

Analysis of Cattle TB Surveillance Data to Identify Wildlife Sources of Infection

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We present an epidemiological analysis of bovine tuberculosis (TB) data derived from routine cattle surveillance. Analysing such data presents opportunities to detect the changes of source of infection throughout time and evaluate wildlife reservoir control strategies for limiting disease transmission. In this study, a range of descriptive and analytical techniques was applied to understand the temporal and spatial features of the disease in the study area during four time periods that coincided with TB and wildlife control measures that were applied. Our objectives were to: (1) describe the geographical patterns of confirmed TB infected cattle and how these relate to changes in possum depopulation strategies that have been applied over time; (2) investigate the contribution of neighbouring-farm contacts to *Mycobacterium bovis* transmission in cattle; and (3) to investigate the influence of environmental and farm-level covariates on the risk of TB infection.

Temporal and spatial patterns of TB in cattle were described using choropleth maps of adjusted incidence. The spatial scan statistic showed a clustering of TB on farms that were close to forest areas in which possums had been less intensively culled. The space-time K-function provided no evidence of spatio-temporal interaction of TB risk ($P = 0.28$), suggesting there was no TB spread between neighbouring farms. A mixed-effects Poisson model was used to quantify the influence of proximity to forest areas and other farm-level factors on the risk of TB in cattle. These analyses showed that proximity to forest areas had the strongest influence on TB risk, which was constant (RR range: 0.54 – 0.77) in spite of increasing levels of vector control intensity throughout the study period. TB risk was not associated with farm type (p -value > 0.2) but was dependent on herd size (RR range: 1.27 – 1.31), consistent with studies conducted elsewhere.

Application of such techniques to cattle surveillance data provided insights into the source of TB in this local area and provided an evaluation of control effectiveness. It enabled us to recommend improvements in TB and wildlife control programs.

ABSTRACT

, to identify the wildlife sources of TB infection associated with the persistence of a low incidence in cattle. We present an epidemiological analysis of bovine tuberculosis (TB) data derived from routine cattle surveillance, to identify the wildlife sources of TB infection associated with the persistence of a low incidence in cattle. A range of descriptive and analytical techniques was applied to understand the temporal and spatial features of the disease in this area during four time periods that coincided with TB and wildlife control measures that were applied. Application of such techniques to cattle surveillance data provided insights into the source of TB in this local area and provided an evaluation of control effectiveness. It enabled us to recommend improvements in TB and wildlife control programs.

INTRODUCTION

Analysis of routinely collected data presents opportunities to detect the changes of source of infection throughout time and evaluate wildlife reservoir control strategies for limiting disease transmission. In this study, spatial and explanatory analyses were conducted to find any geographical and temporal pattern of bovine TB among farms as well as putative variables associated with epidemic spread.

Our objectives were to: (1) describe the geographical patterns of confirmed TB infected cattle and how these relate to changes in possum depopulation strategies that have been applied over time; (2) investigate the contribution of neighbouring-farm contacts to *M. bovis* transmission in cattle; and (3) to investigate the influence of environmental and farm-level covariates on the risk of TB infection

MATERIALS AND METHODS

Data for each cattle farm present in the Featherston Township area between 1980 and 2003 were retrieved from two data sets. The first was the National Livestock DataBase (NLDB) (Ryan, 1997) which provided details of the number of cattle tested for TB and of confirmed cases. The second was AgriBase (Sanson & Pearson, 1997) which records the location and boundaries of farming properties and provides basic information about farms (e.g. type, contacts) of livestock present on farm which enable us to produce digital maps and to generate farm-level geographical putative variables.

We defined four six-year time periods that broadly coincided with possum control policies applied in the Featherston area from 1980 to 2003. These were: (1) 1980 – 1985: test-and-slaughter control (TSC) in cattle which had been in operation since the mid-1970s, and no possum control; (2) 1986 – 1991: intensive TSC in cattle, and no possum control; (3) 1992 – 1997: TSC in cattle, plus bi-annual possum control on farmland and bush-pasture margin, with aerial control of the forest in 1996; and (4) 1998 – 2003: TSC in cattle, plus annual possum control on farmland and bush-pasture margin, with aerial control in the forest in June 2001. Defining the time periods in this way allowed us to crudely evaluate the effectiveness of the various control TB strategies applied over the past twenty years, assuming that the effect of a given control strategy was reflected relatively quickly in the results of cattle TB testing.

Data were analysed in three stages. Firstly, the spatial distribution of TB cases, which were diagnosed within selected phases of the study period, was plotted using choropleth maps of adjusted incidence rate. Using the date of diagnosis and location details the presence of spatio-temporal interaction in farm-level diagnosis patterns was assessed using the space-time K-function (Diggle et al., 1995). Secondly, the spatial pattern of TB-positive animals was described using the spatial scan statistic (Kulldorff and Nagarwalla, 1995). Thirdly, a mixed effect Poisson model was fitted over the count of TB cases for each six-year time periods to estimate the influence of farm-level putative covariates on the fact of experiencing a case of TB.

RESULT

The spatial scan statistic showed a clustering of TB on farms that were close to forest areas in which possums had been less intensively culled. The space-time K-function provided no evidence of spatio-temporal interaction of TB risk, suggesting there was no TB spread between neighbouring farms.

A mixed-effects Poisson model was used to quantify the influence of proximity to forest areas and other farm-level factors on the risk of TB in cattle. These analyses showed that proximity to forest areas had the strongest influence on TB risk, which was constant (RR range: 0.54 – 0.77) in spite of increasing levels of vector control intensity throughout the study period. TB risk was not associated with farm type (p-value > 0.2) but was dependent on herd size (RR range: 1.27 – 1.31), consistent with studies conducted elsewhere.

Our analyses reveal that, thus far, the incidence of cattle herd breakdowns has been 19% lower in proactive trial areas than in survey-only areas (95% CI 6.2–30%)

This result was consistent

Our analyses revealed no significant change in the effect of culling on breakdown incidence over time

We also compared the incidence of cattle

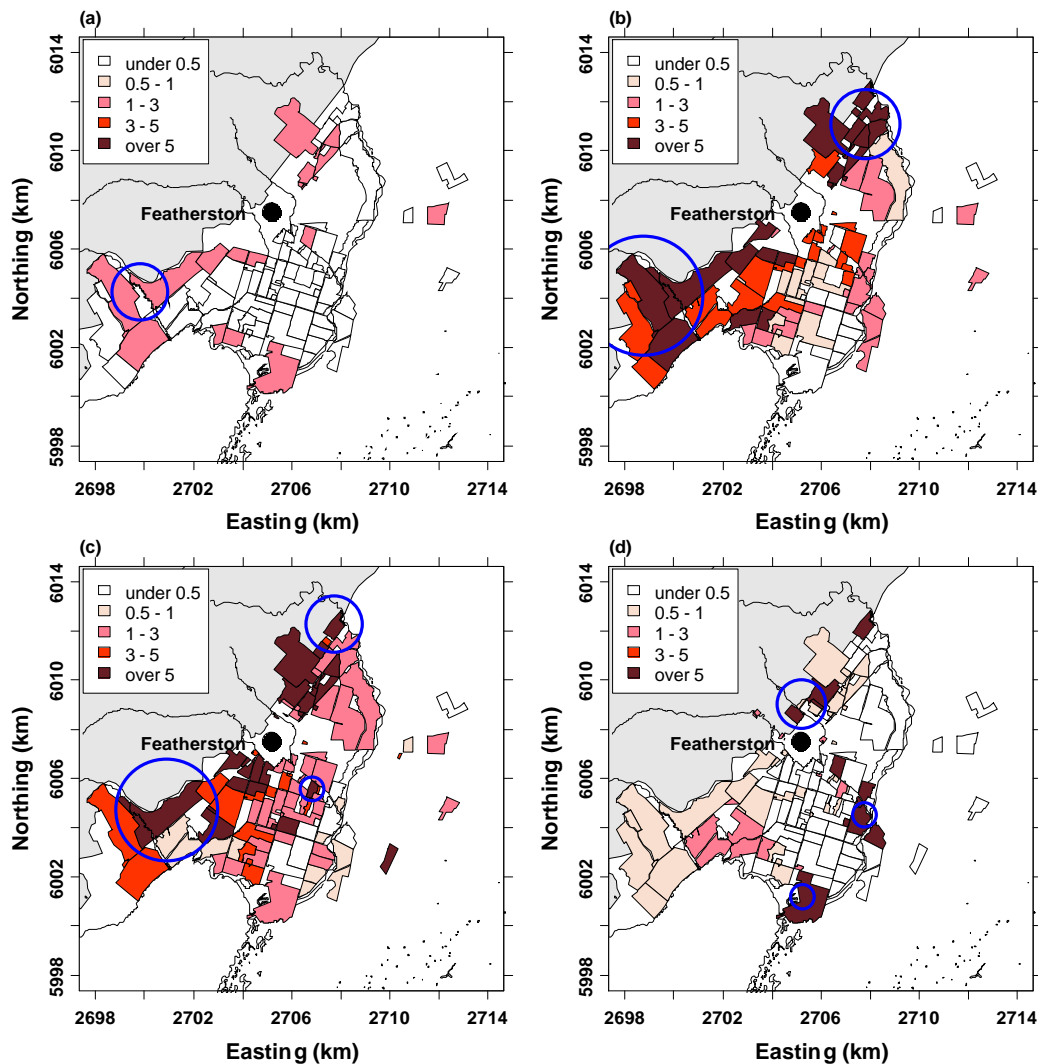


Figure 1: Tuberculosis in the population of cattle in the Featherston area of New Zealand, 1980 – 2003. Choropleth maps showing the empirically Bayesian-adjusted tuberculosis incidence rate in cattle (expressed as cases per 1000 cattle-years at risk) and the location of the most likely spatial clusters (circles) of TB-positive cattle for: (a) 1980 – 1985, (b) 1986 – 1991, (c) 1992 – 1997, and (d) 1998 – 2003.

Table 1: Risk factors for bovine TB on cattle farms in the Featherston area of New Zealand, 1980 – 2003, estimated using a logistic regression model.

Explanatory variables	1980 to 1985			1986 to 1991		
	N	TB	RR (95%CI)	N	TB	RR (95%CI)
Intercept	27949	9		37355	121	
Herd size	27949	9	1.3 (0.7 – 2.4)	37355	121	1.3 (1.1 – 1.5)
Farm type						

Dairy	21922	3	1.0	28080	54	1.0	
Beef	6027	6	2.0 (0.3 – 13.8)	8833	60	0.8 (0.5 – 1.4)	
Other	139	0	–	442	7	0.6 (0.2 – 1.8)	
Prev1	2348	3	2.2 (0.3 – 15.5)	10499	60	1.8 (1.1 – 3.0)	
Bush distance (km)	27949	9	0.7 (0.3 – 1.3)	37355	121	0.5 (0.4 – 0.7)	
		1992 to 1997			1998 to 2003		
Explanatory variables	N	TB	RR (95%CI)	N	TB	RR (95%CI)	
Intercept	53212	183		63108	33		
Herd size	53212	183	1.3 (1.1 – 1.4)	63108	33	1.3 (1.1 – 1.6)	
Farm type							
Dairy	34371	88	1.0	42469	16	1.0	
Beef	16986	88	0.7 (0.4 – 1.2)	16582	16	0.6 (0.2 – 1.9)	
Other	1855	7	0.3 (0.1 – 0.9)	4057	1	0.1 (0.01–0.7)	
Prev1	29618	136	2.1 (1.3 – 3.3)	14341	11	0.9 (0.6 – 1.6)	
Bush distance (km)	53212	183	0.8 (0.6 – 0.9)	63108	33	0.7 (0.5 – 0.9)	

RR. Relative risk.

CI. Confidence interval.

N. Total number of cattle-year considered.

TB. Number of TB positive cattle considered.

CONCLUSION

REFERENCES

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