Endemic Cattle Diseases: Comparative Epidemiology and Governance

David Carslake[1], Wyn Grant[2], Laura E. Green[1], Jonathan Cave[3], Justin Greaves[2], Matt Keeling[1,4], John McEldowney[5], Habtu Weldegebriel[3] and Graham F. Medley[1]

1. School of Life Sciences, Gibbet Hill Campus, University of Warwick CV4 7AL.
2. Department of Politics and International Studies, University of Warwick, Coventry, CV4 7AL.
3. Department of Economics, University of Warwick, Coventry CV4 7AL.
4. Warwick Mathematics Institute, University of Warwick, Coventry CV4 7AL.
5. School of Law, University of Warwick, Coventry CV4 7AL.

Cattle are infected by a community of endemic pathogens with different epidemiological properties which invoke different managerial and governmental responses. We present characteristics of pathogens that influence their ability to persist in the UK, and describe a qualitative framework of factors that influence the political response to a livestock disease. We develop simple transmission models for three pathogens (bovine viral diarrhoea virus, bovine herpesvirus and *Mycobacterium avium* spp *paratuberculosis*) using observed cattle movements, and compare the outcomes to an extensive dataset. The results demonstrate that the epidemiology of the three pathogens is determined by different aspects of within and between farm processes, which has economic, legal and political implications for control. We consider how these pathogens, and *Mycobacterium bovis* (the agent of bovine tuberculosis), may be classified by the process by which they persist and by their political profile. We further consider the dynamic interaction of these classifications with pathogen prevalence and with the action taken by government.

Keywords: bovine viral diarrhoea virus; bovine herpesvirus; *Mycobacterium avium* spp *paratuberculosis*; *Mycobacterium bovis;* governance; mathematical models

Running head: Endemic cattle diseases

1. INTRODUCTION

In the UK, infectious diseases to which livestock are vulnerable are often classified into two major classes: endemic and exotic [1]. Exotic pathogens, such as rinderpest virus or foot and mouth disease virus (FMDV), are by definition normally absent from the UK, but if an introduction occurs, a potentially fast-spreading, highly damaging epidemic can result. Exotic pathogens are legally notifiable, and border and movement controls are used to prevent their (re)introduction. When an outbreak occurs, strenuous efforts are made to re-eliminate the pathogen, often at huge short-term cost to the industry or to a compensating government [2]. By contrast, endemic pathogens, such as bovine viral diarrhoea virus (BVDV) or *Mycobacterium avium* spp *paratuberculosis* (Map), are present in the UK and typically attract less political debate, media attention, legislation or economic analysis. They usually exist at a stable, if often high prevalence, with low apparent mortality and cause less dramatic outbreaks of disease. Individual farmers may seek to eliminate a particular endemic pathogen, but with a high prevalence of infected herds elsewhere a disease-free status is difficult to maintain. Endemic pathogens are often unnoticed, mitigated or tolerated by farmers. Nonetheless, the presence of endemic pathogens causing a reduction in the performance of infected animals and herds represents a considerable, but often underestimated, drain on farm profitability and reduction in animal welfare [3-6].

The labelling of a disease as exotic or endemic is essentially a political decision to "frame" or label a disease in a particular way. Diseases (and the pathogens that cause them) are not *per se* exotic or endemic. For example, FMD is exotic in the United Kingdom but was once endemic, and still is in many parts of the world. Once this labelling has occurred, the political debate is framed around it, particularly in terms of how involved government should be in tackling the disease, and the level of resources that are devoted to its research and management. The political distinction between endemic and exotic pathogens is not, however, an immutable rule and can be influenced by particular political agendas. For example, *Brucella abortus* was recognised as eliminated from Great Britain in 1985 through a government sponsored programme, so that its status has subsequently changed. It was a political decision (motivated by legal requirements and veterinary advice) to use government resources to re-eliminate FMD in 2001 so that it retained its exotic status. The long-term, widespread presence of bovine tuberculosis (bTB) in much of the UK makes it undeniably

endemic; yet the resources devoted to its control are more comparable to the response to a newly introduced exotic pathogen. Managing bTB costs taxpayers some £80m a year, although the true cost is higher because some bTB-related activities are allocated elsewhere [7].

It is evident that there is considerable variation in the political importance attached to a disease. "Political importance" in this context primarily means whether government considers that the disease requires some form of publically-funded intervention. The alternative is that the disease is considered as a production disease (a disease that primarily affects productivity and profitability) that is then considered a matter for animal keepers to deal with either individually or through some form of self-generated collective action. "Government" in this context does not refer only to nation-state governments, but also to sub-national governments and international governance arrangements which have relevant jurisdictions such as the European Union, the World Trade Organisation and the World Organisation for Animal Health (OIE). What is regarded as a production disease might vary between jurisdictions or branches of government and over time, e.g., the Scottish Government conducted a consultation on a BVDV initiative in 2010 (http://www.scotland.gov.uk/Publications/2010/06/29143957/0, accessed 20 July 2010), and has since announced a public intervention (http://www.scotland.gov.uk/News/Releases/2010/09/21145206, accessed 4 October 2010), but in England, BVDV is being treated as a production disease. Extensive government intervention in bTB may reflect historical commitments and stakeholder pressure as much as policy logic, thus indicating other possible determinants of political importance. Elements of path dependency may enter into the picture because once a disease has acquired a high or low profile status, it is difficult for a decision to treat it as an appropriate subject for government policy to be reversed because beneficiaries of the policy among stakeholders are created.

In contrast to the political status of a disease, the epidemiological characterisation of a pathogen as absent, increasing (epidemic) or relatively stable (endemic) is based primarily on some surveillance data. However, the level of surveillance (e.g. whether a disease is notifiable) is largely determined by its political status, so that there is very little surveillance for unregulated endemic diseases. Furthermore, the infection dynamics of pathogens of livestock (a managed host population) are largely determined by socioeconomic processes such as movement of animals between herds, management of herds and decisions to vaccinate.

The endemic pathogens infecting British cattle comprise a diverse, interdependent community of viral, bacterial, protozoan and parasitic species. These infections are not uniformly distributed among British cattle. Farms differ in the scope they provide for the transmission of infection between cattle through, for example, differing management practices and environments. However, herds do not exist in isolation from one another, and cattle movement between herds is a major risk factor for the spread of most pathogens, on which we focus below [8-10]. Cattle moving on to a farm can bring infection with them; cattle moving off a farm can remove infection; so the prevalence of infection in a herd is a balance between introduction, within-farm transmission, birth, death, recovery and emigration. Farm management varies and this influences the numbers and rates of movement of animals on and off farm. Consequently, the prevalence of any pathogen varies between farms, with the pattern of variation reflecting the nature of the pathogen [11]. As well as being non-uniformly distributed among herds, it is also likely that pathogens are not distributed independently from each other since management practices that increase the risk of introducing one pathogen into a herd may also expose the herd to (or protect it from) others. However, all the studies of transmission dynamics of livestock infections of which we are aware consider pathogens separately. Further, the advice given to farmers seeking to avoid the damaging effects of infection is usually pathogen-specific despite the potential for interdependence among endemic pathogens and the influence of farmer responses on other disease risks.

We have recently discussed the management and regulation of animal disease [1]. However, the characteristics that determine how the social system responds to a particular pathogen and how pathogens respond to social systems have not been considered previously; by social system we mean the combined societal processes (economics, culture, politics etc) operating at all levels (farms, governments etc). The epidemiology of both diseases and pathogens are both determined by and determine the social system. For example, a farmer may buy a cow (for purely commercial reasons) that happens to be shedding BVDV and his herd subsequently experiences an abortion storm, which changes the management of the herd (e.g. purchase of recently calved cows) that results in the introduction of Map. Here, we seek to address two questions regarding endemic disease prevalence, in order to explore the interlinked dynamics of disease epidemiology and social system change. First, what determines the political response to a livestock disease? Second, what is the relative role of cattle demography, particularly the movement of animals but including

birth and death, in determining the distribution of infection between farms? We consider three pathogens: BVDV, bovine herpes virus (BHV, which causes several diseases including infectious bovine rhinotracheitis) and Map (which causes Johne's disease); and we also consider the political responses to *Mycobacterium bovis*, the aetiological agent of bTB. These four pathogens were chosen because of their differing natural histories which are expected to produce differing political and epidemiological patterns. Introductions to the properties of BVDV [12], BHV [13], Map [14, 15] and bTB [16, 17] may be found elsewhere. To address the two questions we present and discuss qualitative and quantitative frameworks respectively. Finally, we attempt to pull the two strands together and develop a discussion of interactions between natural and social systems that determine and are determined by infectious disease.

2. A POLITICAL MODEL

(a) Methods

Within the Governance of Livestock Disease (GoLD) project at the University of Warwick we sought to construct a political model which would provide a framework for understanding the varying political priority given to different endemic cattle diseases. This was seen primarily as an academic modelling exercise but with clear policy implications. It consisted of a list of the various questions which might influence a government's response. Not surprisingly, although developed in house, the list resembles the criteria used in Defra's Prioritisation project (http://www.defra.gov.uk/foodfarm/farmanimal/diseases/vetsurveillance/documents/dst_summary.pdf accessed 4 October 2010). An initial draft provided by a member of the team from the political science discipline (WG) was sent to the other team members covering the disciplines of epidemiology, veterinary science, economics and law. Successive iterations of the model were discussed until a final version emerged (table 1). Some subsequent adjustments were made in the light of comments made by anonymous referees. The questions used in the model were intended to be comprehensive in terms of the factors considered by government. Using the four chosen cattle pathogens as examples, the response to each question was scored, again by discussion within the GoLD team, on a scale of 0 (none), 1 (low), 2 (medium) or 3 (high). In order to consider the effect on the political priority of all questions together, it was necessary to combine the scores in some way. Noting that some questions may be more influential than others, it was decided to give the two questions concerning zoonotic risk a weighting factor of 5 in relation to the others.

The National Archives is the UK government's official archive. Government records that have been selected for permanent preservation are sent to the National Archives when they are 30 years old, but many are transferred earlier. The files are extensive and appear to be a complete sequence [18]. National Archive files relevant to each of the four pathogens were identified and studied (by WG), and each pathogen's profile in the National Archives was used as an indication of the attention paid to it by government.

(b) Results

Consensus scores for each question and pathogen are shown in table 1. Weighted sums of the scores were 53 for bTB, 22 for BVDV, 20 for BHV and 14 for Map. The model predicts, as one would expect and in accordance with its high profile in the National Archives, that bTB will attract by far the greatest political attention of the four pathogens. This is particularly true when the zoonosis weighting is included, but applies even without it. The model also predicts correctly that Map will be considered a lower priority than BVDV. The moderately high score (intermediate between BVDV and Map) given to BHV, however, is inconsistent with its complete lack of profile in either the National Archives or current discussions in the cattle industry. In part this reflects the fact that BHV is easier to diagnose and there are effective vaccines. It can be tackled at farm level without government intervention. The ease with which a disease can be managed can affect government decisions about intervention. In Scotland, the selection of BVDV for a policy initiative was influenced by such considerations: 'When BVD came in my team were saying we should be looking at Johne's, potential link to Crohn's disease. Tools are all there [for BVDV], don't have a test for [Map] that works in a practical time scale. Not able to detect the animal early enough.' (Non-attributable interview with policy-maker, Edinburgh, 14 July 2010).

3. EPIDEMIOLOGICAL MODELS

(a) Methods

The primary purpose of the epidemiological modelling was to examine the extent to which the interaction of cattle demography with the natural history of infection explained the observed patterns of

occurrence of each pathogen, rather than to make precise parameter estimates or to predict the infection status of particular herds or individuals. The construction of the models is summarised here: full details are available in the electronic supplementary material.

A stochastic simulation model was devised for each of BVDV, BHV and Map with cattle moving between mutually exclusive infection states (figure 1). Most parameters of the model were determined *a priori* from the literature, but one transmission parameter in each model was adjusted to optimise the fit between the modelled and observed seroprevalence among adults (≥ 2 years old). Transmission coefficients were estimated separately for dairy and beef herds.

Serological data were available for 60 beef and 53 dairy herds in the south west of England, each sampled up to four times at approximately annual intervals [10, 11, 19]. Only animals over two years old were sampled. Serum from each sampled animal was tested by ELISA (details in supplementary material). Samples testing seronegative for BVDV were also tested for the presence of BVDV antigen, and antibody-negative, antigen-positive animals were assumed to be persistently infected with BVDV. Demographic data (births, deaths and transfers between herds) for all cattle on study farms within the simulation period (five years, from 5th December 2002) were supplied on 25th March 2008 by Defra's Rapid Analysis and Detection of Animal-related Risks (RADAR) project. The modelled pathogen transmission process (figure 1) was then applied to the observed demographic history of the study herds during the simulation period, i.e. cattle movement, birth and death were not simulated, but implemented as they had actually occurred. After each five-year iteration, the age-specific distribution of infection states among the cattle of each herd was used to populate that herd for the next iteration. Convergence was apparent after 20 such iterations, after which outcomes were recorded for further 20 iterations. These recorded outcomes were the infection status of simulated cattle, on the dates on which they were sampled in reality. Cattle under two years of age, not sampled in the observed data, were also sampled in the simulation on the same date as the rest of their herd. Finally, a tally was kept of individual or herd-level infection events in the simulation, recording the class of infection responsible.

Simulated serology results were used to calculate age class- and visit-specific seroprevalences, which were compared with the values from the observed data. Correlations between observed and simulated data (the latter averaged over all iterations) at an individual sample level, at a between-visit level and at a within-visit level, were also calculated. Finally, the possible effects of BHV reactivation upon purchase of a latently infected animal [10, 13, 20] were investigated.

(b) Transmission dynamics

Observed adult seroprevalences for BHV and Map fell within the range obtained by varying the transmission coefficient (electronic supplementary material figure S1), allowing the straightforward estimation for each pathogen and herd type (electronic supplementary material table S1). Simulated adult seroprevalences for BVDV levelled off at just below the observed values with increasing transmission coefficient, which was therefore chosen by eye at the point at which the curve became very shallow.

The match between observed and simulated age profiles for each pathogen (electronic supplementary material, figure S2) was good, with BVDV seroprevalence a little lower than expected at all ages, as expected, given that that the overall adult seroprevalence was not reached. In both dairy and beef herds, the simulation overestimated Map seroprevalence in younger age classes and underestimated it in older ones. This is probably because the sensitivity of serological tests for Map increases with age, even within an infection class [21]. The simulation gave a good match to the few BVDV persistently infected animals observed (electronic supplementary material, figure S4) despite not having been optimised for this. The simulations suggest that persistently infected animals under two years of age (not tested for in the observed data) vastly outnumber those over two years of age.

Table 2 lists the transmission events taking place during the simulation, according to the class of infectious animal to which they were attributed. The results from this simulation suggest that within herds, animals persistently and acutely infected with BVDV (classes P and I, respectively) are responsible for approximately equal numbers of new infections. *In utero* infections (resulting in the birth of a persistently infected calf) made up less than 3% of transmission in both herd types, and were usually due to seroconversion of the dam during pregnancy (~90% of cases) rather than to persistently infected dams giving birth. Animals infected with BHV for the first time accounted for about three times as many within-herd transmissions as reactivated latent animals, and the majority (>84% in both herd types) of within-herd Map transmission was due to high-shedding, subclinically infected animals (class H). These animals are

abundant (like class L, but not class C; electronic supplementary material, figure S3) and highly infectious (like class C, but not class L; electronic supplementary material table S1).

The ratio between within-herd and between-herd transmission events was higher in beef herds than in dairy herds. Among dairy herds, BVDV was transmitted between herds far more often than BHV or Map, both in absolute terms and relative to within-herd transmission. Among beef herds, absolute rates of BVDV transmission between herds were higher than those for BHV or Map, but the difference in within-herd transmission was even greater, such that transmission ratios were lower for BHV and Map than for BVDV. Most between-herd transmission for BHV or Map involved latently infected or low-shedding animals, respectively. These are not very infectious, and must be considered less likely to give rise to secondary cases than an animal that is introduced whilst infectious with BVDV. Persistently and acutely infected animals were equally likely to bring BVDV to a previously uninfected herd, although a new herd infection due to an acutely infected animal is more prone to rapid fade-out.

(c) Distributional patterns

Figure 2 shows the herd level distribution of seroprevalence, and table 3 the correlations between simulated and observed herd-level seroprevalence. The three pathogens showed very different distributions of seroprevalence among visits, and the degree to which simulations matched this distribution also varied. For both herd types, observed BVDV data showed a large number of herds with a seroprevalence close to 100%, but a wide range of seroprevalences in other herds, and very few at very low seroprevalence (figure 2a,b). This peak at near total prevalence was successfully reproduced by the simulations, but simulations in dairy herds also predicted a second peak of herds with very low (but not zero) prevalence, which was not seen in reality. Effectively, the simulations predicted a near-dichotomy between high- and low-BVDV dairy herds. Among beef and dairy herds, small herds of fewer than ten animals almost all actually fell into the highest band of seroprevalence. This surprising result was reproduced by the simulation. The correlation between the observed and (average) simulated correlation for each visit differed hugely between herd types (table 3). There was no correlation in dairy herds, but a substantial correlation in beef herds, meaning that the beef herds with high BVDV seroprevalence in the simulation tended also to have high seroprevalence in reality. Moderate correlation at the within-herd level probably indicates that, in the simulation and in reality, older animals are more likely to be seropositive for BVDV (electronic supplementary material, figure S2).

Observed distributions of BHV seroprevalence among visits (figure 2c,d) were bimodal, with one peak at around 80% (albeit rather indistinct among beef herds) and another at very low (dairy herds) or zero (beef herds) seroprevalence. In contrast to BVDV, and in accordance with what we might expect from their relative isolation, small herds tended to be free of BHV. The simulations, however, did not reproduce this bimodality, resulting in a very poor fit among dairy herds, but a moderately good one among beef herds (where the bimodality was far less pronounced). As for BVDV, observed and simulated seroprevalences for each visit were strongly correlated (table 3) in beef herds, but not in dairy herds, and correlation at the within-herd level is probably a result of increasing seroprevalence with age (electronic supplementary material, figure S2). Among dairy herds, the introduction of BHV re-activation on purchase with probability ε (and an associated reduction in the background rate of reactivation, α) improved the match between histograms of observed and simulated visit-level seroprevalence by adding a second peak at low (but not zero) seroprevalence. However, the bimodality remained much less pronounced than in the observed data, even for high ε values of 0.5 or 0.75, and the improved distribution shape was not accompanied by any correlation between observed and simulated seroprevalences (data not shown). Among beef herds, the introduction of re-activation on purchase had only a minimal effect, leading to a slight bimodality that did not improve the overall fit to the observed data.

For Map, which had a much lower overall seroprevalence than the other two pathogens, most herds had very low prevalence (or zero, among beef herds), with declining numbers reaching up to about 20%. This was almost perfectly reproduced by the simulation among beef herds (figure 2f) where small herds all had low seroprevalence. Among dairy herds (figure 2e), the match was also good, but the observed variability in Map seroprevalence was slightly underestimated by the simulation. In contrast to the results for BVDV and BHV, there were no substantial correlations at any level between observed and simulated Map status (table 3). Map seroprevalence does not increase with age as do BVDV and BHV (electronic supplementary material, figure S2). The lack of correlation at the between-visit level indicates that although the simulation reproduced the visit-level distribution, this was not achieved by correctly reproducing the seroprevalence of individual herds.

4. DISCUSSION

We discuss the political and epidemiological models separately before attempting to combine them.

a) Political model

The political diseases model is seen as a heuristic device and a first step in assessing the political importance of a disease. In this analysis it is applied to England, but it could be applied to other jurisdictions and deployed comparatively. It could also be applied to other endemic pathogens of livestock, or to the same pathogen at different points of time. We restricted ourselves here to a very simple system of weightings which recognises the salience of zoonotic factors. However, more elaborate differential weightings (including interactions between questions, such that the weight accorded to one depended on the response to another) could be used to refine predictions, or to explore different understandings of a disease. For example, policy makers or any stakeholder could be asked to assign scores and weightings. It therefore can be regarded as a part of a policy toolkit [22] contributing to the development of decision support. The effect of possible future scenarios can be explored by adjusting scores accordingly. For example, there has been some suggestion, as yet unproven, that Map in milk might be a causative agent of Crohn's disease in humans [23]. If the perception of this link increased in the future (perhaps, but not exclusively, as a result of scientific evidence), it might increase the scores for questions 1a and 1b to 2 and 1, respectively, raising the total score from 13 to 28, suggesting political interest considerably in excess of that presently accorded to BVDV. Map thus has the potential to become considerably more politically significant in the future in England, as seen currently elsewhere e.g. USA, Australia. In this particular sense the model does have a predictive capability.

b) How should government classify livestock diseases?

How livestock diseases are classified by government determines the extent to which public finances are used to research and control them, so there are real consequences for disease prevalence and management. We have proposed a framework to capture the most important factors in the current political classification of disease. However, it does not relate directly to the way in which the farming system interacts with the disease. As a consequence, it does not indicate the degree to which government should get involved in disease control in order to improve farm productivity, animal health and animal welfare directly. It should be noted that this is largely a decision about the role of government in agricultural production, and different bodies will take different views. Thus although the United Kingdom constitutes a single epidemiological unit, devolved (governmental) arrangements have seen the emergence of contrasting approaches to disease management reflecting different political priorities. The Scottish Government considers that Scotland enjoys an international reputation for quality meat production and that this requires a more proactive stance towards endemic as well as exotic diseases. Similarly, the Welsh Assembly Government policy 'has been to improve the "branding" of animals reared in Wales, so that Welsh beef, like Welsh lamb, is synonymous with good quality.' [24]. In relation to the implementation of animal health strategy in Scotland, the Scottish Government comments of endemic diseases in contrast to exotic diseases such as foot and mouth, 'there are diseases found in GB which have much lower profiles but nevertheless require our efforts to control or eradicate them.'
(http://www.scotland.gov.uk/Publications/2003/12/18658/30622, accessed 17 June 2010).

From an economic perspective, the degree to which livestock disease reduction is beneficial to farmers largely depends on the epidemiological drivers of disease, and especially the role of animal movement. We have shown that movement of cattle between farms explains much of the epidemiology of BVDV and BHV in beef herds. Cattle movement is therefore important for these pathogens in this farm type, but is also likely to be important for disease risk for other pathogens in other farm types, so that a reduction in prevalence of infection for these diseases could be beneficial to a large number of farmers. On the other hand, movement does not appear to be a good predictor in dairy herds of the pattern of infection with Map and BHV, whose presence in particular herds seems due to some unidentified non-demographic herd properties. Reduction in disease level is thus beneficial (and the pathogen a problem) only to those farmers with high-prevalence herds, rather than to the industry as a whole. The extent to which government commits to funding a disease control programme is not necessarily determined by a utilitarian consideration of the greatest level of disease reduction for the greatest number of farmers. It is more likely to be determined by a number of other considerations including cost-benefit analysis, the degree to which the

industry commits itself to funding such a programme, the economic manifesto of the government in power and the need to resolve distributional issues which might arise from cost and responsibility sharing debates within the industry [25]. One also has to take account of the attachment or opposition of stakeholder groups to particular programmes or forms of control.

c) The epidemiological model

The simulations include three processes: the natural history of infection, chance and cattle demography. Other processes, such as genetics and differences in management and husbandry (including for example housing) are not included. The same infection model applies to all herds of the same type (dairy or beef), so differences in seroprevalence among simulated herds can arise only though chance, or through their demography. The simulation successfully recreates the distribution of seroprevalence at a herd level (figure 2), as well as the seroprevalence of individual herds (table 3), for BVDV and BHV in beef herds. This strongly suggests that demography (together with stochastic effects) accounts for much of the difference among beef herds in BVDV and BHV seroprevalences. Solis-Calderon *et al.* [26] reported that BVDV status in Mexican beef cattle was related to an interaction between herd size and purchased/homebred origin (two demographic variables that are accounted for indirectly in our model) but not to several non-demographic variables that they recorded. In the case of Map in beef herds (and to some extent, dairy herds), the observed and simulated herd-level distributions of seroprevalence match, but there is no correlation between each herd's observed and simulated seroprevalences, suggesting that differences in seroprevalence between herds are due largely to stochasticity, including factors not included in the simulation. The results for BVDV in dairy herds were similar, except that the simulation predicted a peak at very low seroprevalence that was not observed. The purchase of small numbers of animals having recovered from BVDV (class R) might account for this simulated result, while the assortative matching of source and destination farms (i.e. low-BVDV farms preferentially purchasing from other low-BVDV farms) might explain the absence of this effect in reality. As for Map in beef herds, the lack of correlation between simulated and observed data, and the similar heterogeneity (barring the result discussed above) in seroprevalence among herds suggest that stochasticity might be important in determining a dairy herd's BVDV seroprevalence. In the case of BHV and (to a lesser extent) Map in dairy herds, the simulation underestimates the heterogeneity among herds, suggesting that non-demographic differences between herds are of prime importance in determining their seroprevalence. For example, Raaperi *et al.* [27] reported that the presence of on-farm veterinarians and inseminators, as well as infection with BVDV, increased the risk of BHV in Estonian dairy herds; Scott *et al.* [28] identified low aridity and soil pH as risk factors for Map in Canadian dairy herds; and Çetinkaya *et al.* [29] reported that Channel Island breed and the presence of farmed deer were risk factors for Map in English dairy herds.

It is curious that adding reactivation of BHV upon purchase of animals into dairy herds should improve the fit of the visit-level distribution of seroprevalence, without improving the correlation between the observed and simulated seroprevalence at each visit. Purchase of animals is a demographic process modelled in our simulation, but differences between herds in the number of animals purchased do not seem to have been responsible for differences in BHV seroprevalence. It may be that the peak of herds at very low BHV prevalence is caused by another, unmodelled factor, which reactivation on purchase mimics. The concentration of reactivation among the relatively small number of purchased animals, rather than the whole latent population, would allow greater variation in seroprevalence among herds without necessarily identifying those herds which make up the low-prevalence peak in reality.

Where herds differ in seroprevalence due to factors other than chance, and those factors are within the control of the farmer, changes in management could be used to control the infection. For all three pathogens, our results suggest that the factors influencing seroprevalence in a dairy herd might be different from the factors influencing seroprevalence in a beef herd. Whilst this is not surprising, it does indicate that action to control a pathogen at a national level, which must involve all herd types because of the risk of cross-infection, will require different control measures in different herd types: optimal control of endemic pathogens requires an integrated approach across pathogens and herd types. This result also emphasises the importance of considering herd type when analysing infection data for risk factors.

Medley *et al.* [11] likened the dynamics of pathogens among cattle herds to the metapopulation concept in ecology [30]. Individual herds might become clear of infection, but the pathogen persists in the national herd because susceptible herds get re-infected by other herds. Stable metapopulations, however, exist on a continuum between those in which extinctions and recolonisations are rare, and within-patch

(within-herd) dynamics (transmission) dominate, and those in which extinction and recolonisation are frequent events. By calculating the ratio between within- and between-herd transmission events, we attempted to place each of the three pathogens, in each herd type, on this continuum between those which rely on constant reintroduction for persistence, and those which are relatively stable within herds. The low transmission ratios for BVDV and BHV in beef herds (table 2) suggest that there is considerable transmission between herds, relative to transmission within herds. In the equilibrium situation, which we model, the rate of transmission to previously uninfected herds must be balanced by the rate at which a pathogen is lost from herds. The short infectious period and lack of latency in BVDV means that the virus might relatively easily die out in a herd, particularly if no persistently infected animals are present. Note that such a herd would have residual seroprevalence from the recovered animals, even after active infection was lost. The apparent importance of between-herd transmission is consistent with the suggestion (figure 2, table 3) that demographic factors play an important role in determining a beef herd's seroprevalence of BVDV and BHV. At the other end of the scale, BHV and Map in dairy herds had the highest transmission ratios, suggesting that within-herd transmission is more important than between-herd transmission. Both these pathogens are capable of a long latent period, which would promote long-term persistence within a herd. This is also consistent with the idea that non-demographic, herd-specific factors are at work (figure 2, table 3). It is not clear, however, why BHV latency might prevent the loss of infection in dairy herds, but not beef herds. Map in beef herds had a very low transmission ratio, suggesting frequent reinfection of previously uninfected herds. The fact that Map infects very young animals (i.e. before they are purchased) and usually shows no clinical signs until later in life would make it well adapted to move between herds. However, the majority of these between-herd transmissions involved the transfer of animals in the low-shedding class. These animals can easily live their entire life without moving into the more infectious classes, and so it is likely that many of these apparent between-herd transmissions do not lead to any secondary infections. By a similar argument, the intermediate transmission ratio for BVDV among dairy herds might underestimate the importance of between-herd transmission, because BVDV-infected animals, particularly persistently infected ones, are very infectious, and thus likely to generate secondary cases. The lack of correlation between observed and simulated visit-level seroprevalence (table 3) suggested that demographic factors were not particularly important in determining a dairy herd's BVDV seroprevalence, whilst the heterogeneity generated by the simulation (figure 2a) suggested that non-demographic factors also had limited influence. A dairy herd's seroprevalence of BVDV might be driven largely by the stochastic generation of persistently infected animals within the herd, given an initial herd infection.

The use of real demographic data in the epidemiological model eliminates the approximations and potential biases that would be inherent in reducing a complex system of births, deaths and transfers to a few network parameters and population average demographic rates. However, it has two major disadvantages. First, where demographic data are only known for a short period of time (5 years in our case), the longer simulations necessary to achieve asymptotic behaviour can only be performed by repeating the same demographic time series. Since a farmer's replacement strategy might change from one five-year period to the next, this approach is likely to overestimate the long-term variability between herds in their demographic properties. The longer the demographic time series available, the less this is a problem. Second, the demographic properties of individuals and herds are inflexible and cannot vary in response to the distribution of the pathogen. Infection with any of the three endemic pathogens which we model has only a minimal effect on culling or transfer rates [authors' unpublished data, 31, 32] and for two rare classes of animal where the effects are more profound (those persistently infected with BVDV or clinically infected with Map), we modelled removal of such animals from the infectious population by transferring them to the most abundant non-infectious group. Such an approach would not be suitable for pathogens that frequently cause the death (including culling) of the animal, such as bTB or most exotic pathogens. It should also be noted that our models were parameterised with data from the south west of England; differences in farming practices and intensity mean that our inferences should be applied elsewhere only with caution.

The modelling of Map was difficult because of the uncertain test sensitivity, and the likelihood that sensitivity changes with time since exposure (or its proxy, age), the development of clinical signs and the shedding of bacteria [electronic supplementary material figure S3, 21, 33, 34]. The poor sensitivity of the test is a severe hindrance to the control of Map [35, 36] and a better test would aid both understanding and control of this pathogen. Failing that, a better understanding of the linked development of test sensitivity, infectiousness and clinical signs would improve our ability to model Map.

d) Combining political and epidemiological dimensions

Since the epidemiology of endemic disease is determined by both natural and social processes (the demography of cattle being the social aspect in this paper), a classification that provides a combination of social and epidemiological dimensions is desirable. In figure 3 we propose such a classification system. The two states on the right are those for which there is epidemiologically (and therefore economically) sufficient connexion between herds that it can be argued that disease reduction is a public good. For these diseases, control (restriction) of movement of infection between farms is likely to be an important and effective method of intervention. Diseases in the upper half have a high political profile, for all the reasons previously discussed. Diseases falling in the upper right quadrant have the greatest call on government resources for control – they have a high profile and the epidemiological / economic arguments for creation of a public good. The classification we propose distinguishes different endemic pathogens, but the vast majority of exotic pathogens would fall into the upper right-hand quadrant. This proposed schema thus includes the dichotomous exotic / endemic distinction.

Diseases falling in the lower left quadrant are in the opposite position. However, most interesting are those diseases falling in the upper left and lower right: i.e. those for which there are contradictory indicators for government involvement. Diseases in the upper left quadrant have a relatively high political profile, but they are essentially individual farm-based problems. Historically, when agriculture itself had a higher political salience and there was an emphasis on maximizing production, these diseases might have attracted public funding. However, as they are farm-based problems, public control essentially represents a subsidy to a minority of farmers (if the disease causes production losses), mitigating the impetus for individual farmers to resolve the problem. As government attempts to reduce the resources it puts into livestock disease control, it will increasingly try and persuade farmers, and farmers' organisations, to take responsibility for these diseases, but there will be resistance. For diseases in the lower right quadrant there is good argument and indication for government intervention – those farmers who are experiencing the disease are doing so because it is in the national herd, and there is little, individually that they can do about it. In this case, farmers and farmers' organisations will be arguing for public resources to help control disease, but there will be resistance from government because the disease has a relatively low political profile. A possible solution is private governance arrangements created within the industry or limited public funding to provide a stimulus to action which is what is envisaged in the Scottish BVDV case (http://www.scotland.gov.uk/News/Releases/2010/09/21145206, accessed 4 October 2010). Our results suggested that the factors influencing a dairy herd's seroprevalence of a pathogen were often different from those influencing seroprevalence of the same pathogen in beef herds, resulting in the placement of each herd type in a different quadrant of figure 3. Whether government action (or inaction) on a pathogen can be tailored to different sectors of the cattle industry will depend on the degree of epidemiological connection between the sectors.

This proposed classification is more interesting when considered as a dynamic system. The political profile of a disease is influenced by its prevalence. Consequently, if an intervention programme is successful, then the political profile will fall. Additionally, the role of movement will also be determined by prevalence. Our simulations suggested that demographic processes, including movement, were not an important influence on the prevalence of Map. However, if the prevalence of Map were much higher, then this result might have been different. Thus, *ceteris paribus*, increasing prevalence will move a disease towards the upper right quadrant, resulting in greater chance of concerted control, which might reduce prevalence, which will tend to push the disease back towards the lower left quadrant.

A similar process may have occurred with bTB. There was a national control programme during the twentieth century, inspired by zoonotic infections, which resulted in elimination of disease from all but a few confined geographic areas by 1975 [37]. Bovine TB has an environmental component (including badgers; [38]). This non-demographic, farm-specific factor would tend to move bTB to the left-hand quadrants of our scheme, while the involvement of a wild animal with a positive public profile allowed it to retain its high political profile (i.e. position in the upper quadrants) despite reduced prevalence in the 1970's. In the subsequent epidemic, cattle movement, a demographic factor moving bTB from being a farm-specific to an industry-wide problem, has played a key role in dissemination of infection throughout the UK [9]. Consequently, we suggest that bTB has moved from the upper right to the upper left quadrant and is now back in the upper right quadrant as a result of the current disseminated epidemic. Different diseases - depending on their characteristics, the way in which they are framed politically [18] and their economic and

environmental impact - may trace different policy paths over time, demonstrating the utility of an integrated model.

Cattle pathogens endemic to the UK are able, by definition, to persist in their socioeconomic and epidemiological environment. We have shown that the mechanisms for this persistence differ between pathogens, and for the same pathogen, between sectors of the cattle industry. Elimination or control of an endemic pathogen requires a change in its environment (as broadly defined here), and we have proposed a scheme by which a pathogen's epidemiology, and the political will to intervene in its control, may be classified. Similarly, their persistence in the political environment is influenced by a variety of factors, not least their zoonotic status, but also whether there is a wildlife reservoir that involves an animal with a positive public profile which only applies to bTB of the diseases examined here. We hope that this will provide a useful framework for future research into endemic livestock disease, and promote governance that is appropriate to each pathogen, within an integrated approach to endemic disease control.

Acknowledgements

We thank the Rural Economy and Land Use (RELU) programme (RES -229-25-0016) for funding. RELU is funded jointly by the Economic and Social Research Council, the Biotechnology and Biological Sciences Research Council and the Natural Environment Research Council, with additional funding from the Department for Environment, Food and Rural Affairs and the Scottish Government. Defra (SE3026) and BBSRC (BBS/B/04854**)** funded the epidemiological data collection and analysis. We also acknowledge the contributions made by Steve Moore, Sam Mason, Dr Kerry Woodbine and others to the collection and processing of the serological data.

REFERENCES

1. GoLD. (in press). Animal health and welfare: a case study of science, law and policy in a regulatory environment. *Law, Science and Policy*
2. Woods A. (2004). *A Manufactured Plague: The History of Foot-and-Mouth Disease in Britain*: Earthscan Ltd.
3. Bennett R. (2003). The 'direct costs' of livestock disease: The development of a system of models for the analysis of 30 endemic livestock diseases in Great Britain. *J. Agr. Econ.* **54**: 55-71.
4. Bennett R, Ijpelaar J. (2005). Updated estimates of the costs associated with thirty four endemic livestock diseases in Great Britain: A note. *J. Agr. Econ.* **56**: 135-144.
5. Stott AW, Jones GM, Humphry RW, Gunn GJ. (2005). Financial incentive to control paratuberculosis (Johne's disease) on dairy farms in the United Kingdom. *Vet. Rec.* **156**: 825-831.
6. Tiwari A, VanLeeuwen JA, Dohoo IR, Keefe GP, Haddad JP, Tremblay R, Scott HM, Whiting T. (2007). Production effects of pathogens causing bovine leukosis, bovine viral diarrhea, paratuberculosis, and neosporosis. *J. Dairy Sci.* **90**: 659-669.
7. House of Commons. (2009). The health of livestock and honeybees in England, 36th Report of the Public Accounts Committee, 2008-9.
8. Ezanno P, Fourichon C, Beaudeau F, Seegers H. (2006). Between-herd movements of cattle as a tool for evaluating the risk of introducing infected animals. *Anim. Res.* **55**: 189-208.
9. Carrique-Mas JJ, Medley GF, Green LE. (2008). Risks for bovine tuberculosis in British cattle farms restocked after the foot and mouth disease epidemic of 2001. *Prev. Vet. Med.* **84**: 85-93.
10. Woodbine KA, Medley GF, Moore SJ, Ramirez-Villaescusa AM, Mason S, Green LE. (2009). A four year longitudinal sero-epidemiological study of bovine herpesvirus type-1 (BHV-1) in adult cattle in 107 unvaccinated herds in south west England. *BMC Vet. Res.* **5**: 5.
11. Medley GF, Woodbine KA, Ramirez-Villaescusa A, Moore SJ, Green LE. Comparative transmission dynamics of 6 endemic infections in 114 cattle herds over 3 years: preliminary observations. In: Peeler EJ, Alban L, Russell A, SVEPM Executive Committee, editors. Conference proceedings: Society for Veterinary Epidemiology and Preventive Medicine; 26th-28th March 2008; Liverpool, UK.
12. Brownlie J, Clarke MC, Howard CJ, Pocock DH. (1987). Pathogenesis and epidemiology of bovine virus diarrhoea virus infection of cattle. *Ann. Rech. Vet.* **18**: 157-166.
13. Wentink GH, van Oirschot JT, Verhoeff J. (1993). Risk of infection with bovine herpes virus 1 (BHV1): a review. *Vet. Q.* **15**: 30-33.
14. Ayele WY, Machackova M, Pavlik I. (2001). The transmission and impact of paratuberculosis infection in domestic and wild ruminants. *Vet. Med. (Praha)* **46**: 205-224.
15. SAC. (2001). Assessment of surveillance and control of Johne's disease in farm animals in GB. Edinburgh: SAC Veterinary Science Division.
16. O' Reilly LM, Daborn CJ. (1995). The epidemiology of *Mycobacterium bovis* infections in animals and man: a review. *Tubercle Lung Dis.* **76**: 1-46.
17. Krebs JR, Anderson R, Clutton-Brock TH, Morrison I, Young D, Donnelly C. (1997). Bovine tuberculosis in cattle and badgers. London: Ministry of Agriculture, Fisheries and Food.
18. Grant W. (2009). Intractable policy failure: the case of bovine TB and badgers. *Br. J. Pol. Int. Rel.* **11**: 557-573.
19. Woodbine KA, Schukken YH, Green LE, Ramirez-Villaescusa A, Mason S, Moore SJ, Bilbao C, Swann N, Medley GF. (2009). Seroprevalence and epidemiological characteristics of *Mycobacterium avium* subsp. *paratuberculosis* on 114 cattle farms in south west England. *Prev. Vet. Med.* **89**: 102-109.
20. Winkler MTC, Doster A, Jones C. (2000). Persistence and reactivation of bovine herpesvirus 1 in the tonsils of latently infected calves. *J. Virol.* **74**: 5337-5346.
21. Jubb TF, Sergeant ESG, Callinan APL, Galvin JW. (2004). Estimate of the sensitivity of an ELISA used to detect Johne's disease in Victorian dairy cattle herds. *Aust. Vet. J.* **82**: 569-573.
22. Hood C. (1983). *The Tools of Government*. London: Macmillan.
23. Greenstein RJ. (2003). Is Crohn's disease caused by a mycobacterium? Comparisons with leprosy, tuberculosis, and Johne's disease. *Lancet Infect. Dis.* **3**: 507-514.
24. Caplan P. (2010). Death on the farm: Culling badgers in North Pembrokeshire. *Anthropol. Today* **26(2)**: 14-18.

25. Weldegebriel HT, Gunn GJ, Stott AW. (2009). Evaluation of producer and consumer benefits resulting from eradication of bovine viral diarrhoea (BVD) in Scotland, United Kingdom. *Prev. Vet. Med.* **88**: 49-56.
26. Solis-Calderon JJ, Segura-Correa VM, Segura-Correa JC. (2005). Bovine viral diarrhoea virus in beef cattle herds of Yucatan, Mexico: Seroprevalence and risk factors. *Prev. Vet. Med.* **72**: 253-262.
27. Raaperi K, Nurmoja I, Orro T, Viltrop A. (2010). Seroepidemiology of bovine herpesvirus 1 (BHV1) infection among Estonian dairy herds and risk factors for the spread within herds. *Prev Vet Med* **96**: 74-81.
28. Scott HM, Sorensen O, Wu JTY, Chow EYW, Manninen K, VanLeeuwen JA. (2006). Seroprevalence of *Mycobacterium avium* subspecies *paratuberculosis*, *Neospora caninum*, Bovine leukemia virus, and Bovine viral diarrhea virus infection among dairy cattle and herds in Alberta and agroecological risk factors associated with seropositivity. *Can. Vet. J.* **47**: 981-991.
29. Çetinkaya B, Erdogan HM, Morgan KL. (1997). Relationships between the presence of Johne's disease and farm and management factors in dairy cattle in England. *Prev. Vet. Med.* **32**: 253-266.
30. Hanski I. (1989). Metapopulation dynamics: does it help to have more of the same? *Trends Ecol. Evol.* **4**: 113-114.
31. Beaudeau F, Fourichon C, Robert A, Joly A, Seegars H. (2005). Bulk milk somatic cell counts and bovine viral diarrhoea virus (BVDV) infection in 7252 dairy herds in Brittany (western France). *Prev. Vet. Med.* **72**: 163-167.
32. Tiwari A, VanLeeuwen JA, Dohoo IR, Stryhn H, Keefe GP, Haddad JP. (2005). Effects of seropositivity for bovine leukemia virus, bovine viral diarrhoea virus, *Mycobacterium avium* subspecies *paratuberculosis*, and *Neospora caninum* on culling in dairy cattle in four Canadian provinces. *Vet. Microbiol.* **109**: 147-158.
33. Sockett DC, Conrad TA, Thomas CB, Collins MT. (1992). Evaluation of four serological tests for bovine paratuberculosis. *J. Clin. Microbiol.* **30**: 1134-1139.
34. Whitlock RH, Wells SJ, Sweeney RW, Van Tiem J. (2000). ELISA and fecal culture for paratuberculosis (Johne's disease): sensitivity and specificity of each method. *Vet. Microbiol.* **77**: 387-398.
35. Milner AR, Mack WN, Coates KJ, Hill J, Gill I, Sheldrick P. (1990). The sensitivity and specificity of a modified ELISA for the diagnosis of Johne's disease from a field trial in cattle. *Vet. Microbiol.* **25**: 193-198.
36. Çetinkaya B, Egan K, Harbour DA, Morgan KL. (1996). An abattoir-based study of the prevalence of subclinical Johne's disease in adult cattle in south west England. *Epidemiol. Infect.* **116**: 373-379.
37. Bourne FJ. (2007). Bovine TB: The scientific evidence: Independent scientific group on cattle TB; DEFRA.
38. Donnelly CA, Woodroffe R, Cox DR, Bourne FJ, Cheeseman CL, Clifton-Hadley RS, Wei G, Gettinby G, Gilks P, Jenkins H, et al. (2006). Positive and negative effects of widespread badger culling on tuberculosis in cattle. *Nature* **439**: 843-846.
39. Nuotio L, Neuvonen E, Hyytiäinen M. (2007). Epidemiology and eradication of infectious bovine rhinotracheitis/infectious pustular vulvovaginitis (IBR/IPV) virus in Finland. *Acta Vet. Scand.* **49**: 3.

Tables

Table 1. A framework for assessing the political priority accorded to endemic livestock diseases, with consensus scores for four examples in England.

To achieve an overall assessment of an individual disease, each question was scored: 0 (none); 1 (low); 2 (medium); 3 (high); and the scores were aggregated, all questions being weighted equally, except for questions 1a and 1b, which were each given a weighting factor of 5.

Questions	***bTB***	***BVDV***	***BHV***	***Map***
Links with human health				
1a: Is there a significant zoonotic transmission risk, i.e., does it occur more often than an occasional case? (x5)	1	0	0	0
1b: Does zoonotic infection lead to serious or long-term illness that requires hospital treatment as an inpatient or is potentially fatal? (x5)	3	0	0	0
Political factors				
2: What is the level of public/media awareness of the disease?	3[(1)]	0	0	1
3: Do key industry stakeholder groups have a policy position they use resources to pursue on control of the disease?	3	2	1	2
4: Does controlling the disease involve a wild animal with a positive public profile?	3	0	0	0[(2)]
5: Is government significantly concerned about its international reputation in animal health?	3	2[(3)]	2[(3)]	2[(3)]
Management factors				
6: Is the disease diagnosable and, if so, at what stage in the cycle (e.g., before or after the infectious period)? Are there specific clinical signs, readily useable diagnostic tests, what is the range of hosts?	1[(4)]	3	3	1[(4)]
7: Are there good, cost-effective technologies (e.g., vaccines, treatment) that can be used with diagnosis to eliminate infection from a herd?	0	3	3	0
8: Is there a 'demonstration' project that has eliminated/controlled the disease in some defined population?	3	3	3[(5)]	0
Economic impacts				
9: What is the importance of livestock industries in the national economy?	1	1	1	1
10: What is the impact of the disease on the farmer's income stream? Does it entail considerable losses in production for farmers?	3[(6)]	2	2	1
11: What is the effect on commodity prices and hence the final consumer? This will be influenced by supply and demand considerations and consumer product perceptions.	1	2	1	1
12: What is the impact on trade?	3	1[(7)]	1[(7)]	2
International effects				
13: Is the disease notifiable outside the UK?	3	0	0	0
14: Is it on the OIE list of diseases?	3	3	3	3
15: Is there an EU policy on the disease?	3	0	0	0
Total	**53**	**22**	**20**	**14**

Footnotes:
1. High awareness for some aspects
2. Possible rabbit involvement, sheep can be hosts.
3. Potential concern
4. Test has low accuracy
5. e.g. Finland [39].
6. Variable by dairy/beef herd type and farmer experience of living with bTB.
7. Likely future impact

Table 2. Within- and between-herd infections attributed to each infectious class.

Totals are for all herds over 20 iterations of the five year simulation period. The birth of a calf persistently infected with BVDV was attributed to class P if it was due to the calf's dam being persistently infected and to class I if it was due to the dam seroconverting during pregnancy. A herd with no active infection (i.e. all animals susceptible or recovered immune) was considered newly infected when an infectious (or potentially infectious, in the case of animals latently infected with BHV) animal was introduced to it. Within- and between-herd transmissions thus represent counts of cattle infected, and herds infected, respectively. The transmission ratio is the ratio between within-herd transmission and between-herd transmissions for a class of infectious animal.

pathogen	herd type	class	within-herd transmissions	between-herd transmissions	transmission ratio
BVDV	dairy	P	56716	187	303
		I	66753	194	344
	beef	P	78767	325	242
		I	100846	323	312
BHV	dairy	I1	94616	2	47308
		L	NA	41	NA
		I2	30592	0	∞
	beef	I1	43420	10	4342
		L	NA	366	NA
		I2	11006	3	3669
Map	dairy	L	6589	46	143
		H	60096	31	1939
		C	1969	1	1969
	beef	L	3892	305	13
		H	25787	161	160
		C	796	3	265

Table 3. Correlations between the simulated and observed serological status of samples and herds

Overall correlation is the crude correlation at the individual sample level. Between-visit correlations were calculated for seroprevalence at the level of the herd visit, weighted by herd size. Within-visit correlation is calculated at the individual sample level, after recalculating each sampled animal's status relative to the seroprevalence of their herd. Values of β for each pathogen were optimised separately for each herd type. Simulated serological status was averaged over all simulations for each sample and visit.

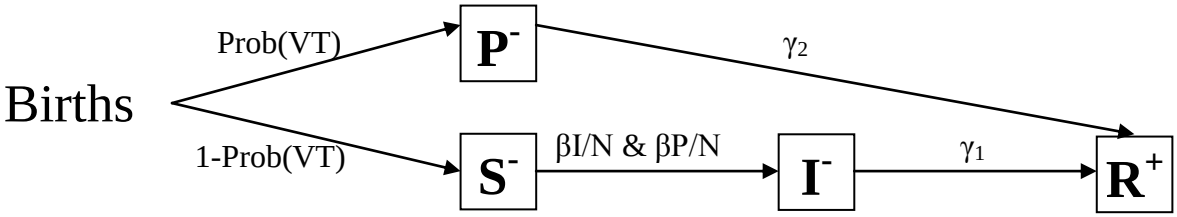
Pathogen	herd type	within	between	overall
BVDV	dairy	18.1%	0.4%	5.4%
BVDV	beef	23.3%	46.6%	36.1%
BHV	dairy	26.0%	2.5%	18.6%
BHV	beef	17.6%	42.6%	28.1%
Map	dairy	0.4%	-4.8%	0.1%
Map	beef	-0.9%	-10.7%	-1.8%

Figures

Figure 1. Epidemiological Models for BVDV, BHV and Map

In the BVDV model, animals were susceptible (S), infectious (I), recovered (R) or persistently infected (P). In the BHV model, cattle were susceptible (S), primarily infectious (I_1), latent (L) or secondarily infectious (I_2). In the Map model, they were susceptible (S), low-shedding (L), high-shedding (H) or clinically infected (C). The +/- superscripts indicate the assumed serological status of each class, subject to test sensitivity and specificity. The subscript 'ad' indicates the number of adult (≥ 2 years old) animals of the given infection class. Parameter values are given in the electronic supplementary material (table S1). Where two infection processes are shown for the same transition, they were combined by calculating the probability of either occurring.

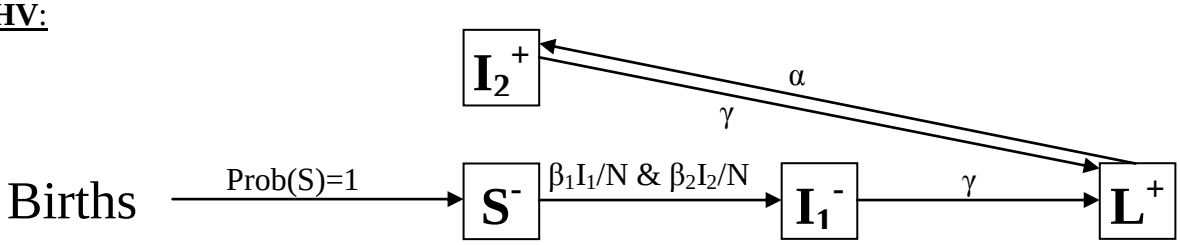
BVDV:



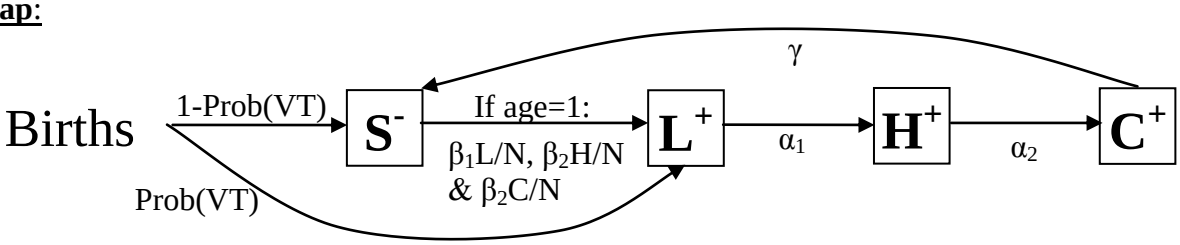
where:

$$\text{Prob(VT)} = \frac{\varepsilon_1 P_{ad,t-280}}{N_{ad,t-280}} + \varepsilon_2\left(1 - \prod_{t-280}^{t-160}\left(1 - \frac{\text{serocon}_{ad,t}}{N_{ad,t}}\right)\right)$$

BHV:



Map:



Where:

$$\text{Prob(VT)} = \varepsilon_1 \frac{(L_{ad} + H_{ad})}{N_{ad}} + \varepsilon_2 \frac{C_{ad}}{N_{ad}}$$

Figure 2. Frequency distributions of seroprevalence among visits

The observed (circles) and simulated (bars) distribution of the seroprevalence of BVDV (a, b), BHV (c, d) and Map (e, f) among visits to dairy (left) and beef (right) herds. Filled circles and the entire bars represent data from all herds, whereas the lower part of the bars and the unfilled circles, where distinguishable, represent data only from herds of 10 or more animals. Visits with exactly zero prevalence were counted separately (left-most bars and circles).

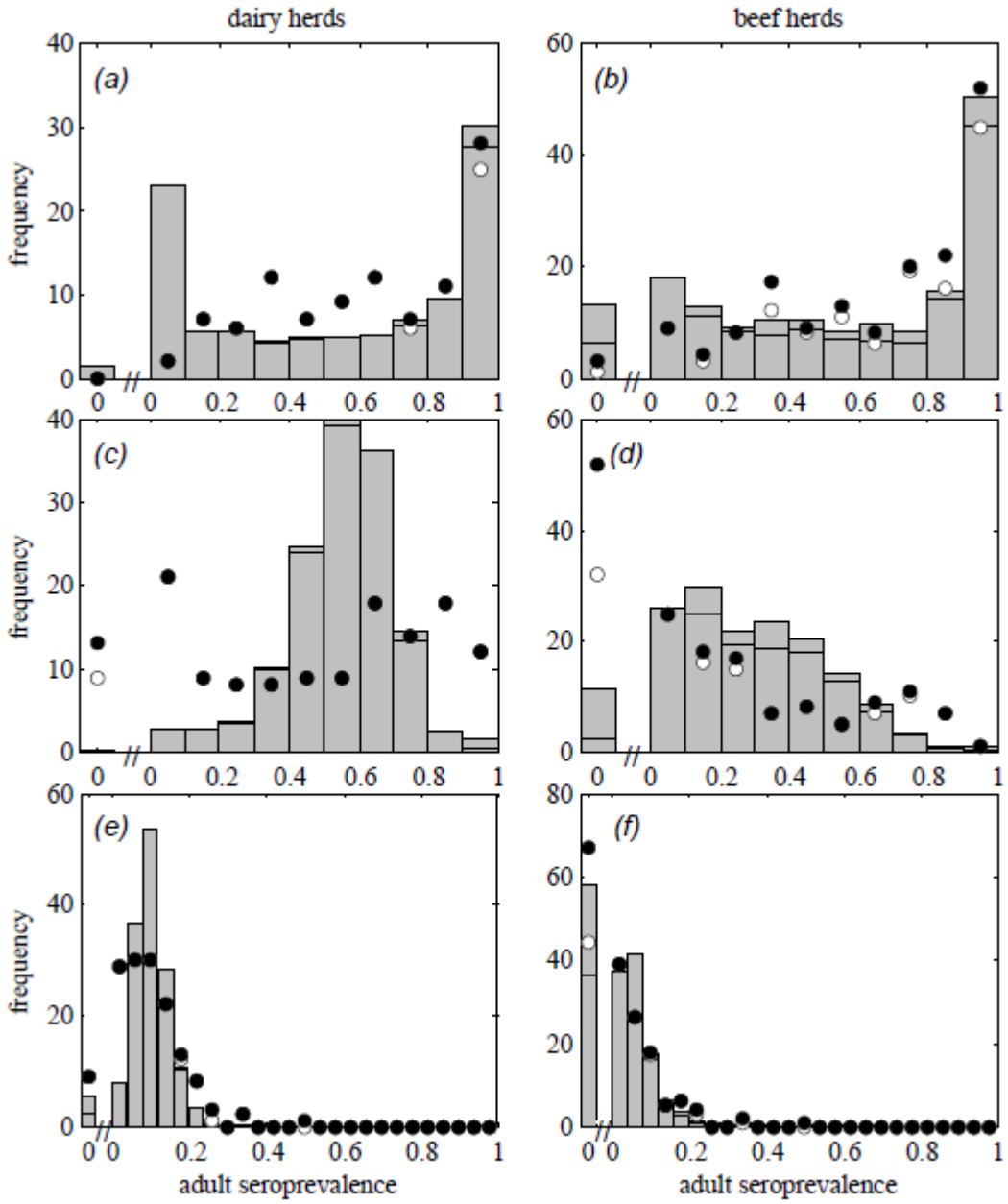


Figure 3. Schematic epidemiological and political classification of cattle diseases

		Epidemiological Classification	
		Farm: Movement of animals plays a relatively small role; or the disease is geographically restricted	*Industry: Transmission between farms through animal movement is relatively common; disease threatens the whole of the national cattle herd*
Political Profile	*High*	Public money used to control, although industry increasingly encouraged to deal with problem farms/areas E.g. bTB 1970-2000	Public money and government resources used to control infection E.g. bTB currently Most exotic pathogens, e.g. FMD
	Low	No public money or resources; it is an individual farm issue E.g. Map, BHV (dairy herds),	Industry will claim help from government, or government will seek to encourage industry. E.g. BVDV (beef herds), BHV (beef herds)