR areas (Fig. 4) (1.1% more of infected premises), and accounted for more cases via onward spread through movements (~2% of total cases).

Figure 4: Estimated causes



## Implications for BTB control strategies

Attribution of risk by areas centred on breakdown herds in 2003 might have identified substantially greater number of BTB infected herds in 2004. Better attribution of these high-risk areas as in our model could be used to limit their further growth.

Eliminating transmission associated with our high-risk areas would have reduced the number of BTB breakdowns by 82% in 2004, whereas eliminating all movement transmission out of high-risk areas achieves a 13% reduction in our model.

**References:** <sup>1</sup><http://www.defra.gov.uk/animalh/tb/stats/expenditure.htm> <sup>2</sup>Gilbert, M. et al. (2005). Nature 435: 491–496.

<sup>3</sup>Gallagher, J. & Clifton-Hadley, R.S. (2000). Res. Vet. Sci. 69: 203–217.

**Acknowledgements:** This work was supported by DEFRA and the Wellcome Trust.