



Livestock as sentinels for an infectious disease in a sympatric or adjacent-living wildlife reservoir host



D.P. Anderson^{a,*}, A.M. Gormley^a, M. Bosson^b, P.G. Livingstone^c, G. Nugent^a

^a Manaaki Whenua Landcare Research, Wildlife Ecology and Management, P.O. Box 69040, Lincoln 7640, New Zealand

^b TBfree New Zealand, P.O. Box 10522, Hamilton 3241, New Zealand

^c TBfree New Zealand, P.O. Box 3412, Wellington 6140, New Zealand

ARTICLE INFO

Keywords:

Bayesian logic
Bovine tuberculosis
Eradication
Mycobacterium bovis
Surveillance

ABSTRACT

A central question to address in managing wildlife diseases is how much effort and resources are required to reduce infection prevalence to below a requisite threshold? This requires surveillance for infection in at least one species involved in the infection cycle, a process that is often expensive and time-consuming but one which could be enhanced using additional sources of readily-obtainable surveillance data. We demonstrate how surveillance data from ruminant livestock monitored for bovine tuberculosis (bTB) in New Zealand can be employed in spatially-explicit modelling to help predict the probability of freedom from *Mycobacterium bovis* infection in a sympatric wildlife reservoir species, the brushtail possum (*Trichosurus vulpecula*). We apply the model to a case study and compare resulting probabilities of freedom when utilizing (1) livestock data only, (2) wildlife data only, and (3) combined livestock-plus-wildlife surveillance data. Results indicated that the greatest probability of *M. bovis* eradication was achieved using wildlife monitoring data supplemented with livestock surveillance data. This combined approach lessened the time required for a confident (95% probability) declaration of regional eradication. However, the combined model was sensitive to the precision of the input parameters, and we describe ways to account for this. In a broad sense, this modelling approach is flexible in that any spatial arrangement of wildlife habitat and farms can be analysed, provided infection is readily detectable in both the wild and domestic animal(s) of interest. It is applicable to monitoring any communicable wildlife disease that affects regularly-tested livestock. The potential benefits to wildlife disease management include reduced surveillance costs and more rapid achievement of targeted reductions in disease prevalence.

1. Introduction

Wildlife disease management aims to control or eradicate diseases that present risks to human health, domestic animals and endangered wildlife (Gortázar et al., 2007). Local reduction in disease prevalence is readily achievable (Corner et al., 2003; Gortázar et al., 2007), but broad spatial-scale wildlife disease management is far more challenging and requires extensive intervention over large areas for extended periods of time (Caley et al., 1999; Coleman et al., 2006). Information about the changing disease status should be updated during and following any practical management action aimed at mitigating the disease, whether that is via prophylactic vaccination or reduction of host population density (Couacy-Hymann et al., 2005; Townsend et al., 2013). Such information helps the wildlife disease manager answer a central question: how much more effort and resources are required to achieve the stated objective? To address this with precision requires some level of surveillance, often across a large proportion of the geographical area of

concern, to obtain a quantitative probability that the disease level in at least one of the species affected has been reduced to the requisite threshold, or even eradicated. This information could include surveillance of the wildlife maintenance host(s) and sympatric spillover hosts (de Lisle et al., 2005; Nugent, 2005). However such information is often expensive to obtain, hence the financial feasibility of operations aimed at mitigating wildlife disease could be enhanced if multiple, widespread and readily-available but inexpensive sources of surveillance data were utilized.

In New Zealand, efforts to eliminate bovine tuberculosis (bTB) from farmed cattle and deer have been complicated by the presence of wildlife reservoirs of *Mycobacterium bovis* infection (Livingstone et al., 2015b; Nugent et al., 2015). The introduced brushtail possum (*Trichosurus vulpecula*) is the primary wildlife maintenance host of *M. bovis* (Jackson et al., 1995; Coleman and Caley, 2000). Additionally wild ferrets (*Mustela furo*; (Caley, 1998)), pigs (*Sus scrofa*; (de Lisle, 1994)) and red deer (*Cervus elaphus*; (Lugton et al., 1997)) have been found

* Corresponding author.

E-mail address: andersond@landcareresearch.co.nz (D.P. Anderson).

infected, oftentimes when sympatric with possums, but in most places are regarded as spillover hosts at the densities at which they occur in the wild, so are often utilized as sentinels to indicate presence/persistence of *M. bovis* infection in possums (Nugent, 2011; Livingstone et al., 2015a). Achieving freedom from *M. bovis* infection in local possum populations is a critical part of New Zealand's effort to progressively eradicate infection from the whole country. That aim is being achieved by intensive lethal control of possum populations in *M. bovis*-endemic areas, an approach that while only transiently successful when practised on a local scale (Corner et al., 2003) has been shown to both mitigate wildlife infection and offer protection to livestock against bTB when undertaken at a regional level (Nugent et al., 2015). Over the last 20 years, sustained possum control operations have helped in reducing the national cattle and farmed deer herd bTB reactor rates by greater than 95% (Livingstone et al., 2015a). However, *M. bovis* infection remains among some residual possum populations and continues to present a threat to livestock, hence surveillance data are routinely collected from possums and from sentinel species in order to make robust inference on the on-going infection status among wildlife (Anderson et al., 2015; Nugent et al., 2015). Such data are analysed using tools developed to quantitatively assess any remaining infection risk (Anderson et al., 2013).

Aside from data accrued from possum population control operations and from wildlife sentinels, an additional valuable source of information on the *M. bovis* infection status of possum populations that has yet to be considered is the bTB status of livestock herds that share, or live immediately adjacent to possum habitats. New Zealand ruminant livestock (dairy and beef cattle, and red deer farmed for venison) are farmed under outdoors conditions, are widely distributed and are highly susceptible to infection from tuberculous possums. The country's bTB control program involves routine *ante mortem* diagnostic screening of livestock, i.e. annually, biennially or triennially (OSPRI, 2015) depending on the perceived level of risk from *M. bovis*-infected possums (Buddle et al., 2015). In addition, slaughtered animals undergo *post mortem* carcass examination for visible bTB lesions at abattoirs. If a possum population is maintaining *M. bovis*, then experience has shown that infection will, eventually, spill-over to sympatric or adjacent-living livestock, at which point it will be detected by *ante mortem* diagnostic testing and/or abattoir surveillance (Livingstone et al., 2015a). Via this mechanism, livestock can thus act as sentinels – in addition to other wildlife sentinels – to indicate the on-going presence of *M. bovis* infection in local possum population(s). The data accrued from the livestock surveillance program are readily available and inexpensive (because they are collected anyway), and could theoretically be used to make important inference on infection persistence in possums.

New Zealand's national bTB eradication strategy (Livingstone et al., 2015a) is progressing in a two-stage process (Anderson et al., 2017), and the use of livestock as sentinels will play an important role in both stages. In *Stage I*, managers use a combination of wildlife vector control and surveillance to declare freedom from infection in vector control zones (VCZs; management zones of approximately 10,000 ha), which enables the freeing-up of financial resources for re-allocation elsewhere. In open farmland areas, where livestock and possums are sympatric, the empirical surveillance required to quantitatively declare a VCZ free of *M. bovis* infection relies largely on monitoring of possum population densities (using interference devices and traps) and on necropsy surveys of wildlife carcasses for tuberculous lesions (which includes bacteriological culture for *M. bovis* (Anderson et al., 2015)). Such surveillance can cost in excess of \$100/ha, although it can be reduced to < \$40/ha if low-cost wildlife sentinels (such as pigs or ferrets) are common; however, they often are not. Thus indirect surveillance of *M. bovis* infection in possums using 'free' livestock surveillance data could potentially provide additional quantitative data on the probability of freedom from infection. This would reduce the amount of costly possum (and wildlife sentinel) surveying required.

In *Stage II* of the eradication process (the 'assurance' phase of the

process), there is an ongoing need for surveillance in VCZs declared free of *M. bovis* infection, because of both the inherent risk of failure (i.e. making a wrong decision) and of the need to estimate VCZ surveillance sensitivities (which would eventually be used collectively to calculate a probability of biological eradication for the entire country; Anderson et al., 2017). To be clear, we use the term 'freedom' to refer to the complete removal of *M. bovis* infection from both livestock and wildlife in a VCZ, and the term 'eradication' for the total area of interest (e.g. New Zealand). Surveillance in *Stage II* needs to be inexpensive and available on a widespread basis, and so surveillance of livestock as sentinels could be a very important data source for VCZs previously declared free of *M. bovis* infection.

In this paper we describe and demonstrate a statistical methodology that uses livestock surveillance data, based on the New Zealand bTB example, to contribute to predictions of *M. bovis* infection freedom in a possum population given negative surveillance results. The model is spatially explicit because it incorporates the spatial arrangement of livestock herds and possum habitat in the area of interest, which will influence disease transmission from wildlife to livestock and therefore the probability of disease detection. We focus on *Stage I* of the *M. bovis* eradication strategy, and apply the modelling examples at the VCZ level. We address three objectives: (1) to describe the probabilistic relationships in the spatial surveillance-data model for quantifying the probability of freedom from *M. bovis* infection among possums based on livestock surveillance data; (2) to assess sensitivity of model predictions to model parameters; and (3) to demonstrate application of the model to the local vector control operation currently being undertaken in the Blythe Valley VCZ (a farmland region on the east coast of the South Island of New Zealand) using livestock-, host- and sentinel-surveillance data.

2. Materials and methods

2.1. Model description

The following logic was used to develop a model that uses livestock bTB surveillance data to make inference on the probability of freedom of *M. bovis* infection in a sympatric possum population. To detect *M. bovis* infection in an infected possum population using livestock data the following sequence of events must occur: 1) a livestock animal encounters an infected possum and becomes infected with *M. bovis*; 2) the infection is detected by either (a) a positive *ante mortem* diagnostic screening result that is then followed by slaughter and confirmation of bTB during abattoir inspection or (b) at routine slaughter unrelated to recent *ante mortem* testing (by identification of archetypal bTB lesions); and 3) the subsequent confirmation of *M. bovis* infection in lesions or suspect tissues by PCR or culture for viable bacilli. The model uses livestock bTB surveillance data organized by herd/farm, and parameters from the literature related to disease transmission from possums to livestock, possum homerange movement behavior, and bTB test sensitivity. The model is written in the Python computing language (pseudo-code available in Appendix S1).

The modelling approach employs a similar spatial sampling procedure to that previously described for estimating the probability of eradication of *M. bovis* infection in possums based on wildlife surveillance data (Anderson et al., 2013). To implement the method, a spatial grid-cell system is super-imposed over the area of interest, with each grid cell as the spatial sampling unit. The model can use any resolution, but we used 1 ha grid cells as these are smaller than the expected possum home-range size (Pech et al., 2010). The surveillance system quantifies the probability of detecting *M. bovis* infection in each grid cell given an infected possum has its home-range center in the grid cell. The grid cells in which livestock are exposed include the grid cells accessible by livestock within all farms' boundaries, plus a small buffer around all farms that could harbor home-range centers of possums. Spatial raster or polygon-vector data are used to assign farms and

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