Geographic Modeling of the Distribution of Tuberculosis in Possums in New Zealand

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Abstract

The significance of spatially explicit habitat factors in the distribution of TB in possums makes geographic information systems (GIS) a useful tool to manage and analyse data associated with TB-related possum control programmes. This paper describes two studies in which we explored how a GIS could be used to model the distribution of TB in possums at two scales. We developed a model comprising three possum TB risk categories at a scale of 20-meter pixels in ArcView from vegetation and slope grid maps. In a second study we used ArcView to obtain data on possum habitat and other geographic features of farms. Binomial logistic regression modelling was used to identify the variables that were significantly associated with the probability of cattle on a farm being infected with TB by possums and being detected under the MAF Quality Management TB surveillance system. The resulting probabilities were then displayed on a farm map using a GIS.

These models provide a useful means of displaying possum TB risk information at different scales within a GIS. They are useful tools for the development of possum control strategies as they facilitate decisions on targetted use of resources based on an area's possum TB risk. The models have been incorporated into a decision support system, known as EpiMAN(TB), to facilitate their application at an operational level.

1. Introduction

The brushtail possum (*Trichosurus vulpecula*) is the major source of tuberculosis (TB) infection for farmed cattle and deer in New Zealand (Livingstone, 1997; Morris & Pfeiffer, 1995; Hennessy, 1986). The presence of this wildlife vector is seriously complicating the eradication of TB from farmed animals and has resulted in an extremely expensive control programme. The resource spent on possum control has increased dramatically over the past ten years, from a low of less than $1 million dollars in the early 1980s to an estimated $19 million (standardised to 1990 dollars) in 1996/97 (Livingstone, 1997). This has resulted in a decline in the incidence of TB in farmed cattle and deer. However, we believe that additional strategies and planning tools are needed to maintain the cost-effectiveness of control programmes in low-density possum populations where the prevalence of TB is very low. Such strategies and tools can utilise recent information that has become available on environmental factors associated with the distribution if TB in possums.

The spatial distribution of TB in possums is clustered at three scales. It is present in possum populations only in certain regions of New Zealand, and within these affected regions certain farms or groups of farms have a TB problem while others have no (or very infrequent) infection. The smallest unit of clustering is associated with possum denning areas occupying as little as 0.25-0.5 hectares (Pfeiffer, 1994; Hickling, 1995). Field research indicates that

TB clusters in possums fall into two categories: permanent (sometimes referred to as endemic) and temporary (sometimes referred to as sporadic), and the distribution of these clusters is associated with specific habitat factors (McKenzie et al, 1997). Permanent clusters are more likely to occur at locations where there are multiple dens that are fully enclosed, providing an environment that favours the transmission of TB between possums. This results in the disease remaining in the possum population at such locations on a permanent basis, albeit with a prevalence that fluctuates over time. Temporary TB clusters occur at sites that differ from negative TB sites in terms of the structure of the habitat, for example, they are more likely to be associated with taller trees. However, there is no significant difference in the abundance of fully enclosed dens, suggesting that such sites do not favour the transmission of TB between possums, hence the cluster disappears after a relatively short period of time. It is highly likely that TB is maintained in possum populations at the sites of permanent clusters even after the population density has been reduced to a low level by control measures (Hickling, 1991). It is the perpetuation of TB at such locations that means possum populations must continually be kept at a low level to reduce the risk of TB spreading from possums to farmed cattle and deer. This is a major expense to the industry, and the ability to target control measures at areas where the effect is likely to be greatest would improve the efficiency with which possum control resources are used.

Given the importance of spatial factors in the distribution of TB in possums, Geographic Information Systems (GISs) can be a useful tool for the management and analysis of data to support TB-related possum control programmes. However, there has been very limited application of GISs in this area to date. To maximise the application of GISs in this possum control context further research is needed to identify how field research results can be matched to spatial data available in GIS databases to predict the distribution of TB in possums.

This paper describes two projects in which we have applied a GIS to produce models of the distribution of TB in possums using spatial data. The first is a geographic model of the distribution of possum TB clusters at the scale of the individual cluster. The second is a study that we conducted using a GIS to manage and analyse spatial data to identify geographic and habitat factors that can be used to classify farms according to the risk of cattle being infected by possums. Finally we briefly describe how these models are incorporated into a decision support system, known as EpiMAN(TB), to facilitate their application at an operational level.

2. Geographic Model of the Distribution of Possum TB Clusters

Recent research has shown that slope of the land and the presence of multiple dens that are almost fully enclosed were the most significant factors in predicting the location of permanent clusters of TB in possums (McKenzie et al, 1997). Slope of the land and height of the canopy layer were the most significant factors in predicting the distribution of temporary clusters of TB in possums. The research also showed that the specific types of habitat that provided these conditions varied between areas. For example, in the central North Island permanent TB clusters were associated with tall large-diameter trees on flat ground as these provided enclosed den sites within their trunks, under their roots or in old hollow logs and stumps. In contrast, in the coastal Wairarapa permanent TB clusters tended to be associated with a lower dense canopy of old gorse located on very steep slopes. Thus, models of the distribution of TB in possums need to be specific to an area, taking into consideration the types of habitat available and identifying those that are more likely to provide den sites that are enclosed.

Our aim was to build a geographic model of the distribution of possum TB hot spots by applying field research results to available digital data. Details of the geographic data used to model TB hot spot distribution are described below.

2.1 Geographic Data

The model was developed in ArcView version 3.0a (Environmental Systems Research Inc, Redlands California, USA) using the Spatial Analyst extension. Geographic data sets used in the model are described below.

2.1.1 Slope data

A slope map was derived from a 20-meter digital elevation model (DEM) using the SLOPE algorithm in Spatial Analyst. The slope grid was then reclassified into 10° categories using the RECLASSIFY function in Spatial Analyst. We used a 20-meter DEM that had been generated by the Landcare remote sensing group. Height data was interpolated from 20-meter contour lines (purchased from Terralink) to a resolution of 10 meters, and then generalising the resulting DEM to 20 meter resolution.

2.1.2 Vegetation data

The most important characteristic of vegetation that related to the distribution of possum TB clusters was the abundance of enclosed den sites (McKenzie et al, 1997). However, there were no maps that displayed vegetation classes in terms of this factor. It was not practical to collect this information over large areas of land as it involved detailed investigation of all potential locations to identify the nature of the available den sites. We thus needed to identify features in available vegetation maps that would represent the likelihood of enclosed dens occurring, and also represent different tree heights. Enclosed dens most commonly occur under roots and within hollow trunks of large trees, in old logs or stumps, (Cole, 1995; Green & Coleman, 1986) or under dense canopy which is near ground level such as that provided by dense gorse with dry litter underneath. The most detailed digital vegetation data that was available at the time of conducting this study (1994-96) at a scale large enough to identify small patches of possum habitat was that derived from a SPOT3 satellite image. While this had adequate spatial resolution at 20 metres, the spectral information was limited. Given this was the only multispectral imagery at this scale that was likely to be available in

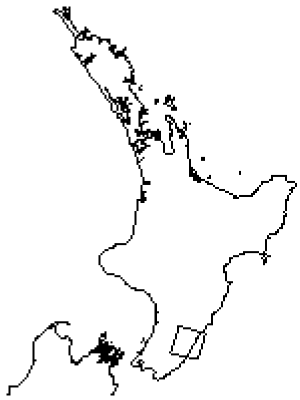

Figure 1. Map showing the location of the SPOT3 satellite image

the short term, we felt it would be useful to determine how useful it would be in modelling the distribution of possum TB clusters.

We used a SPOT3 multi-spectral image of northern Wairarapa that was acquired on 3 March 1994 (Figure 1). The image was rectified to the New Zealand Map Grid (NZMG), and was orthorectified using a 20-meter raster digital elevation model. Image analysis was conducted in ERDAS Imagine (ERDAS Inc, Atlanta, Georgia, USA), using a supervised classification approach. We were able to identify eight vegetation classes with an acceptable level of accuracy. These are listed in the first column of Table 1. Error checking of the data showed that five of the eight classes were specific to either one species or a group of related species that had been identified with a high level of accuracy, while the remaining classes were quite heterogeneous and contained a wide range of unrelated species. Pine (*Pinus radiata*) was the most specific class, followed by podocarp/broadleaf, manuka/kanuka (*Leptospermum scoparium, L. ericoides)*, manuka-kanuka-pasture, and pasture. Manuka/gorse (*Ulex europaeus)*, shrubland and beech (*Nothofagus* species) were the most heterogeneous classes. Beech represented both large stands of beech trees and scattered trees on pasture, particularly pine and podocarp species. Shrubland represented smaller trees scattered on pasture, such as willows (*Salix* species), kowhai (*Sophora* species) and manuka/kanuka plus low density gorse on pasture. Manuka/gorse represented patches of pure gorse, mixed gorse

Vegetation classes	Slope categories (degrees)									
	0 – 10		**11 – 20**		**21 – 30**		**31 – 40**		**41 - 60**	
	CNI[1]	Wair[2]	CNI[1]	Wair[2]	CNI[1]	Wair[2]	CNI[1]	Wair[2]	CNI[1]	Wair[2]
Podocarp/broadleaf	High	Mod	Mod	Low	Low	Low	Low	Low	Low	Low
Beech	Mod	Low	Low	Mod	Low	Mod	Low	Low	Low	Low
Pine	Mod	Mod	Mod	Mod	Low	Low	Low	Low	Low	Low
Manuka/Pasture	Mod	Low	Low	Low	Low	Low	Low	Low	Low	Low
Manuka	Mod	Low	Low	Low	Low	Low	Low	Low	Low	Low
Manuka/Gorse	Low	Mod	Low	Mod	Mod	Mod	Low	High	Low	High
Shrubland	High	High	Mod	Mod	Mod	Mod	Low	Mod	Low	Mod
Pasture	Low	Low	Low	Low	Low	Low	Low	Low	Low	Low

[1] CNI: Central North Island (Turangi, Western Bays of Lake Taupo, Taumarunui)

[2] Wair: Wairarapa (Wairarapa and Wellington)

Table 1: Rules that combine vegetation and slope categories in a model of the distribution of possum TB clusters in the Wairarapa and the central North Island.

and manuka, patches of short dense manuka and some broadleaf species.

Smoothing of the vegetation map was not conducted as clustering of TB in possums can occur in association with habitat patches at a scale as small as 50 m^2 and we wanted to retain the full extent of habitat heterogeneity. The map was retained in a 20-meter grid format as this managed the heterogeneity of the resulting map better than a vector format that would have had many tiny polygons. It also enabled us to use the Spatial Analyst functions for grid maps in ArcView.

As a combination of vegetation and slope influenced the abundance and quality of dens that in turn influenced the TB risk in possums, we generated categories of vegetation by 10^o slope class using MAP QUERY. A separate grid was generated for each vegetation-slope category from the original vegetation and slope grids.

2.2 Hot spot model

TB hot spot risk was represented as 3 categories: high, medium and low. High and medium categories represented permanent and temporary TB cluster sites respectively, and the low risk category represented TB-negative sites. Each combination of vegetation class and 10^o slope category was allocated a risk value according to the likelihood of their representing the variables found to be significantly associated with possum TB clusters. Given the variation between areas in the vegetation classes that are associated with these risk factors we developed a model for the central North Island area and another for the Wairarapa. The former model was based on the findings of the hot spot study (McKenzie et al, 1997), and the latter was based on combined information from the hot spot study and the longitudinal study conducted in the Wairarapa (Pfeiffer 1994; Jackson 1995). The rules for these two models are presented in Table 1.

A separate grid for each of the three risk categories was generated from the individual vegetation-slope grids using MAP QUERY. The medium and high-risk maps were then displayed over the original vegetation map so that the risk areas could be seen within the context of the vegetation on the farm. This is important as control measures are most likely be applied to the entire vegetation patch within which the hot spot lies. We also built the model using the matrix presented in Table 1 in a decision support system, known as EpiMAN(TB) which is briefly described later in this paper.

2.3 Hot spot model validation

Validation of this model is very difficult as there are relatively few accurate records of the locations where tuberculous possums have been found in the area for which we have the digital data, and most of the known locations were used to develop the model. It is difficult to locate TB-positive possums. The most common approach is to conduct necropsy surveys in which possums are trapped and necropsied to look for the presence of TB lesions. Some such surveys have been conducted in the Wairarapa, however, accurate records of the locations of TB-positive possums were not kept. Some locations are known to the level of the patch of bush or scrub and these will be used together with a small number of accurate locations of TB possums that have been found since the study was conducted, to validate the model.

3. Farm TB Risk Study

The aim of this study was to identify habitat and geographic factors that could be used to classify farms according to the risk of cattle being infected with TB from possums, using data available within a GIS.

3.1 Study area

The study area covered a 60 square kilometer area in the northern Wairarapa (figure 1). The location and extent of this area was dictated by the satellite image that we obtained to generate a vegetation map. This area is a pastoral farming area dominated by extensive sheep and beef farming. The topography of the land is rolling to steep hills. Vegetation is predominantly improved pasture species. The coastal region is dominated by a range of hills that runs parallel to the coast and is covered predominantly with pine forest. The areas of these hills that are not planted in pine are covered by either large areas of beech or podocarp – broadleaf forest or a mixture of gorse and manuka in areas where forest has been cleared. Further inland there are patches of predominantly manuka/kanuka in gullies, some pine plantations and podocarp forest remnants. There are some plantings of exotic species such as willows and poplars for soil conservation purposes, and willows are the dominant species lining river banks.

3.2 Geographic data

3.2.1 Vegetation and slope data

Details of these data sets are provided in section 2.1.

3.2.2 Rivers map

We used a rivers map that had been digitised from NZ topographic maps at a scale of 1:250000.

3.2.3 Farm map

A map of farm boundaries was obtained from MAF Quality Management's (MQM) national farm database, Agribase. This database contains digital farm boundary information plus descriptive information for each farm such as land owner, main enterprise type, farm area and stock numbers. Each farm is identified by an unique Farm Identification (FarmID) number. Agribase is built up from the Digitial Cadastral Database (DCDB) and is registered to the NZMG. The map was not complete for the Wairarapa at the time of the study, thus we were only able to use the farms for which accurate boundary information was available.

3.3 Farm selection

A total of 171 beef breeding farms was included in the study. Only beef breeding farms were used in the study to reduce the confounding effect of TB in purchased cattle, as we were interested in measuring the TB in cattle acquired from possums on the farm. Beef breeding farms purchased a smaller proportion of their cattle than dry stock farms which purchase almost all their stock. Dairy farms were excluded as they tend to graze their cattle off-farm during the winter thus the TB incidence in cattle may not have been a true reflection of the possum TB situation on the home farm. Only farms with a land area greater than 10 hectares were included in the study.

3.4 Outcome variable

This study used the incidence of TB in cattle as an indicator of the incidence of TB in possums on each farm. All cattle on the study farms were tested annually for TB and animals reacting positively to the test were sent for slaughter. In addition to on-farm testing of cattle, TB surveillance is conducted in all slaughter plants. All cattle carcases are inspected for the presence of TB lesions, and suspect positive lesions are confirmed using laboratory diagnosis. The TB control program is administered by MQM, and all TB surveillance results are recorded in the National

Livestock Database (NLDB). This data can be linked to farm data by the FarmID.

We used the maximum annual incidence of TB in cattle from the testing history for each farm as the outcome variable, as we believed that this represented the maximum expression of the disease in possums associated with maximum contact between cattle and infective possums on each farm. Incidence was measured as the total number of cattle that reacted to the TB test plus cattle that had not reacted but were detected as having lesions at slaughter. The denominator was the total number of cattle tested at the whole herd test in that year.

3.5 Independent variables

The land-based independent variables were all collected for an area that included the farm plus a buffer of 100 meters surrounding the farm. This was to allow for the influence of possums on a neighbouring property, given that the movement of possums is not stopped by farm boundary fences. Data for spatial variables was generated within ArcView version 3.0a (Environmental Systems Research Inc, Redlands, California, USA) using the Spatial Analyst extension. Data were then exported to Microsoft Access for Windows version 7.0 (Microsoft Corporation, Redmond, WA, USA) for collation into a format suitable for statistical analysis.

3.5.1 Habitat data

The total area of each vegetation-slope category was calculated using the TABULATE AREA function in Spatial Analyst. The area of each category was tabulated by farm polygon and by buffer polygon. These areas were then summed in Access to give a total for the farm plus 100-meter buffer.

3.5.2 River data

To estimate the length of river on each farm, we converted the line coverage to a grid file and then tabulated the area of river for each farm and buffer polygon. This was represented in the analysis as proportion of the farm plus buffer area covered by rivers.

3.5.3 Distance from coastal forest

Farms surrounding the coastal forest are thought to have a worse TB problem than other farms so we created a variable for distance from coastal forest using spatial analyst. We did this by converting the farm shape file to a 50-meter grid file then used the DISTANCE function in Spatial Analyst to determine the distance of each 50-meter cell from the forest polygons. We then calculated the average distance from all cells on each farm.

3.5.4 Farm factors

Total area represented the area of the farm plus the area of the 100-meter buffer in hectares. *Ratio of buffer area to farm area* was used to represent the shape of the farm. *Livestock density* was calculated by determining the livestock units (LSUs) present on the farm. We used a multiplication factor of 4 and 1 for cattle and sheep respectively to convert them to livestock units. This number was then related to the area of the farm as LSUs per hectare.

3.6 Statistical modelling

The association between farm-based risk factors and the maximum annual incidence of TB in cattle was modelled using a binomial logistic regression model adjusted for overdispersion. The numerator was the number of TB-positive cattle recorded during the year of maximum annual incidence, and the denominator was the number of cattle tested by MQM during the whole herd test for that year. Adjustment was made for overdispersion as the model assumption of independent observations was violated by including all tested cattle from each farm (McDermott et al, 1992). Stepwise regression was first conducted without adjustment for overdispersion to identify the variables that were significantly associated with the outcome probability. The resulting model was then run again with an adjustment for overdispersion. Stepwise binomial logistic regression was conducted in Egret version 1.02.07 (Statistics and Epidemiology Research Corporation and Cytel Software Corporation, Seattle, Washington, USA). Logistic regression with the overdispersion factor was conducted using PROC LOGISTIC in SAS for Windows version 6.12 (SAS Institute, Cary, NC, USA).

Variable	Unadjusted model	Adjusted model
ForestDistance (2 km units)	0.95 (0.94-0.96)	0.94 (0.91-0.97)
Grass on 0-10º slopes (Ha)	0.99 (0.998-0.999)	
PctRivers	1.34 (1.21-1.57)	1.50 (1.09-1.99)
Beech on 11–30º slopes (Ha)	1.30 (1.24-1.37)	
Manuka/Pasture on 21-30º slopes(Ha)	0.91 (0.89-0.94)	
TotalBeech (Ha)	0.86 (0.83-0.90)	
Manuka/Pasture on 41-60⁰ slopes (Ha)	14.7 (6.12-34.52)	
Shrub on 0º – 10º slopes (Ha)	1.03 (1.02-1.04)	
Manuka/Pasture on 0-10º slopes (Ha)	1.03 (1.02-1.04)	
Manuka on 41º – 60º slopes (Ha)	0.40 (0.26-0.62)	
Total Manuka (Ha)	1.01 (1.002-1.006)	
Grass on 41–60º slopes (Ha)	0.92 (0.87-0.97)	
Podocarp on 41º – 60º slopes (Ha)	0.76 (0.61-0.91)	
Manuka/Pasture on 31-40º slopes (Ha)	1.13 (1.01-1.26)	

Table 2: Significant variables in two binomial logistic regression models of the probability of finding TB-positive cattle on farms in the Wairarapa, the first unadjusted and the second adjusted for an overdispersion factor.

3.7 Results

A total of 44 farm-based risk factors was examined. The initial stepwise binomial logistic regression produced a model with 15 variables. However, once the model was adjusted for overdispersion only two variables: distance to the coastal forest and percent rivers, remained significant. The significant variables in both models are listed in Table 2 together with their odds ratios and associated 95% confidence limits.

3.8 Discussion

The two significant factors shown to be associated with the probability of possum-associated TB in cattle at the farm level were distance from the coastal forest and percent of the farm covered with rivers. While no individual vegetation-slope categories were shown to be significant once overdispersion was accounted for, these two significant variables are most likely representing vegetation factors on farms. Rivers are predominantly lined by willow trees, and these provide very favourable habitat for possums. As willows become older they often develop holes in their trunks and under their roots which provide a favourable environment for the transmission of TB between possums. The increased TB risk associated with being closer to the coastal forest is most likely due to closer farms having more scrub cover that provides favourable habitat for high densities of possums, and in many cases for the transmission of TB between possums. The effect of individual vegetation-slope categories appeared to be accounted for by these two variables. The lack of significance of individual vegetation-slope categories may also have related to the lack of specificity of vegetation species in the vegetation map, particularly for the shrubland and manuka-gorse categories. Field testing showed that these categories represented different plant species at different locations on the map. If the plant species represented within one category are associated with different possum TB risks, then the effects of these on TB risk in cattle at a farm level may have been cancelled out. Modelling with a more detailed vegetation map that has more specific differentiation of plant species may result in an improved model that includes risks associated with individual vegetation-slope categories. New satellite imagery with greater spectral resolution and high spatial resolution will enable more detailed vegetation maps to be produced. Such imagery is now becoming available with the recent launch of SPOT4 and others planned for the future.

Our aim was to build a logistic regression model that could be used to identify farms in an area that have a higher risk of possum-related TB. This would be useful in an area bordering a known endemic area or in an area where TB has recently entered the possum population as it would help identify farms on which the possums are likely to have a higher incidence of TB. This information could be used in conjunction with the hot spot predictor model to then develop a strategy for controlling possums in the area to prevent the spread of the disease.

4. Summary

We have described the application of spatial data to develop two models of the spatial distribution of TB in possums. Firstly a geographic model that used spatial analytical tools available within a GIS to combine data layers in a way that represents the distribution of tuberculous possums at the individual cluster scale (50 – 100 meters). Secondly, a logistic regression model that utilises data from a spatial database to predict the distribution of farms by the probability of possum-related TB infection occurring in cattle. Logistic regression models using spatial data have been shown to be a useful tool to predict the distribution of disease risk, and displaying the results as maps within a GIS provides a visual distribution of the data that can be used in disease control decisions (Pfeiffer et al, 1997).

These models are useful tools for the development of more cost-effective possum control strategies as they facilitate differential targeting of resources at areas based on the risk of TB in possums. We have incorporated the resulting models into a decision support system known as EpiMAN(TB) to help facilitate their application in an operational environment (McKenzie et al, 1997). EpiMAN(TB) incorporates two other models: PossPOP, a geographically referenced stochastic model of the spread of TB amongst possums, and a model of the spread of TB between possums at a regional level. (This latter model is still in the conceptual stage). These models combine to provide tools that can identify high risk areas of TB and compare different control strategies at a farm and regional level. The models are embedded in software that displays the TB-risk information for areas defined by the user, in an easy-to-use format.

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