Application of Remote Sensing to Enhance the Control of Wildlife-Associated Mycobacterium bovis Infection

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Abstract

The brushtail possum (Trichosurus vulpecula) is a wildlife vector for tuberculosis (TB) caused by Mycobacterium bovis in New Zealand. Supervised automatic classification of a SPOT3 multi spectral image was used to generate a vegetation map, which was used together with slope data to model the risk of TB-infected possums being present in habitat patches. The vegetation data were also used to identify habitat patterns which, together with other geographic variables, were incorporated into logistic regression models to identify predictors of possum TB risk of farms. The impact of the predicted possum TB risk data on the cost-effectiveness of vector control programs at both individual farm and larger regional control areas is discussed, plus issues associated with the uptake of the models by operational managers.

Introduction

Implications for Humans of Cattle TB Infection

Tuberculosis (TB) in cattle, caused by *Mycobacterium bovis*, is an important disease both as a risk for human health and as a cause of reduced productivity in farm animals. *M. bovis* infection was a major public health problem prior to the introduction of milk pasteurization, when this organism was transmitted to humans in milk from infected cows (O'Reilly and Daborn, 1995). Pasteurization, combined with a major reduction in the incidence of TB in cattle in many countries, has significantly reduced the threat of *M. bovis* infection to human health. TB due to *M. bovis* in man, however, still remains a public health problem in many areas of the world, particularly among abattoir and farm workers. It is thus important that TB in livestock continue to be controlled to reduce the risk of transmission to the human population and to reduce its impact on farming productivity.

Involvement of a Wildlife Vector

In a number of countries the control of TB has been complicated by wildlife species acting as vectors of *M. bovis* for farmed animals. The brushtail possum (*Trichosurus vulpecula*) in New Zealand (Morris *et al.*, 1994) and the badger (*Meles meles*) in the United Kingdom and Ireland (Stuart and Wilesmith, 1988)

are important wildlife vectors for bovine TB. The involvement of the possum in the epidemiology of TB in New Zealand seriously complicates the program to eradicate this disease, because M. bovis infection must be controlled in possum populations as well as in farmed cattle and deer. Infected possum populations are present in approximately 24 percent of the land area of New Zealand (Livingstone, 1997). Within these areas, the disease is clustered in small patches of less than one hectare, commonly referred to as "hot spots" (McKenzie, 1999). The spatial distribution of possum TB hot spots is associated with habitat and topographic factors that provide favorable denning sites for possums (McKenzie, 1999). This leads to localized crowding of possums which in turn supports the transmission of M. bovis between possums. The locations of residual possum clusters following population control are also strongly associated with favorable denning sites, indicating the risk that such residual clusters could be residual foci of TB from which the infection could rebuild (McKenzie and Meenken. 2001)

Approximately US \$13 million is spent annually on possum control in New Zealand. The principal approach to possum control has been large scale culling of possum populations in areas where there is evidence of wildlife infection, to reduce the density of possums to a level below which transmission of the disease does not occur, both between possums and between possums and livestock. Control programs involve intensive culling of possums throughout 20,000- to 30,000-hectare operational areas during the first two years, and less intensive culling in subsequent years to maintain possum populations at a low density. In a few geographic areas there is evidence that intensive possum control has eradicated TB from possum populations. In the majority of areas the pattern of disease in livestock, however, indicates that the prevalence of infection in possums has been reduced to a very low level, but residual pockets of infection remain. Therefore, continual control of possum populations is necessary in these areas to prevent the disease reestablishing.

To date, the *modus operandi* of most possum control operators has been a broadcast approach, applying control with equal intensity to all habitat throughout an operational area with no differentiation according to TB risk. Such uniform control may not be the most cost-effective means of controlling the spread of TB once possum populations have been reduced to a very low density. The application of a risk-based approach to

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control, whereby the intensity of control is related to the risk of TB, is likely to improve the efficiency with which possum control dollars are spent and may also improve control effectiveness in eradicating TB. At the broader scale of a farm or a group of farms, the risk of TB-infected possums being present can be identified from the pattern of TB in the cattle exposed to possums on the farm(s) (McKenzie, 1999). At a more detailed scale, particular patches of habitat that are more likely to support possum TB hot spots can be identified by means of a combination of land cover and topographic factors (McKenzie, 1999).

A further problem lies in the fact that current control methods have not been able to prevent the outward spread of infection into possum populations in neighboring areas that were previously uninfected. Identification of risk factors for locations to which infection is likely to spread would help develop control strategies for containment.

Incorporation of GIS and Remote Sensing Tools in Vector Control

Geographic information systems (GISs) are useful tools to manage possum control, given the association of the distribution of possum populations and of infected sub-populations with explicit spatial factors such as particular habitat types. Digital land-cover data sets that are sufficiently detailed to represent possum TB risk are not yet widely available in New Zealand. Remote sensing however, provides a cost-effective solution to obtaining such data (Dymond *et al.*, 1996). Methods of automatic classification of satellite imagery in a country that has much steep terrain are currently being researched to produce data that are sufficiently detailed and accurate for this purpose (Dymond *et al.*, 2001).

Remotely sensed imagery has been used in many health studies to represent habitat and/or climatic factors that influence the distribution of both vertebrate and invertebrate species acting as vectors of disease (Boone *et al.*, 2000; Hay, 2000; Thomson and Conner, 2000). The principal approach in applying remote sensing and GIS to human and animal health has been to identify species—habitat correlations at a localized scale, and then "scale-up" to regional control programs using high spatial resolution satellite data (Curran *et al.*, 2000; Hay *et al.*, 1997). The information has been used to target control efforts on a risk basis, leading to significant cost savings and reduced environmental contamination, where insecticides are used for control.

At the scale of large geographic areas, habitat data can be aggregated and landscape indices used to identify areas that are suitable for particular vector species. It is known that the pattern of landscape elements has a strong influence on the distribution and abundance of organisms, particularly factors such as fragmentation of habitat, proximity of patches, and species' richness (Griffiths *et al.*, 2000). Using analytical methods that provide information on habitat patterns may provide more accurate models for predicting the distribution of species of interest. An aim of this study was to gain an understanding of how landscape pattern variables influence the occurrence of TB-infected possums on farms, and to evaluate whether these were better predictors of possum TB risk than the simpler variables representing absolute and relative area of habitat classes.

Decision support systems (DSS) are a useful tool for health management programs because they assist managers to make complex decisions by presenting information that is critical to key decisions in a user-friendly interface (Sprague, 1993). The systems help improve management decisions both by providing useful information and by promoting deliberation and analysis of the different options available. A number of DSS have been developed to manage animal health problems at both the farm level and the national level (Morris *et al.*, 1993). EpiMAN-FMD is a spatial DSS that has been developed in New Zealand to manage an outbreak of foot-and-mouth disease (FMD) (Sanson and Morris, 1999; Sanson, 1993). When Epi-MAN-FMD was developed, it was envisaged that the system could in the future be further enhanced to develop a DSS to help manage other exotic diseases such as swine fever (EpiMAN-SF) (Stark *et al.*, 1998) and endemic diseases such as TB (McKenzie *et al.*, 1997).

Objective

This paper describes how GIS and remotely sensed data can be utilized to improve the cost-effectiveness of possum control for TB management in New Zealand. The research objectives were to (1) develop a digital database of vegetation coverage using satellite imagery; and to use this to (2) develop a model to classify habitat according to possum TB risk, at a scale related to the size of a possum denning area; (3) to identify geographic and habitat factors associated with possum TB risk at the farm scale; and (4) to develop a decision support system that incorporated the results of this research into a tool for field-level managers.

Data

Study Area

The study area was a 60-kilometer-square area in the southeastern part of the North Island of New Zealand (Figure 1). The area corresponded with the coverage of a SPOT3 satellite image that was used to develop a vegetation map for this study. This is a pastoral farming area dominated by extensive sheep and cattle farming, with topography of rolling to steep hills. TB has been endemic in cattle in this area since at least the 1950s. It was first



Figure 1. Map of the North Island of New Zealand showing the location of the study area.

discovered in possums here in 1968, and since then tuberculous possums have been found throughout the region. Intensive possum control has been conducted on an annual basis in parts of this area since 1989.

Remotely Sensed Data

Satellite imagery was considered the most cost-effective source of land-cover data for the study area. SPOT multispectral imagery was chosen for this study in preference to Landsat TM imagery because of its greater spatial resolution of 20-meter pixels versus Landsat's 30-meter pixels. This enabled the identification of smaller patches of land cover which may be important possum habitat, down to individual rows of trees. While Landsat TM images have a higher spectral resolution due to the collection of data in seven spectral bands, we considered SPOT multispectral imagery, with three spectral bands, to provide sufficient detail to differentiate broad vegetation classes.

An image of the study area was acquired on 03 March 1994 (Figure 1). The image was ortho-rectified to the New Zealand Map Grid using a 20-meter digital elevation model. Image analysis was conducted in ERDAS Imagine (ERDAS Inc, Atlanta, Georgia) using a supervised classification approach. The initial aim of the classification was to identify as many classes of habitat as possible. An initial list was made of 13 habitat classes associated with the distribution of tuberculous possums, and thought likely to be distinguishable on a SPOT3 multispectral image. All the proposed habitat classes could not be differentiated, however, and the final map legend comprised eight vegetation classes plus a bare ground and a water class (Table 1). The seven non-pasture vegetation classes represented variation in both species composition and/or density of plants as

TABLE 1.	DESCRIPTION OF THE CLASSES IN A VEGETATION	MAP THAT WAS
PRODUCED	BY A SUPERVISED CLASSIFICATION OF A SPOT3	MULTISPECTRAL
	IMAGE	

Vegetation Class	Description					
Tree classes						
Pine	Pinus radiata of all ages, except very young; small patches of beech (<i>Nothofagus</i> species)					
Podocarp/broadleaf	Podocarp species and some broadleaved forest and scrub species. Also includes Eucalypt spe- cies, poplars (<i>Populus</i> species), exotic garden species, and dense stands of tree ferns (<i>Dick- sonia</i> and <i>Cyathea</i> species), willow (<i>Salix</i> spe- cies), and kowhai (<i>Sophora</i> species)					
Woodland	Low-density patches of large tree species com- bined with pasture					
Shrub classes						
Manuka/kanuka	Pure stands of <i>Leptospermum scoparium</i> and <i>Kunzea ericoides</i> (higher than 2 meters)					
Manuka/pasture	Low-density stands of <i>L. scoparium</i> and <i>K. eri- coides</i> on pasture					
Shrubland	Kowhai (<i>Sophora</i> species), willow (<i>Salix</i> spe- cies), low-density gorse (<i>Ulex europaeus</i>), scat- tered manuka/kanuka					
Manuka/gorse	Short dense manuka (<i>Leptospermum scopa-</i> rium), mingimingi (<i>Leucopogon fasciculatus</i>), and gorse (<i>Ulex europaeus</i>) in pure or mixed patches. In some areas includes broadleaved shrub species mixed with manuka/kanuka.					
Other classes						
Pasture	High quality and rough pasture comprising native and introduced grass species					
Water	Rivers, lakes, and sea					
Bare ground	Areas of soil with no pasture cover, sand and rock					
Unclassified	Residential areas, cloud cover, and steep shaded faces					

described in Table 1. Some classes included a particularly heterogeneous mixture of plant species. This resulted in the Shrubland and Manuka/gorse classes in particular, incorporating a wide range of habitats with respect to possum TB risk, which influenced the specificity with which these classes reflected TB risk.

Due to budget and time constraints, we were not able to undertake extensive field checking of the vegetation map. About 50 accessible sites were checked in the field. A further 127 sites in five different areas of the vegetation map were checked using existing data collected for the Protected Natural Areas Programme (PNAP) (Leathwick, 1994). The species present within each remnant of natural vegetation within the study area were recorded in detail in 1998. They were divided into dominant species and other species, but the relative proportions of each were not recorded; thus, an accuracy assessment could only be based on the presence or absence of species rather than the relative proportion of each species. Results of classification error checking at the 127 PNA sites are shown in Table 2. An overall accuracy of 93 percent was achieved, with a range among the classes of 73 to 100 percent. Four classes were classified with 100 percent accuracy. In the case of Woodland, Shrubland, and Manuka/gorse, this was due to the heterogeneous nature of these classes, resulting in at least one of the constituent species being present at each of the test sites. Field checking showed that pine was classified with a high degree of accuracy except where it was present in a mixed pixel with pasture, such as on the perimeter of pine forest stands, when it was classified as "Woodland." Field checking also showed that podocarp and broadleaf forest species were classified with a high degree of accuracy. Broadleaved shrub species, however, could not be differentiated from manuka/kanuka mixed with gorse, particularly in areas where the broadleaved shrubs were mixed with manuka/kanuka.

Obvious errors in the spectral classification were manually corrected using raster-editing software. Small areas covered by cloud were edited with the use of aerial photographs, and large areas of cloud were left unclassified. The data were not smoothed because this would have eliminated small patches of habitat, and it was necessary to retain the full extent of habitat heterogeneity for the subsequent analyses.

Other Geographic Data

Slope and River Maps

Slope data was classified into five categories: $0-10^\circ$, $11-20^\circ$, $21-30^\circ$, $31-40^\circ$, and $>40^\circ$ in a raster format with a spatial resolution of 20 meters. River data were digitized from New Zealand topographic maps at a scale of 1:250,000.

Farm Map (Agribase)

Farm boundary data were obtained from Agribase (Sanson and Pearson, 1997). This database contains digital farm boundary information in vector format plus descriptive information for each farm, such as land owner, main enterprise type, farm area, and stock numbers.

Application of Remote Sensing Data in Disease Control

Two models were developed to predict possum TB risk at different scales. A geographic model was developed to predict TB risk of habitat at a scale that related to the size of possum denning areas. At the larger farm scale, a statistical model was developed using logistic regression to identify geographic and habitat factors associated with the risk of a possum TB hot spot being located on a farm.

TABLE 2. PROPORTIONS OF THE PNA SURVEY SITES USED FOR ACCURACY CHECKING WHERE EACH CLASS WAS ACCURATELY CLASSIFIED AS BEING PRESENT IN THE SATELLITE-DERIVED VEGETATION MAP

PNA Survey	Vegetation Map							
	Pine	Woodland	Pod/ broadleaf	Manuka/ kanuka	Shrubland	Manuka/ gorse	Pasture	Num. PNA sites where class present
Pine	0.73	*						41
Woodland		1.0						16
Pod/broadleaf	*	*	0.87	*	*	*		93
Manuka/kanuka				1.0	*			123
Shrubland					1.0		*	124
Manuka/gorse						1.0		60
Pasture			*				$< 1.0^{1}$	n.a.1

*Indicates the classes into which species groupings were mis-classified. There was insufficient information in the PNA data set to quantify results. ¹Classification results for pasture could not be quantified because pasture was not recorded in the PNA data set.

Predicting TB Risk at the Individual Possum Scale

In a preliminary study, logistic regression was used to identify habitat factors associated with the spatial distribution of possums infected with TB (McKenzie, 1999). TB-infected possums were more likely to be trapped at locations with a slope less than 20° where multiple fully enclosed dens were present. Such dens offer full protection from the environment, and are often the preferred denning locations of possums. They are most likely to be located within the trunks or under the roots of large living trees or in the logs and stumps of large dead trees.

To "scale up" this statistical model to predict the TB risk of habitat over a wider geographic area, it was necessary to represent the abundance of high-quality dens indirectly by vegetation class, based on an understanding of the types of dens that different species or species groupings were likely to provide. Fully enclosed dens were most likely to be found in large mature indigenous tree species and in willow trees (*Salix* species) that commonly grew along river banks, or on very steep slopes where exposure to wind had caused low dense scrub coverage. The vegetation map derived from a SPOT3 multispectral satellite image was used to provide the vegetation data. These data were combined in a GIS with slope data to improve the prediction accuracy of TB risk.

TB hot-spot risk was represented in three categories: high, medium, and low. The high-risk category represented locations where clusters of TB possums were likely to persist over many years because they provided conditions that favored the transmission of TB between possums. The medium-risk category represented locations where tuberculous possums may be found but on a more sporadic basis because they provided conditions that were less favorable for the transmission of TB between possums. The low-risk category represented locations where TB possums were unlikely to be found at any time.

A program was written to combine the data from the vegetation and slope raster layers in a two-dimensional matrix to produce a third layer of possum TB risk for each 20-meter pixel on the map. This was produced independently of any commercial GIS software so that the model could be incorporated into customized decision support software developed at Massey University (refer to later section). It was also possible to produce a hot-spot risk map from the raster slope and vegetation data in ArcView (Environmental Systems Research Inc., Redlands, California) using the Spatial Analyst extension.

Application of TB Risk Model in Farm-Level TB Management Programs

This risk map provides information that enables targeting of habitat on the basis of possum TB risk rather than on possum risk alone. The information can be used to design vector control programs at both the individual farm and larger operational area levels. The value of applying TB hot-spot risk information to develop individual farm TB management programs was evaluated in a separate study (Sauter-Louis, 2001). Predicted hotspot information was used in conjunction with individual farmers' knowledge of where they believed cattle were becoming infected in order to identify high-risk patches of habitat. The TB control program included supplementing the routine possum control provided by the regional pest control agency with additional targeted control of possums in the high-risk areas. In addition, cattle grazing programs were altered to avoid high-risk paddocks during winter and summer, when possums have the highest risk of dying from TB. After a period of three years, TB incidence in cattle on 35 program farms was compared with that on 35 control farms which only implemented the routine control provided by the regional pest control agency. The incidence of TB was 48 percent lower in extensive beef cattle breeding farms that implemented the control program compared with control farms. Furthermore, 27 percent more farms were disease-free and were thus no longer under movement control restrictions. There was no difference in TB incidence between intervention and control farms for intensive farming systems such as dairy and beef cattle fattening units. Beef cattle breeding farms were located on steeper, less productive country that had more extensive possum habitat compared with more intensive farming systems which were located on more productive flat to rolling land. This project showed that applying additional possum control in high-risk habitat plus altering grazing management was cost-effective on extensive farms with considerable areas of possum habitat.

Application of TB Risk Model in Regional-Level TB Management Programs

A further study was conducted to identify the impact of incorporating predicted TB hot-spot risk information into larger scale regional possum control operations which covered several thousand hectares (McKenzie, 2000). Four different control programs were designed with varying combinations of standard uniform control plus targeted control which focused on predicted high and medium TB-risk habitat patches. For example, the most intensive program involved two years of standard control plus additional targeted control in high-risk areas each year, and control in only high-risk areas in the third year. The least intensive program involved standard control in the first year with no additional targeting, and only targeted control in the subsequent two years. Each of the four programs was costed for three different geographic areas that had different land-cover patterns. There were considerable savings in control costs associated with all four programs in each of the

three geographic areas. The influence of the programs on TB incidence in cattle was predicted to vary in accordance with farm management systems as described in the section above. Evaluating a range of control programs enabled us to identify which program was most cost-effective for areas with different land-cover patterns. This provided more information than merely having one option of using targeted control or not, and it also enabled managers to consider the concept of using a mixture of strategies within a large area rather than applying a uniform approach.

Predicting TB Risk at the Farm Scale

The farm is the smallest administrative unit used in the management of TB, and decisions regarding cattle testing and movement restrictions plus possum control are applied at this level. It is thus useful to identify risk factors for possum TB infection at the farm level. Having information that could be used to predict farms or geographic areas in which TB-infected possums are most likely to be located could be used to predict farms that are more likely to become infected as a result of the spread of TB from known infected areas. This would help target surveillance more intensively at such farms and/or target possum control as a measure to preempt the establishment of infection.

A study was undertaken in an area with a history of wildlife TB to identify risk factors at the farm level using the vegetation coverage derived from a SPOT3 multispectral satellite image and other spatial data described above. The prevalence of TB-infected years was shown to be a good indicator of possum TB risk on a farm, and logistic regression was used to identify significant risk factors. A major aim of this study was to identify landscape pattern indices that were predictors of possum TB risk. Spatial variables were calculated using ArcView Version 3.1 (Environmental Systems Research Inc, Redlands, California) and the Spatial Analyst extension for grid data. Landscape patterns were analyzed using FRAGSTATS (McGarigal and Marks, 1994), a spatial pattern analysis program for quantifying habitat structure.

Three different groups of habitat variables were calculated for this study using the seven non-pasture vegetation categories identified from satellite imagery. The first group of variables was total area and percent of the farm area covered by each vegetation class. The second was the area of each combined vegetation-slope class, given that these two variables were found to be significantly associated with the distribution of possum TB hot spots. The third was habitat pattern variables calculated using FRAGSTATS.

FRAGSTATS calculates variables at three levels of aggregation: individual patches, individual vegetation classes, and the farm as a whole. The software produces a large number of variables, which are divided into the following groups: area metrics, patch density metrics, patch size and variability metrics, edge metrics, shape metrics, core area metrics, nearest-neighbor metrics, diversity metrics, and contagion and interspersion metrics. We selected a subset of the variables output by FRAG-STATS that represented patterns for each vegetation class and summary patterns at the farm level. Other variables included in the model were: distance from the coastal forest (which supported a high density of possums), total area of the farm and 100-meter buffer, ratio of buffer area to farm area, livestock density, and length of rivers on the farm.

The model that best predicted TB status of farms included total area of the farm, distance from the coastal forest, area of pine, area of manuka/pasture, and percent area of podocarp/ broadleaf species. While this was the best model, it only provided a moderate fit to the data. Other models that included habitat pattern variables showed that heterogeneity factors were most strongly associated with a high TB risk; however, these models did not fit the data as well as the best model described above. This is because the forest distance variable represented the gradient of heterogeneity of habitat across the study area, which was highest on farms near the forest and lowest on farms furthest from the forest. This variable appeared to be a proxy for a combination of habitat factors that are associated with the probability of TB-infected possums and had a stronger effect than did individual habitat pattern variables.

Incorporation into a Decision Support System, EpiMAN-TB

EpiMAN-TB is a DSS that is being developed at Massey University as a tool to help design vector control programs both at individual farm levels and at operational area levels. The system is designed for the use of field veterinarians and pest control managers, providing them with access to expert knowledge on the epidemiology of TB in possums, TB simulation models, and tools to display and analyze geographic data in an interface that is easy to use. It is a stand-alone system designed to run on PCs under Windows. Further details on EpiMAN-TB can be found at the following website: http://EpiCentre.ac.nz.

Conclusions and Discussion

Vegetation coverage is a fundamental data set for possum management because it has the greatest influence on the distribution of possums by means of its influence on food sources and den sites. Remote sensing is a cost-effective means of obtaining current vegetation data. We were interested in investigating the degree of accuracy that could be achieved with an automatic classification procedure, this being a more efficient way to produce maps of vegetation data for large areas of the country compared with manual classification. In choosing SPOT multispectral imagery over Landsat TM, some spectral detail was sacrificed to obtain adequate spatial detail to capture all potential cover that could act as possum habitat. The final vegetation map comprised eight classes and had considerably more detail than any existing digital vegetation data available in New Zealand, enabling us to obtain more information on landscape patterns such as heterogeneity of habitat patches. There was adequate spatial detail in the vegetation data, and the accuracy of the classification was sufficiently high for our purposes. The broad range of plant species in some classes, however, reduced the specificity of a TB risk classification system based on this data. The remote sensing industry is rapidly expanding at present with the development of imagery with higher spatial and spectral resolution. This is likely to result in the accurate identification of more specific vegetation classes, making the data more useful for possum control purposes.

Despite the broad vegetation classes used to produce a geographic model of possum TB risk, incorporating predicted TB hot-spot risk information into possum control programs at both an individual farm level and at a regional level improved the cost-effectiveness of the programs. Supplementing standard broadcast control methods with additional targeted control during the first two years of the program improved the effectiveness of control on farms with more extensive possum habitat, but not on those with less extensive habitat. A likely explanation for this is that, where standard control is applied to areas of extensive habitat, there is a greater chance of either missing or ineffectively controlling some patches of habitat. The greater the area of habitat, the greater the absolute number of residual possum clusters. Because TB hot spots are more likely to occur at locations where possums are clustered, this can be a significant problem, because any residual foci can reseed infection back into the wider population. Additional targeted control in high-risk habitat "mops up" many of these residual possums. The increased costs incurred through adding targeted control to standard broadcast control in the first two years can more than be offset by applying only targeted control in the third year, when the average possum density should

already be at a very low level. In open country with less extensive possum habitat, standard control is more likely to be effective in a higher proportion of habitat. In such areas effectiveness is not improved by additional targeted control, but efficiency of control can be improved by substituting standard control with targeted control in the second and third years of the program, once the average possum density has been reduced to a very low level.

Major savings in the cost of possum control can be achieved by adopting a portfolio approach and applying a suite of control programs within a larger area, with the intensity of control varying in conjunction with the risk of TB and the nature of the habitat. Following this research, vector control managers are beginning to incorporate TB possum risk at the scale of a farm or group of farms into possum control programs; however, they are still reluctant to incorporate risk data at the habitat patch level. A major practical reason is that managers find it more straightforward to have operators control all habitat with equal intensity rather than have operators work from maps and vary the intensity of control in different habitat patches. Another factor relates to the mind set of possum control managers and operators who are tuned into culling possums everywhere, and are reluctant to leave some patches uncontrolled in certain years in case the possum population should build up in these patches, even though such patches are considered low risk in terms of possum TB. Further research is required to identify the dynamics of very-low-density possum populations in different habitat types when subject to different control pressures, in order to overcome some of the concerns shown by possum control managers. Having ready access to accurate and detailed vegetation data will also help managers incorporate these data into possum control programs.

The decision support system, EpiMAN-TB, is potentially a useful tool to assist field managers develop and implement a risk-based approach to possum control for TB management purposes; however, it has not yet reached the stage of being implemented as a field tool. Part of the reason is that further research is required to refine the way in which habitat predictors are used to target possum control programs, and time is required for vector control managers to think routinely in terms of using a TB risk-based approach. As current possum control strategies achieve the initial disease control objectives, strategies to eradicate TB from possum populations and prevent the recrudescence of TB will undoubtedly become more complex because the remaining problem areas have not responded to the standard approach already implemented. To ensure that cost-effective strategies are developed to handle these situations, TB managers need access to all the information and information processing tools available.

In conclusion, remote sensing provides a valuable source of vegetation data to model the distribution of possums and of sub-populations of TB-infected possums with a level of accuracy that is adequate to enhance the cost-effectiveness of possum control for TB management purposes in New Zealand. These data are an important means of facilitating the implementation of a TB risk-based approach to vector control. Research utilizing these data has helped increase vector control managers' awareness of the potential value of incorporating habitat data into the design of possum control programs. This puts managers in a strong position to take advantage of the more detailed vegetation data that are coming on-line with recent developments in the remote sensing and image analysis areas.

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References

- Boone, J.D., K.C. McGwire, E.W. Otteson, R.S. DeBaca, E.A. Kuhn, P. Villard, P.F. Brussard, and S.C. St. Jeor, 2000. Remote Sensing and Geographic Information Systems: Charting Sin Nombre Virus Infections in Deer Mice, *Emerging Infectious Diseases*, 6(3):248–258.
- Curran, P.J., P.M. Atkinson, G.M. Foody, and E.J. Milton, 2000. Linking Remote Sensing, Land Cover and Disease, Advances in Parasitology, 47:37–80.
- Dymond, J.R., M.J. Page, and L.J. Brown, 1996. Large Area Vegetation Mapping in the Gisborne District, New Zealand, from Landsat TM, International Journal of Remote Sensing, 17(2):263-275.
- Dymond, J.R., J.D. Shepherd, and J. Qi, 2001. A Simple Physical Model of Vegetation Reflectance for Standardising Optical Satellite Imagery, *Remote Sensing of Environment*, 77:230–239.
- Griffiths, G.H., J. Lee, and B.C. Eversham, 2000. Landscape Pattern and Species Richness; Regional Scale Analysis from Remote Sensing, International Journal of Remote Sensing, 21(13 & 14): 2685–2704.
- Hay, S.I., 2000. An Overview of Remote Sensing and Geodesy for Epidemiology and Public Health Application, Advances in Parasitology, 47:1–35.
- Hay, S.I., M.J. Packer, and D.J. Rogers, 1997. The Impact of Remote Sensing on the Study and Control of Invertebrate Intermediate Hosts and Vectors for Disease, *International Journal of Remote* Sensing, 18(14):2899–2930.
- Leathwick, J., B. Clarkson, and C. Ward, 1994. Use of GIS for Protected Natural Area Programme Surveys: Waiapu Ecological District, a Case Study, Proceedings of the 4th National Remote Sensing and Geographic Information Systems Workshop, 07–08 April, Aokautere, New Zealand (Manaaki Whenua—Landcare Research New Zealand Ltd, Private Bag 11052, Palmerston North, New Zealand), pp. 69–74.
- Livingstone, P.G., 1997. Update on the New Zealand TB Situation, Proceedings of a Seminar on Possum and Mustelid Control Research, 26–27 November, Wellington, New Zealand (National Possum Control Agencies, Wellington, New Zealand), pp. 17–30.
- McGarigal, K., and B.J. Marks, 1994. Fragstats: Spatial Pattern Analysis Program for Quantifying Landscape Structure, Version 1.0, Reference Manual, Forest Science Department, Oregon State University, Corvallis, Oregon, 62 p.
- McKenzie, J.S., 1999. The Use of Habitat Analysis in the Control of Wildlife Tuberculosis in New Zealand, unpublished PhD thesis, Massey University, Palmerston North, New Zealand, 212 p.
- ———, 2000. Implementation of EpiMAN(TB): Impact of Predicted TB Hot Spots on Possum Control Strategies, Animal Health Board Report, EpiCentre, Massey University, Palmerston North, New Zealand, 25 p.
- McKenzie, J.S., and D. Meenken, 2001. Spatial Clustering of Low-Density Possum Populations and Association with Habitat, Animal Health Board Report, EpiCentre, Massey University, Palmerston North, New Zealand, 58 p.
- McKenzie, J.S., R.S. Morris, C.J. Tutty, and D.U. Pfeiffer, 1997. EpiMAN-TB, a Decision Support System Using Spatial Information for the Management of Tuberculosis in Cattle and Deer in New Zealand, Proceedings of the Second Annual Conference on Geocomputation (R.T. Pascoe, editor), 26–29 August, Dunedin, New Zealand (Spatial Information Research Centre, University of Otago, Dunedin, New Zealand), pp. 271–277.
- Morris, R.S., R.L. Sanson, J.S. McKenzie, and W.E. Marsh, 1993. Decision Support Systems in Animal Health, *Proceedings of the Society for Veterinary Epidemiology and Preventive Medicine* (M. Thrushfield, editor), 31 March–02 April, Exeter, England, pp. 188–199.
- Morris, R.S., D.U. Pfeiffer, and R. Jackson, 1994. The Epidemiology of Mycobacterium bovis Infections, Veterinary Microbiology, 40(1):153-177.
- O'Reilly, L.M., and C.J. Daborn, 1995. The Epidemiology of *Mycobacte*rium bovis Infections in Animals and Man: A Review, *Tubercle* and Lung Disease, 76(Supplement 1):1-46.

Sanson, R.L., 1993. *Development of a Decision Support System for an Animal Disease Emergency*, unpublished PhD thesis, Massey University, Palmerston North, New Zealand, 317 p.

Sanson, R.L., and A.P. Pearson, 1997. Agribase—A National Spatial Farm Database, Proceedings of the 8th International Symposium on Veterinary Epidemiology and Economics, 11–14 July, Paris, France, pp. 12.16.1–12.16.3.

Sanson, R.L., R.S. Morris, and M.W. Stern, 1999. EpiMAN-FMD: A Decision Support System for Managing Epidemics of Vesicular Disease, *Review Scientifique Technical*, Office Internationale Epizooties, 18(3):593-605.

Sauter-Louis, C.M., 2001. The Effectiveness of On-Farm Control Programmes against Wildlife-Derived Bovine Tuberculosis in New Zealand, unpublished PhD thesis, Massey University, Palmerston North, New Zealand, 373 p. Sprague, Jr., R.H., 1993. A Framework for the Development of Decision Support Systems, *Decision Support Systems. Putting Theory into Practice*, Third edition (R.H. Sprague, Jr. and H.J. Watson, editors), Prentice Hall International, Englewood Cliffs, New Jersey, pp. 3–28.

Stark, K.D.C., R.S. Morris, H.J. Benard, and M.W. Stern, 1998. EpiMAN-SF: A Decision Support System for Managing Swine Fever Outbreaks, *Review Scientifique Technical*, Office Internationale Epizooties, 17(3):682–690.

Stuart, F.A., and J.W. Wilesmith, 1988. Tuberculosis in Badgers: A Review, Review Scientifique Technical, Office Internationale Epizooties, 7:929–935.

Thomson, M.C., and J. Conner, 2000. Environmental Information Systems for the Control of Arthropod Vectors of Disease, *Medical* and Veterinary Entomology, 14:227–244.

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