Identification of risk factors associated with new and persistent infection in cattle herds at Karamea

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Landcare Research
Manaaki Whenua

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Bruce Warburton, Dean Anderson, Graham Nugent, Jackie Whitford

Landcare Research

Mark Neill

Animal Health Board

Prepared for:

Animal Health Board

PO Box 3412
Wellington

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Landcare Research, Gerald Street, PO Box 40, Lincoln 7640, New Zealand, Ph +64 3 321 9999, Fax +64 3 321 9998, www.landcareresearch.co.nz

Animal Health Board, PO Box 3412, Wellington

Reviewed by:	*Approved for release by:*
Phil Cowan Research Priority Leader Landcare Research	Graham Nugent Research Priority Area TB Freedom

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Extended Summary

Project and Client

- There has been persistent herd TB infection within the Karamea district since the early 1970s despite possum control having been carried out on the farmland and in adjacent forest, and a higher than average level of herd testing. Because of this disease persistence and uncertainty about its cause, the Animal Health Board (AHB) contracted Landcare Research, in collaboration with the AHB District Disease Control Manager for the area, to examine both possum-related and herd-testing factors to try and identify the most likely causes of continuing TB infection at Karamea. This work was carried out between July 2009 and July 2012.

Objectives

- To identify the critical gaps in herd and/or possum management preventing eradication of TB from chronic infection areas by using infection in Karamea cattle herds to:
    - Identify through socio-epidemiological study of herds, owners and management, the factors associated with repeated infection or persistent infection in infected herds (June 2013).
    - Identify the relationship between herd infection and possum-related factors such as density, patchiness and immigration.
- Sub-objectives included:
    - Determining what livestock and wildlife factors influence the probability that a livestock animal on a given farm would be infected at a specified time.
    - Determining the probability that TB had been eradicated from possums in the central area of Karamea.

Methods

- Herds with a history of recurrent breakdowns or persistent infection were selected as case-control herds. Selection was not random, but based on infected farms within an area where infected herds were clustered (Arapito Valley) or TB persistence was ‘atypical’ given location of the farms (Market Cross). Control herds (mostly uninfected) were also selected, but with difficulty, because a large proportion of Karamea herds have experienced TB at some point in their history.
- Nineteen out of the 29 dairy herds in the area were visited and a survey questionnaire completed for each. Each farmer was asked a standard set of questions related to herd composition, grazing management, farm management practices, and pest control.
- In 2009 and 2010 relative possum abundance and possum distribution were determined for an area that included the case and control farms, using chewcards placed every 50 m around habitat patches and located so no potential on- or near-farm habitat was more than 100 m from a card. All possum carcasses retrieved from AHB-funded control or following the detection surveys were necropsied and their lymph nodes pooled for culture.

- An individual-based spatial possum model was used to evaluate the likely annual number of infected immigrant possums arriving on the farmland given a 5-km-wide buffer was in place.
- A hierarchical Bayesian model was developed for making inference on wildlife and livestock factors that influence the probability that an individual animal on a farm is infected at a specified time.
- Chewcard survey data collected in 2010 and 2011 and the Proof-of-Freedom model were used to calculate the probability of disease eradication from possums. We restricted the area of analysis to the central part of Karamea, the focal area of the detection surveys in 2010.

Results

Herd factors

- Dairy herds made up 34% of all herds in the Karamea dataset during 1989 to 2011, and 57% of all the current herds.
- Parallel blood testing (Bovigam™) has been used sparingly in Karamea in the past either as required for pre-movement testing or on specific risk cohorts rather than on whole herds Where it has been applied, the results have been variable and, despite negative parallel test results, herds still go on to produce TB reactors and /or TB culls.
- There have been a number of long-standing infected herds including one herd with a disease history that pre-dates computerised records of herd data.
- During 1993 to 2011 there has been a steady overall downward trend in the number of herds infected, as a result of both possum control and the testing programme. The largest declines in infected herd number (i.e. in 1994, 1999, 2004, 2008) followed an aerial control operation against possums, but all of these declines were relatively short-lived.
- Although possum control, along with the test and slaughter programme, has reduced the proportion of herds infected, there appears to be a base level of period prevalence of about 0.2 (i.e. 20% of herds with infected status over the past 12 months) that is proving difficult to reduce further and that has persisted since early 2001.
- Most Karamea dairy herds are completely ‘closed’ and do not trade in livestock (other than sending culls directly to slaughter). Purchasing stock is rare and where it does occur most farmers buy from non-movement-control areas (e.g. Nelson and Canterbury).
- The survey of farmer factors found a significant correlation between herd status and use of a run-off block, but none with factors including bush–pasture margins, offal pits, home kill, stock water, carry-over cows, and cull slaughter. Milk productivity per pasture hectare did not differ between case and control farms.

Possum control

- Possum control was first undertaken in the Karamea district in the 1970s and control operations have been carried out annually since the contractor-based control industry was developed in 1996.

- In the winter of 2008 all forest adjacent to Karamea farmland, from Blue Duck creek in the south to Kohaihai in the north and extending 5 km into the forest interior, was aerial sown with 1080 baits which was considerably more extensive than the previous three aerial operations carried out in this area.
- Chewcard surveys carried out in 2009/10 indicated CCI-predicted RTC equivalents of 0.03% to 0.9%. In 2011 the interference rate from chewcards placed along the forest margin was 2.8% (192/6789), with an RTC equivalent of 0.4%.
- Although possum numbers were low they were not uniform across all habitats. Comparison of the mean distance between the sites where closest neighbouring possums were trapped with the mean distance between closest neighbours when the same number of possums were distributed at random between all trap sites showed they were significantly aggregated, with these aggregations tending to be concentrated at the forest ends of farms.

Possum TB and risk model

- Between 2006 and 2011 only four TB-infected possums were identified, all from the 2006 survey in which 249 possums were necropsied, and cultured. Since then, a further 386 possums have been sampled with no TB detected. However, in the winter of 2012 a control operation detected at least two infected possums from a sample of 50 in the Arapito Valley.
- Using an individual-based possum model, the number of infected immigrant possums turning up on adjacent farmland in a 12-month period was predicted to be one per 10 km, which equates to 3–4 annually for the full length of forest–pasture margin on Karamea farmland.
- In 2006, 187 stoats were trapped from 14 030 trap nights (from 1403 trap sites), and two were confirmed with TB. No other species have been identified with TB on the farmland although two infected deer have been recovered from the adjacent forest.
- Using a risk model, the probability that an individual animal on a farm is infected at a specified time was best predicted by models that included the exposure of the farm to forest before 2009, whether the farm had had previous infections, and exposure of the farm to aerial 1080 exclusion zones post-2008.
- Using data from the 2010 and 2011 chewcard detection surveys and the Proof of Freedom utility, the median probabilities of TB freedom in possums were 0.74 and 0.78, for 2010 and 2011 respectively.

Conclusions

- The period prevalence of infected herds at Karamea was as high as 40% in the early 1990s, but even with ground-based on-farm control and aerial control of the adjacent forest over a number of years, the period prevalence has not been reduced below 20%.
- Parallel blood testing has been used, but it has not been as effective for resolving problem herds as in other areas of New Zealand.
- All case and control herds were essentially closed herds, therefore posing very low risk of introducing new infection from outside the area.

- Based on chewcard detection surveys in 2009 and 2010, possum abundance was low (i.e. less than 1% equivalent RTC), and therefore met the AHB operational requirements.
- Although average abundance of possums was low, those present were not distributed randomly and some sites may have had sufficient numbers of possums to enable TB to persist.
- The apparent rapid recovery of possum numbers between 2006 and 2007 (from numbers of possums killed in control operations) suggests the immigration rate of possums from the adjacent forest onto farmland was very high, but since the 2008 aerial control of the forest, immigration is likely to be low (i.e. as indicated by the possum model).
- Karamea geography (long strip of farmland sandwiched between the forest and coast) lends itself to be a sink (i.e. an area for migrating possums to settle in) for a large number of immigrant possums, and this appears likely to have played a significant role in maintaining TB prior to the 2008 aerial control operation.
- Prevalence of TB in possums is low (surveys up until 2011 suggested a prevalence of about 1%), but recent surveillance using possums recovered during 2012 control operations has identified two confirmed infected possums (and possibly four) from a sample of 50.
- Given a 2% prevalence of TB in possums and the potential number needed for each new herd infection (i.e. 3.5), then there needs to be at least 150 possums sympatric with several farms for at least one of them to become newly infected. Given the apparent low abundance of possums, it seems unlikely that possums are driving infection in all herds.
- Although other wildlife species are present (e.g. rats, stoats, hedgehogs, seals, deer), there is nothing to suggest they play a greater role in TB persistence in herds at Karamea than the generally negligible role they appear to play elsewhere.
- The sensitivity of the range of herd testing protocols used at Karamea is relatively low (0.43–0.65) suggesting a high risk of allowing TB to persist in herds.
- The likely presence of non-specificity, recrudescence, and anergy will contribute to decreasing the sensitivity of the different testing protocols.
- Some farms (e.g. Meidema) are likely to be exposed to a higher risk of immigrant infected possums than others more distant from aerial exclusion areas or from likely ‘corridors’ for dispersal.
- The long-term persistence of infection on some farms, but not on their immediate neighbours, suggests that either wildlife is not the main cause of infection or that movement and settlement of infected wildlife are not random.
- The risk modelling indicates that TB infection in Karamea livestock is mostly influenced by wildlife factors acting through exposure to forest, and to a lesser extent by previous infection history.

Recommendations

- Use of parallel testing should be increased to more confidently identify which farms might have persistent in-herd infection.
- Current skin-testing protocols should be evaluated to ensure skin test sensitivity is maximised, and staff should be trained in best practice.
- Contracted possum control should continue as planned, with all device locations recorded by GPS and possums collected for necropsy and culture. This will help identify any persistent 'hotspots' of TB in possums and enable their treatment with more focused control effort. Locations where TB possums are found should be immediately trapped to extinction, over about a radius of 500–1000 m, both to eliminate the focus and begin to characterise the absolute local possum densities at which TB is occurring.
- Research should be undertaken to better understand:
    - the influence that patchiness of possum distribution has on TB persistence even if average RTC levels are low
    - if possum abundance changes seasonally and increases significantly at expected times of seasonal dispersal (i.e. February–April) by monitoring possum abundance monthly or bimonthly on 2–3 selected farms (e.g. Jones, Meidema)
    - the extent to which immigrant infected possums are contributing to the ongoing infection in livestock, by (1) measuring TB prevalence and possum abundance at the most likely source (behind the control buffer); (2) over two years, using DNA genotyping of possums, surveyed during control, to determine the likely rate of immigration.
- A farmer self-help programme should be developed that aims to reduce abundance of possums on their farms by establishing permanent bait stations that are rat and weka proof (i.e. Weka-proof Sentry bait stations). This approach is to ensure any infected possums (immigrant or resident) have the minimum time to interact with livestock.

1 Introduction

There has been persistent bovine tuberculosis (TB) infection in cattle herds within the Karamea district since the early 1970s, despite possum control having been carried out on the farmland and in adjacent forest, and despite a higher than average level of herd testing. Because of this persistence and uncertainty about its cause, the AHB contracted Landcare Research, in collaboration with the AHB District Disease Control Manager for the area, to examine both possum-related and herd-testing factors to try and identify the most likely causes of the problem. This work was carried out between July 2009 and July 2012.

2 Background

Dairy and beef herds in the Karamea district have consistently been infected with TB at a relatively high herd prevalence level since the early 1970s when possums (*Trichosurus vulpecula*) with TB were first identified in the area. Over the last 10 years, at least 50% of all Karamea cattle herds have been infected at least once and at least 60% of infected herds have had multiple instances of an infection or multiple cases of infected animals over time (i.e. herd status has remained continually infected). One herd has retained its infected status for 29 years. This is despite some possum control having been undertaken regularly on all farms and in the adjacent forest margin for more than two decades.

In 2008, a large area of forest adjacent to the farmland (i.e. forest extending from the pasture edge to about 5 km into the interior) was aerially poisoned (following a single prefeed), in anticipation that such an operation would have a significant impact on infected animal and herd rates in Karamea. The working hypothesis for this operation was that reducing numbers of forest possums would lower the number of infected possums moving from the forest onto adjacent farms. The prediction was that the rate of herd infection on farms would therefore decline. The control operation was designed by AHB staff to reduce or potentially eliminate the contribution that immigrant possums made to maintaining infection. The presumption was that if reactor rates did not decline and/or some herds continued to become infected, then immigration could be disregarded as one of main causes of TB persistence in Karamea herds.

There are four main possibilities that contribute to cattle herd infection at Karamea. These are: (1) within-herd (and associated testing problems with anergic/recrudescent animals); (2) purchase of infected cattle; (3) infection from off-site grazing (i.e. away from Karamea); and (4) TB-infected possums (or another wildlife vector) either resident on near the home or off-site grazing properties, or immigrants. This project aimed to clarify, using a risk modelling approach, the contribution of each of these factors to herd breakdowns and/or disease persistence in the Karamea farming district over the period of the project.

The probability that an animal in a given herd becomes infected at a specific time is related to its exposure to infected wildlife or livestock management practices that facilitate the establishment or propagation of disease in the herd. We used two different datasets and modelling techniques to tease apart the relative risks posed by wildlife and livestock factors and address two questions related to persistence of TB in Karamea. First, using livestock disease surveillance data, we ask what livestock and wildlife factors influenced the probability that a cow on a given farm would be infected at a specified time, while accounting for an imperfect surveillance regime? Second, using possum disease surveillance

data (and assuming that possums are the primary wildlife reservoir), what was the probability that possums in the central area of Karamea were free of TB?

While the Karamea district is obviously not free of TB, as it is present in livestock there, calculating the probability of TB freedom in possums provides some insight into the likelihood that possums are causing most of the persistent infection in livestock. If the outcome of the hierarchical modelling of the infection risk to herds (question 1) concurs with the findings of the probability of eradication analysis, conclusions will be stronger.

It is essential to determine the management (herd and possum), biological, and/or social factors that are driving the disease system. Identifying these risk factors will allow disease and vector control managers and farmers to adapt their control and management programmes to mitigate these factors. This will not only assist in understanding the reasons for the breakdown rates of herds in Karamea, but will also help improve the management of TB infection elsewhere in New Zealand where farmlands adjoin large tracts of indigenous forest.

We emphasise that this work is not questioning the validity of the currently-accepted possum control paradigm for disease eradication from possums (i.e. reducing possums to uniformly low densities and maintaining those for 7+ years), but is focused on answering the question: What factor is driving the persistent infection in herds at Karamea?

3 Objectives

To identify the critical gaps in herd and/or possum management preventing eradication of TB from chronic infection areas by using infection in Karamea cattle herds to:

- Identify through socio-epidemiological study of herds, owners and management, the factors associated with repeated infection or persistent infection in infected herds (June 2013).
- Identify the relationship between herd infection and possum-related factors such as density, patchiness and immigration.

Sub-objectives included:

- Determining what livestock and wildlife factors influence the probability that a livestock animal on a given farm would be infected at a specified time.
- Determining the probability that TB had been eradicated from possums in the central area of Karamea.

4 Methods

4.1 Research design

This project comprised three interlinked components: (1) a case-control investigation conducted in 2010/11 to compare infected and uninfected herds and determine if any herd or farm management practices predisposed herds to infection; (2) development of a probability risk model incorporating herd-testing histories and farm exposure to possum habitat, including the main adjacent forest margin; and (3) a detection survey of case-control farms to identify if any had residual high numbers of possums.

4.2 Case and control herds

All cattle herds within the full Karamea district (29 dairy, 6 dairy dry, 13 beef dry, 11 beef breeding) continued to be monitored routinely, and farmers with new herd infection were visited and interviewed to determine the likely risk of the infection being in-herd-, movement-, or wildlife-vector-related. Herds in specific locations with a history of recurrent breakdowns or persistent infection were selected as infected 'case' herds (Figure 1). The selection was not random, but based on infected farms within an area where infected herds were clustered (Arapito Valley – Karamea River) or TB persistence was 'atypical' given the location of the farms (Market Cross, i.e. very low possum habitat present on farm and distant from forest margin). The uninfected 'control' herds were more difficult to select because a large portion of Karamea herds have experienced TB in their history. A few herds were excluded because of recent management changes. For the selected herds the core population of animals was assumed to be resident (i.e. at risk).

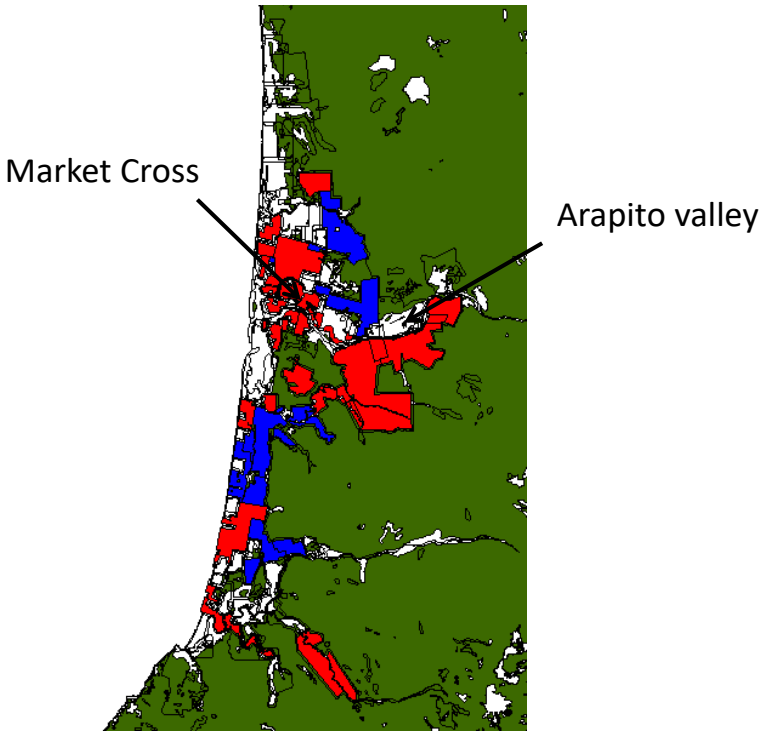

Figure 1 Location of case (red) and control (blue) herds.

4.3 Farmer survey

Nineteen of the 29 dairy herds in the area were visited and a survey questionnaire completed for each. All farmers participated, but some would not or could not provide answers to all questions. The 19 herds included seven herds with at least C3 status including two with C10 status. Each farmer was asked a standard set of questions (Appendix 1) as follows:

1 *Herd composition:* Included different farming enterprises that run on the farm, herd demographics, stock purchasing preferences (if any) and numbers culled, and destination.

2 *Grazing management:* Included fence quality, type and continuity, stock water sources, grazing practices around bush–pasture margin (BPM).

3 *Farm management practices:* Included type of dairy shed, presence of offal pits, stage of farm development, supplementary feeding practices, whether non-pregnant cattle were carried over winter and where they were run. The calf-rearing arrangements were also investigated and the use of run-off blocks (contiguous or non-contiguous blocks of land used for grazing young or dry stock and producing supplementary feed).

4 *Pest control:* Included whether the farmers carried out their own pest control/hunting activities on their properties, and the abundance of different wildlife species present.

Four respondents to this survey admitted using offal pits to dispose of dead animals. Three of these four owned ‘long-standing infected herds’, prompting further investigation through a phone survey of all Karamea herd owners/managers, which was carried out by AHB contact centre staff member Harry Atkinson.

In this survey, up to seven questions were asked of each participant:

1 How many cattle or deer, of any age, do you have on your property at the moment?

2 Do you use an offal pit for your farm? if yes:

3 Is it an open or lidded offal pit?

4 On average, how many animals do you send to the freezing works each year?

5 Do you have animals killed on-farm for your own consumption? If yes:

6 What happens to the waste?

   a. Buried

   b. Offal pit

   c. Carted away by the operator

   d. Other

For dry stock herds only:

7 Where do you usually source your stock from?

a. Local dairy farmers

b. Sales yards

c. TradeMe

d. Through agent

e. Other

8 Comments

Of 56 owners/managers identified, only three could not be contacted. A further contactee was an absentee farmer with none of his own stock on the property (other local farmers lease the block for grazing young stock).

Survey data were explored and analysed using Microsoft Access, Excel and NCSS (Hintze 2001). Although we sampled over half of the population of dairy herd farmers in Karamea, the small number of herds precluded us from using the survey data for a multi-covariate analysis. Instead we assessed the uni-covariate ratios of herds for each risk factor and present those worthy of note. Contingency table analyses of individual risk factors were examined using the Fisher's exact test. Because sample sizes were small, there is a risk that significant differences were not detected because of low statistical power.

4.4 Possum control history and TB prevalence

Recent control history (2004 onwards) was obtained from records kept by the AHB. We also sought clarification of details from Barrie Petrie (AHB West Coast and formerly West Coast Regional Council), Ron Walker, and Paul Livingstone (AHB).

4.5 Abundance and patchiness of possums on farmland at Karamea

In 2009 and 2010 relative possum abundance and possum distribution were determined for an area that included the case and control farms (Figure1 and Appendix 2), using chewcards placed every 50 m around habitat patches and located so no potential habitat was more than 100 m from a card. Cards were nailed to trees and posts where appropriate, as per standard best practice, and left in place for 7 days before checking for possum tooth marks. Chewcards were used to enable all areas to be surveyed at ground level without posing any risk to weka (*Gallirallus australis*).

We carried out three separate surveys each with different follow-up control treatments (Table 1). All possum carcasses were necropsied and nodes pooled for culture except those significantly decomposed.

Table 1 Landcare Research detection surveys and post survey activity/control

Date	Survey type	Location	Following activity (control)
Oct–Dec 2009	Pre-control detection	Karamea south	EPRO ground contract
March 2010	Post-control detection	Karamea south	June 2010, bait stations set at positive detections and then spotlight shot after one week. A Sentinel kill trap also set at each station
June 2010	Detection only	Karamea north	-
2011	Pre-control detection	Total length of Karamea farm–forest margin	Positive detection sites were trapped with arrays of 8–12 traps

In 2011 a control operation was planned by the AHB, using chewcards to first detect possums along the total length of Karamea's farm–forest margin, so this was used as an additional survey with the results integrated into this research programme. In this operation the attachment of chewcards was varied from standard practice in order to reduce interference from ship rats (*Rattus rattus*) whose numbers had been high in previous surveys. The cards had a wire spoke placed through the centre flute that allowed the card to sit out from a tree and rotate, thus allowing possums access to the outer edge of the card but preventing rats from gaining access from the tree side. These cards were placed every 50 m and left for seven nights before being read and control applied. A subsample of possums killed was collected for necropsy.

To determine relative possum abundance we used a six-times conversion to convert a chewcard interference index (CCI) to a Residual Trap-Catch Index (RTCI) value (i.e. a 12% CCI = 2% RTCI) (Nugent et al. 2012). To determine if captured possums were randomly distributed we compared the mean distance between neighbouring captured possums to that of neighbours if the same number of possums had been randomly distributed at all possible detection points. The distribution of random mean distances was estimated from 100 simulations.

4.6 TB prevalence in farmland possums at Karamea

TB prevalence was obtained from necropsy and culture data from surveys carried out in 2006–2011. Most surveys only included necropsy and searches for visible lesions. The Landcare Research samples from 2009/10 were necropsied, with pooled nodes sent for culture.

4.7 Modelling TB-possum Immigration

The TB-possum model (Ramsey & Efford 2010) was used to predict the number of TB-infected immigrant possums that might disperse to farm margins in a farmed area adjacent to an aerially-controlled forest 'buffer' 5 km wide in which possums had been reduced to 1%

RTC, with the possum population on the far side (interior source) of the control zone having a carrying capacity of 10 possums/ha and being uncontrolled. Both the residual possums in the aerial control area and in the interior uncontrolled 'source' had an assumed TB prevalence of 2%. The model simulated an area 10 km long. The numbers were then multiplied up by 3.8 to represent the full 38 km of the farm–forest boundary in the Karamea district.

4.7.1 Modelling the risk of infection in cattle

We developed a hierarchical Bayesian model for drawing inference from wildlife and livestock factors that influence the probability that an individual animal in a farm is infected at a specified time (Figure 2). That inference was based on the following data.

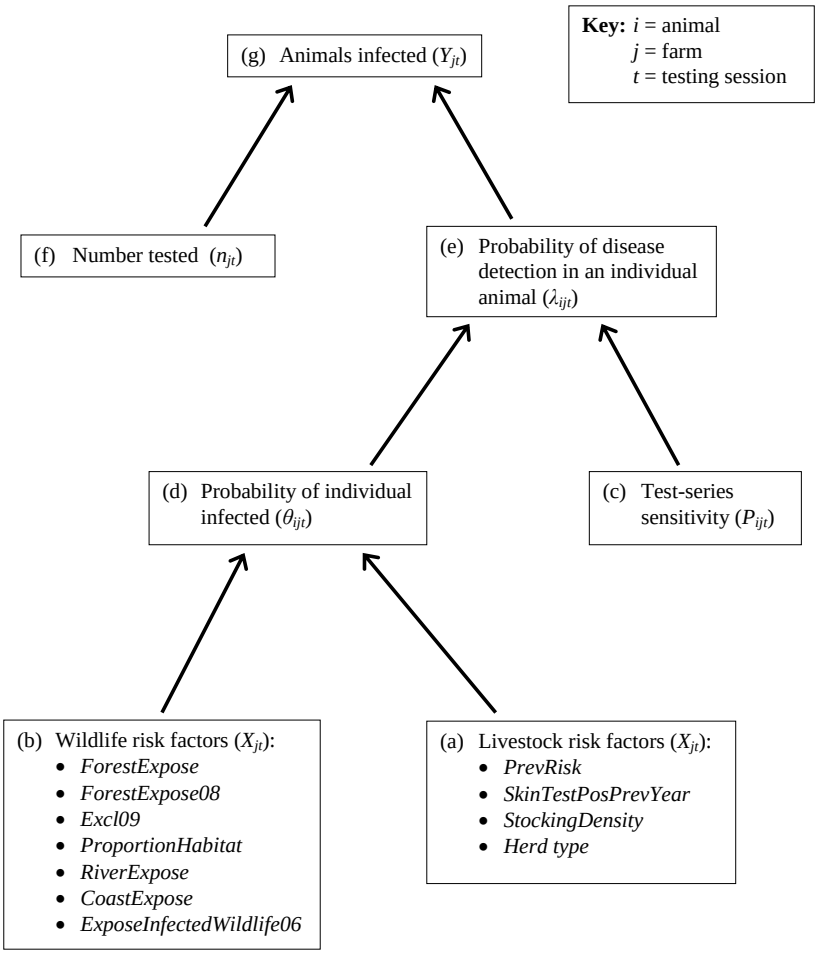

Figure 2 A hierarchical model showing the livestock and wildlife parameters.

Livestock data

Cattle in New Zealand are routinely TB-tested as part of the TB management scheme. The programme includes a combination of tuberculin skin testing, ancillary testing of skin test positives, parallel blood-testing[1] to increase sensitivity, and slaughter surveillance.

TB skin testing is carried out at least once annually for all Karamea breeding herds. Dry herd owners may test stock or send them all directly to slaughter. Herds with an infected status or herds that are moving animals between farms may test more frequently (up to 3–4 times per year).

Karamea test data were extracted from DMIS (Disease Management Information System) and other sources for each herd for the study period (1 January 2003 to 1 August 2011). The data included the farms associated with a herd, numbers of animals tested, test type, number

[1] Blood testing tuberculin-skin-test-negative cattle 13–33 days after the tuberculin injection day, using interferon – gamma enzyme immunoassay (Bovigam™) applied to heparinised blood samples within 30 h of collection.

of TB cases, farm area and the proportion of each farm that comprised possum habitat on the farm and within a 100-m buffer of the farm boundary.

From these data we derived testing regimes (combinations of surveillance tests) and associated sensitivities, and estimates of population size of each herd and numbers of animals deemed infected.

Livestock factors that we examined included stocking density and the risk of infection at the time of the preceding testing. We expected the probability of infection to increase with increasing stocking density because we suspected that within-herd transmission was occurring on at least some occasions, and, if so, that the disease should be transmitted more readily with increased contact rates in high density herds. Risk of infection at the time of the preceding testing was included in the modelling to account for the expectation that a herd at high risk at a given time should have an increased chance of remaining at high risk due to residual within-herd infection and imperfect testing regimes.

Wildlife data

Wildlife factors were indirect measures of TB risk from wildlife (i.e. not direct measures of wildlife abundance and disease prevalence), and included closeness to forest, rivers and coast, the proportion of a farm covered by possum habitat, and the distance to TB-infected wildlife captured in 2006 (3 possums and 1 stoat (*Mustela erminea*)). The probability of an animal becoming infected was expected to increase with increasing closeness to forest, the proportion of possum habitat on a farm, and with decreasing distance to known wildlife infections (in 2006). Because rivers and waterways are known to guide possum movements, and in pastoral landscapes their riparian vegetation provides the only significant habitat for possums, we expected the probability of infection to increase with increasing closeness to rivers and waterways. Lastly, we included exposure to the coast to test the hypothesis that the source of TB in livestock could have been from pinnipeds (NZ fur seals, *Arctocephalus forsteri*).

Covariates

We used covariates in the modelling to assess whether livestock and wildlife factors influenced the probability that an animal in a herd became infected. Stocking density was calculated as the number of animals divided by the area of the farm. Risk of infection at the time of the preceding testing (*PrevRisk*) was an autoregressive variable that was generated in the modelling process (see details below). We also created a variable to test whether the serial testing regimes were inadequate and allowed infected animals to persist in the herd (i.e. animals with positive skin tests that were later deemed infection free; *PrevSkinTestPos*). While the *PrevSkinTestPos* was a management-related variable and did not represent an epidemiological risk of disease, its inclusion in the modelling could have potentially explained some of the variance in the data and allowed for better inference on the covariates of interest. In addition, it could have potentially helped identify weaknesses in the testing regimes.

Several covariates were developed to assess influence of wildlife factors on the probability of TB infection in a given herd. Herd exposure to forest represented the risk that a TB-infected wildlife animal would come onto a given farm, and was therefore proportional to the farm

area and proximity to the forest block. A two-step procedure was used to calculate exposure to forest (*ForestExposej*) for each herd *j*. First, ArcGIS (ESRI 2008) was used to place a regular grid of points *p* with 200-m spacing within each farm. ForestExpose was calculated as:

$$ForestExpose_j = \sum_{p=1}^{P} \frac{1}{d_{jp}}, \quad (1)$$

where d_{jp} was the shortest distance from point *p* to the nearest point of the main forest block.

An aerial drop of 1080 over the main forest block occurred in 2008, and several zones on the farm–forest boundary were excluded from aerial control, but ground-based control was conducted to reduce the possum population in these exclusion zones. To explore the potential differential risk posed by these areas, we created two covariates: exposure to forest up to and through 2008 (*ForestExpose08*); and exposure to the exclusion zones from 2009 (*Excl09*). These were calculated in the same way as *ForestExposej* (Eqn 1).

Using ArcGIS (ESRI 2008) and native forest cover in the Land Cover Database (LCDB2) we calculated the proportion of each farm covered by possum habitat (*ProportionHabitat*).

The same grid points used in the calculation of *ForestExposej* (Eqn 1) were used to calculate the risk of infection from areas where TB-infected wildlife were captured in 2006 (*ExposeInfectedWildlife06j*):

$$ExposeInfectedWildlife06_j = \sum_{p=1}^{P} \sum_{q=1}^{Q} \frac{1}{d_{jpq}}, \quad (2)$$

where d_{jpq} was the distance from point *p* on farm *j* to location *q* where a TB-infected wildlife animal was captured in 2006. Lastly, ArcGIS was used to calculate the exposure of farm *j* to water ways (*ExposeRivers*) and the coast (*ExposeCoast*) as in Eqn 1:

$$River\ Expose_j = \sum_{p=1}^{P} \frac{1}{d_{jp}}, \quad (3)$$

$$Coast\ Expose_j = \sum_{p=1}^{P} \frac{1}{d_{jp}}. \quad (4)$$

Model description

The data available for the modelling were the number of infected animals in herd *j* at time *t* (Y_{jt}; Figure 2a), number of animals tested (*njt*; Figure 2b), and the wildlife and livestock covariates (Figure 2f, g). The surveillance sensitivity for individual *i* (P_{ijt}; Figure 2e) was a parameter derived from the test sensitivities in the serial testing for seven regimes we identified (Table 2 and Appendix 3).

The probabilities of an individual being infected and disease detected (θ_{ijt} , λ_{ijt}; Figure 2c, d) were estimated latent variables (i.e. inferred variables) from the modelling. The principal relationship of interest was how wildlife and livestock factors influenced the probability that an individual was infected (Figure 2d, f, g). The data were modelled with the following procedure:

$$Y_{jt} \sim Binomial(n_{jt}, \lambda_{ijt}) \quad (5)$$

$$\lambda_{ijt} = \theta_{ijt} P_{ijt} \quad (6)$$

$$logit(\theta_{ijt}) \sim Normal(\mu_{jt,} \sigma^2) \quad (7)$$

$$\mu_{jt} = X' \beta_{kh} \quad (8)$$

$$\beta_{kh} \sim Normal(\mu_{kh}, \sigma^2_{kh}) \quad (9)$$

$$\sigma^2 \sim InverseGamma(0.1,0.1) \quad (10)$$

$$\mu_{kh} \sim Normal(0,1000) \quad (11)$$

$$\sigma^2_{kh} \sim InverseGamma(0.1,0.1) \quad (12)$$

where μ_{jt} was a linear prediction of covariates (X') and associated parameters (β_{kh}) for covariate k and herd type h. This was done because the different herd types (beef breeding, beef dry, dairy dry, and dairy wet) could vary in their respective susceptibility to wildlife and livestock management factors. All covariates were scaled to have mean 0 and standard deviation 1, which allowed for comparison of the relative influence of covariates within a model. The βkh parameters were constrained by priors (Eqn 9) and hyperpriors (Eqns 11 and 12). The variance parameter σ^2 allowed for over-dispersion of θ_{ijt} (Eqn 7). The covariate $PrevRisk_t$ was used as a temporal autoregressive 'latent' variable (AR1; θ_{ijt-1}) instead of an autoregressive variable of the response variable (Y_{jt-1}; animals infected), because of the imperfect testing regime and related risk of underestimating $PrevRisk_t$ due to negative tests of infected animals.

We used Markov Chain Monte Carlo (MCMC) to fit the models numerically (Clark 2007, chapter 7). Within-chain serial autocorrelation was assessed to determine the appropriate thinning rate. Convergence on the posterior target distribution was confirmed with a scale reduction factor ($\hat{R}$) < 1.2 calculated on four parallel chains (Gelman & Rubin 1992; Gelman et al. 2004). Convergence for all models was achieved with 100 000 iterations, and posterior summaries were taken from four chains containing 40 000 samples with a thinning rate of 20 (i.e. 8000 samples).

Table 2 Total test sensitivities for each of seven testing protocols (see Appendix 3 for details).

Test protocol	Total sensitivity
Dairy testing of clear herds	0.438
Dairy testing of infected herds	0.650
Beef breeding	0.464
Beef dry	0.564
Beef dry works surveillance	0.477
Movement testing 1	0.447
Movement testing 2	0.568

We explored models with various combinations of variables (Eqn 8) to make inference on herd and wildlife factors that influence the risk of TB infection. Our approach to comparing models and assessing goodness of fit was first to assess uni-covariate models, and then form multi-covariate models using covariates with relatively high explanatory strength. Three indices were used to compare and assess explanatory strength. First, we used the Deviance Information Criterion (DIC), which is a generalisation of the more familiar Akaike Information Criterion (AIC; Akaike 1973; Burnham & Anderson 2002). Explanatory strength of models increases with decreasing DIC (Spiegelhalter et al. 2002). Second, Bayesian p-values were used to compare how well the models fitted the data (Kéry & Schaub 2012; Link & Barker 2010). Bayesian p-values approaching 0.50 indicate that the model fits the data very well, whereas values near 0 or 1 suggest very poor fit. Lastly, we used parametric estimation methods to calculate the area under the curve (AUC) of receiver-operating characteristic curves (ROC, Lusted 1971; Zou et al. 2007). An AUC value of 0.5 indicates that the model predictions are completely random, and a value of 1.0 corresponds to perfect prediction accuracy.

Modelling the probability of eradication

We used chewcard survey data collected in 2010 and 2011 and the spatial-survey-data model to calculate the probability of TB freedom in possums (Anderson et al. in review). We restricted the area of analysis to the central part of Karamea covered by the 2010 Landcare Research chewcard survey (Appendix 2).

Standard default parameters were generally used for chewcards in the spatial-survey-data model (Table 3 and 4).

Table 3 Chewcard (CC) parameters for the spatial survey-data model

	σ mean	σ SD	CC mean	CC SD	g_0 mean	g_0 SD	Test Se mean	Test Se SD	λ_0 mean	λ_0 SD
Chewcard	90	8	0.2	0.05	0.13	0.05	0.74	0.1	1	1

Table 4 Model parameters for the spatial survey-data model

Element	Value
Cell size (m)	100
Cell design prevalence	1
Traps per chewcard	3
Probability of introduction	Pert: Min: 0.0, Mode: 0.01, Max: 0.05
Prior probability	Pert: Min: 0.3, Mode: 0.65, Max: 0.90
Year range	2010– 2011
Iterations	200
CIV threshold	0.9

The exceptions are that we used a pert prior distribution of min = 0.3, likely = 0.65, and max = 0.9 (0.65 was selected based on the amount of possums control that had been carried out and the lack of TB possums identified, but knowing there was still a risk of TB-infected immigrant possums). In addition, because only 78% of captured possums were necropsied, we used a test sensitivity of 0.74 instead of the default 0.95 (i.e. 0.95 * 0.78 = 0.74). We evaluated the median and 95% credible intervals (CI) of the posterior probability of eradication and surveillance-system sensitivity. We also present the credible interval value (CIV), which is the proportion of the posterior distribution of the probability of eradication that is greater than 0.90. A target CIV of 0.90 would be regarded as being TB free.

5 Results

5.1 General background on herds and testing

Dairy herds persist on a farm longer (mean of 25.7 years) than beef dry herds (10 years) and beef breeding herds (15 years). Actual stock time on farms cannot be estimated from the available data as individual animals are not currently recorded in the database. Dairy herds made up 34% of herds in the Karamea dataset during 1989–2011, and 57% of the current herds.

There have been a number of long-standing infected herds including one herd (B. Jones) with a disease history that pre-dates computerised records of herd data.

Some Karamea herds have remained under movement restrictions continuously for prolonged periods while others have alternated between clear and infected herd status (Appendix 4).The average number of separate breakdown episodes per herd (i.e. when a herd is under movement control restrictions due to being classified as an infected (I) herd) is 3.3 for dairy herds and 0.6 for beef breeding herds.

The effort for ‘on-farm’ TB testing appears to have been relatively constant each year, except in 1999–2000 when a short-term Karamea project was undertaken that included an increased test frequency (up to three times a year) and parallel testing of some herds.

Parallel blood testing has been used sparingly in Karamea due to the significant cost for whole-herd testing and the constant risk of reinfection from external sources. Parallel blood testing (Bovigam™) was not used much in Karamea up until 2000. Where it has been applied, the results have been variable. In some herds, parallel blood testing identified small numbers of tuberculous cattle, while in others its application failed to identify any test-positive animals. Despite negative parallel test results, herds still produce TB reactors and /or TB culls. For example, in 1999, three chronically-infected herds were parallel tested, and 11 blood-test-positive animals were slaughtered, but none had visible lesions. In addition, pooled lymph nodes were collected and cultured but no *Mycobacterium* was isolated (Ryan et al. 2000). TB cases have subsequently been found in all three herds on a number of occasions, strongly suggesting wildlife infection. Both nationally and at Karamea, parallel tests are sometimes applied to a subset of herds (either a cohort considered to be of greater risk or as part of a pre-movement test for animals to be moved from the property to some place other than directly to slaughter).

5.2 Spatial and temporal herd infection

Bovine TB infection in cattle in Karamea pre-dates the introduction of compulsory skin testing. Small dairy herds sourced animals from outside the district and may have inadvertently introduced the disease by 'importing' infected stock. All dairy stock were required to be TB-tested from 1961, and testing of beef stock became compulsory in 1971 (de Lisle 1993). During the early period of the TB control scheme, the numbers of herds increased throughout Buller District and Karamea. Despite the test-and-slaughter policy of the day, TB infection was hard to clear and some herds had repeated detections of infected animals. Actual data from these early times are difficult to locate, but Karamea became, and still remains, the area with the highest prevalence of TB-infected herds in the country. Nevertheless, available data show that most herds in Karamea have had some period of infection and movement restrictions (Figure 3).

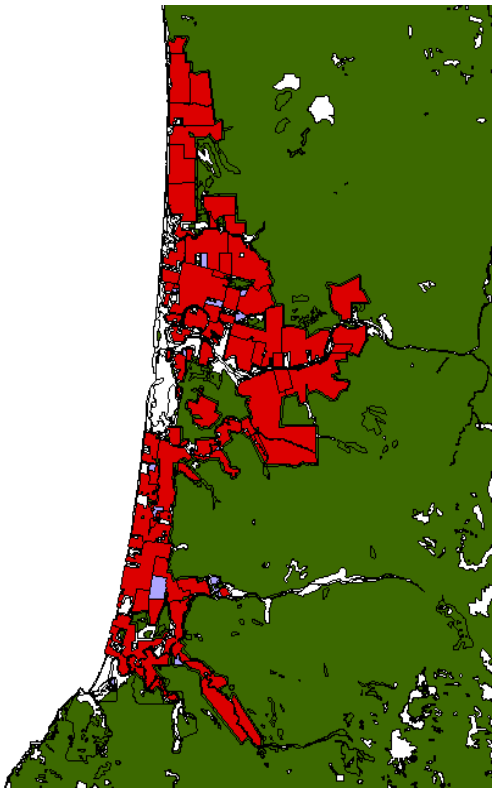

Figure 3 Map of Karamea showing the properties that have been under movement restrictions due to bovine tuberculosis since 1987. Red polygons indicate that TB has been diagnosed on the property. Blue polygons have no record of infection, no linkage with a herd, or do not carry stock. White areas are unidentified Crown land.

The distribution of stock throughout Karamea is relatively uniform and there is good coverage with surveillance units (TB-tested and works surveillance animals) (Figure 4).

During 1993–2011 there has been a steady overall downward trend in the number of herds infected, as a result of both possum control and the testing programme (Figure 5). The only large declines (of five or more) in the number of infected herds occurred within 1–2 years of aerial 1080 poisoning operations in the continuous native forest immediately east of Karamea

farmland in 1994, 1999, 2004, 2008. The numbers of infected herds increased again in the periods 3–5 years after these operations, but usually not to quite the same level as at the time (or just before) the operation. The same pattern is apparent in the period prevalence data for herds except that, by 2011, the period prevalence exceeded that recorded in 2008 (Figure 6). Although all four aerial operations were followed by reduced infection in herds, only the first two or three possum control operations appear to have produced declines that were greater than the subsequent increase. The overall decline therefore appears to be slowing, as suggested by the better fit of a polynomial than a linear trend line (Figure 6).

This suggests a plateauing of period prevalence in herds at about 0.25, even though the most recent aerial operation in 2008 was larger and occurred sooner after previous control than did the earlier operations (Figure 6).

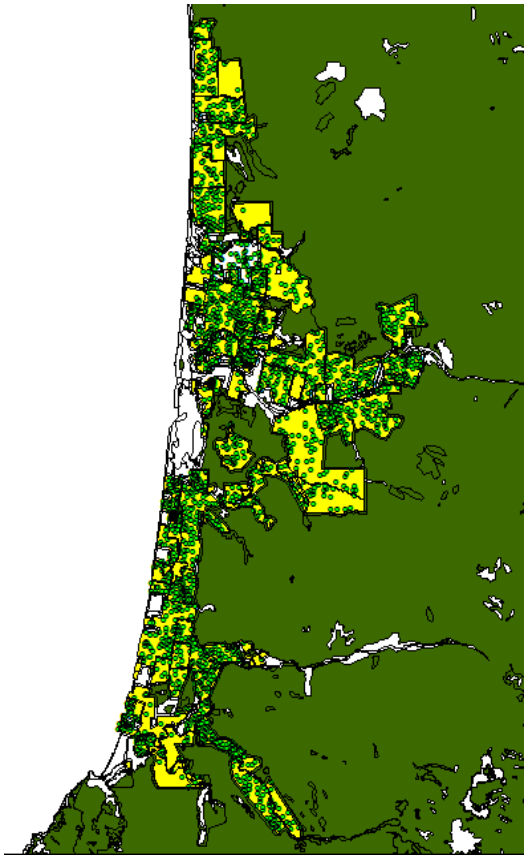

Figure 4 Map showing the simulated distribution of livestock throughout Karamea district. Points are randomly generated within farm polygons and may appear to fall within non-productive parts of properties (one green dot = 10 cattle).

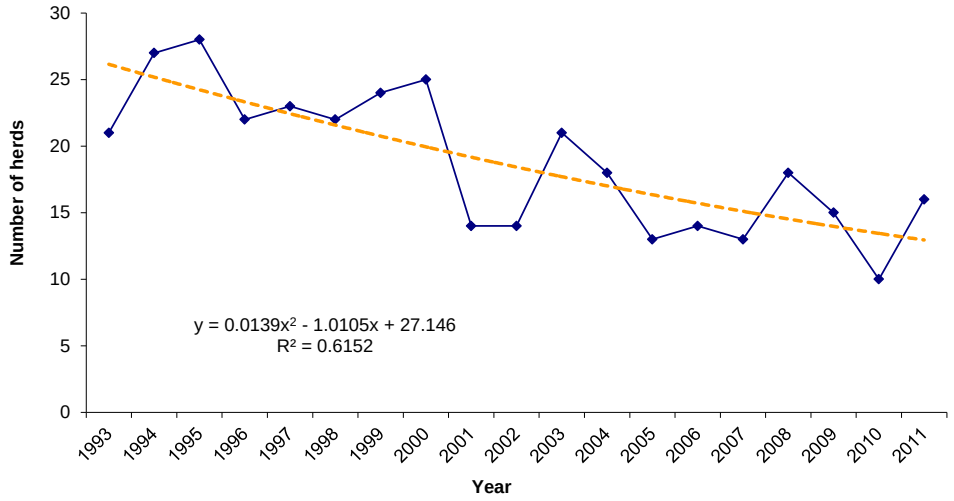

Figure 5 Number of herds with an infected status at any time during a calendar year from 1993 to 2011 (this is a similar measure to the period I herds used to calculate period prevalence). A polynomial trend line has been used to illustrate the overall trend.

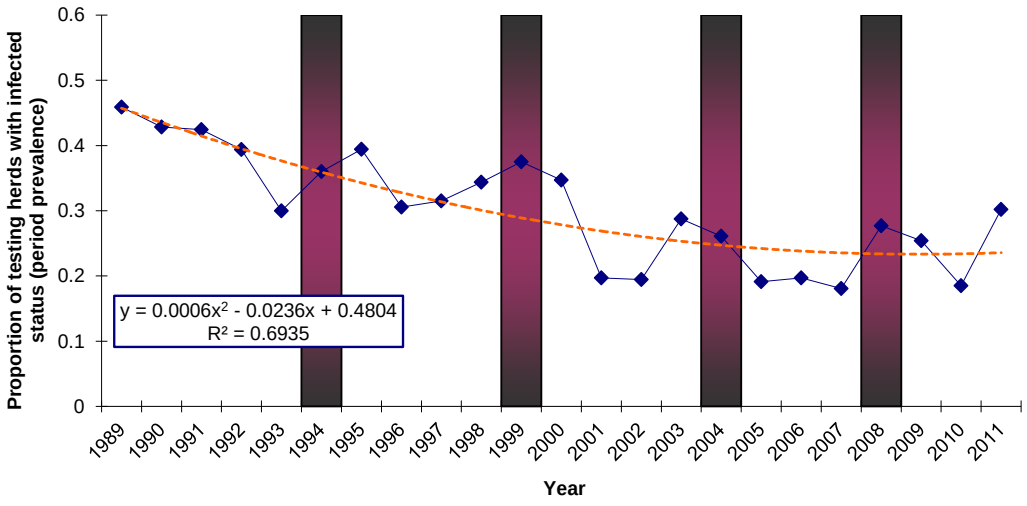

Figure 6 Period prevalence for tested herds in Karamea district. Purple bars indicate aerial operations. (Aerial operations before 2008 were carried out with fixed-wing aircraft and were not prefed.) Note bars denoting aerial control in Figure 6 do not align with declines in infected herds in Figure 5 because aerial operations were sometimes in June or July and therefore in different financial years and did not always have a herd test immediately.

5.2.1 Case/control herds

A summary of case and control herds follows, and detailed descriptions of these herds' histories are in Appendix 5. Note the farm details below are from only the seven specific farms among the case and control herds that had chewcard surveys.

Karamea dairy herds share a number of management practices. Most are completely 'closed' and do not trade in livestock (other than sending culls directly to slaughter). Purchasing stock is rare and, where it does occur, most farmers buy from non-movement-control areas (e.g. Nelson and Canterbury).

Many local farmers breed their own replacement bulls and do not sell stock to others for fear of a subsequent TB breakdown and a bad reputation with buyers.

Case #1: Scarlett/Heal

This dairy herd has an I13 herd status, indicating the herd has had infected status continuously for 13 years. The herd had a major breakdown in 2000/01 and TB has been found in the herd in most years since. Multiple parallel tests and frequent skin testing reduced the number of infected animals from 23 TB-infected animals after a single test in 2001 down to five, with 1–5 cases over the last few years. This infection has persisted for a long time despite the significant testing effort.

Cattle were seen investigating a possum behaving strangely in a paddock by the farmer one afternoon in 2007.

The herd backs onto a solid bush–pasture margin, and uses several run-off blocks including one (Kimberley block) located at the end of Granite Creek Road surrounded by forest and accessed by a narrow dirt track cut through the forest behind the farm.

Case #2: Scarlett/Pender

This dairy herd is also owned by Mr Scarlett but is managed separately. The animals are never mixed or traded. The history of this herd is quite different to the herd above.

This herd has little possum habitat on or immediately adjacent to the farm. It is situated amidst the Market Cross (Karamea) township. Baker's Creek runs behind the farm and there is modest possum habitat along its banks. The herd has grazed a run-off block near the beach in the past, but that run-off area also has little possum habitat.

The herd currently has I13 herd status. Usually, one, or sometimes two, TB cases are identified at a test or in cull cattle sent for routine slaughter. Cases are generally identified at intervals between 6 months to 3 years. This pattern has continued since the early 1990s. The TB cases are usually older (adult) animals. Several parallel herd tests on the herd have failed to identify any infection at all. The herd had almost completed two clear tests at the time this report was written.

Case #3: Miedema

This dairy herd is situated at the end of Arapito Valley immediately adjacent to forest at the lower end of the Karamea Gorge. The herd has had a long history of TB infection at variable intervals, and is currently clear (C1). Like the Scarlett/Pender herd, TB cases are usually single animals, either reacting to TB testing or identified as TB culls at routine slaughter. The recent TB cases have tended to be younger cows.

Calves are grazed off the farm in Canterbury (in TB-free areas) and return as in-calf heifers. This practice is relatively rare for Karamea farmers as most maintain their herds within the Karamea district and many are restricted to their own home properties.

Case #4: Jones

This is another dairy herd with a long history of TB infection and is currently I2. This herd has been in the family for many generations and TB cases have been identified sporadically in the herd for more than 40 years. Cases usually involve small numbers of cows or singletons. Parallel testing has been carried out on the herd multiple times and initially small numbers of animals with TB were discovered. More recent parallel tests have failed to identify any test-positive animals with TB.

The farm has very little possum habitat and is located along the beach. The farmer grazes on the spit between the lagoon and the sea. The farm's dry-stock block is close to the south-west corner of Karamea's 'South Terrace', which is covered in bush and scrub.

5.2.2 Control herds

Control #1: Hyndman

This dairy herd had a C10 status (clear for at least 10 years) prior to having a single young cow react to a skin test in 2011. This TB case was found after the project was initiated. A further case of TB has since been identified in 2012. This is a closed herd with a minimal history of trading stock and located close to the bush at the back of the property.

Control #2: Hislop

The Hislops have only been on the farm for 3 years, but they are milking the original herd that has been on the farm for many years. The dairy herd has C10 status and no infection has been found in the herd since the mid-1990s. The farm is located on the Wangapeka Road and remains clear to date. The property has a bush–pasture interface along the back fence.

Control #3: Kees

This C9-status dairy herd is located across the road from the Hislop herd on the Wangapeka Road. A single cull was found in 2002.

5.3 Farmer survey

Key findings from the two surveys are tabulated in Appendix 5. Caution is needed in interpreting results as virtually all herds have been infected at some point and, as stated above, some of the control herds (or other C10 herds) broke down before the end of the study or have broken down since then.

5.3.1 Bush–pasture margin

Although not all Karamea farms have an immediate bush interface, all are within 2 km of the bush edge, and most infected herds have run-off blocks that are associated with bush.

Of the herds infected for three or more years between 2005 and 2010, 9 out of 10 farmers said they did not believe that their home farms had an immediate boundary that interfaced with the contiguous Karamea bush (i.e. a bush pasture margin on their property). Note that farmers considered their properties separate from the bush if there was a road or double fence between their grazing paddocks and the bush edge. Farmers appear unaware that fences usually prevent the movement of stock from the paddocks to the bush but provide no barrier for wildlife.

In contrast, for herds that were not infected at all during this period, 1 out of 5 farmers considered their property had a bush–pasture margin (Fisher exact test $p = 0.02$). However, since the survey was completed, three out of five herds that did not have an infected status between 2005 and 2010 have broken down.

All eight farmers whose herds had an infected status during 2010 (study year) considered that they did not have an immediate bush–pasture margin compared to 5 out of 12 with herds that were not infected during 2010 ($p = 0.01$).

From the survey herds, 9 out of 10 farmers that had an infected status during the 2 years preceding the latest aerial control (2006–2008) considered that they did not have an immediate bush–pasture margin. This was significantly different to the 2 out of 6 owners of herds that were not infected during this period who considered that they did not have an immediate bush–pasture margin ($p = 0.03$).

Eleven out of 13 farmers with longstanding infected herds (herds infected for 10 consecutive years or greater from available test records) did not consider they had an immediate bush–pasture margin compared to 2 out of 7 farmers that did not have longstanding infected herds ($p = 0.02$).

Offal pits

Offal pits are used to dispose of carcasses of animals that die on the farm, or by-products from home-kill. The open carcasses of TB-reactor cattle that have been necropsied on-farm could end up in an offal pit and be a source of tuberculous material for wildlife. A higher proportion of ‘problem herds’ surveyed had offal pits, although this was not statistically significant ($p = 0.11$ for herds with an infected status since the last aerial operation) with the small sample sizes available. Exposure to offal pits is not a simple variable to model as an offal pit located on one property may actually be closer to stock on a neighbouring property

than animals on the property itself. Offal pit data were not included in the Bayesian risk model as the survey only captured data for a single point in time and the location/presence of a pit is unlikely to have been constant throughout the herds' test histories.

Home kill

There was no significant difference in infection rate between herds where the farmer kills stock on farm and those where farmers do not. It must be noted that no surveillance information is collected from routine 'on farm' slaughter material so the TB status of these animals is unknown (especially where farmers of dry-stock herds are not testing stock).

Run-offs

From the study herds that had an infected-herd status during the 2 years preceding the last aerial control, 9 out of 10 had a 'run-off' block, compared with 4 out of 10 herds with such blocks but not infected during the same period ($p = 0.03$). Of the case-study herds, 10 out of 12 had run-off blocks (and only 2 did not have a bush–pasture margin) compared with 2 out of 7 control herds ($p < 0.03$).

This was by far the most significant variable examined. Herds that had infection for multiple years over the past 5 years, herds that were infected 2 years prior to the 2008 aerial 1080 drop, and case herds were all significantly more likely to break down compared with control herds. A crude index of 'Movement Restriction Risk' was calculated for each herd based on having a run-off or not. The Movement Restriction Risk was approximately 5 times higher where the herd used a run-off. The risk was similar for herds under restrictions before or after the latest aerial operation.

Virtually all West Coast run-off blocks are less developed and are usually associated with bush or scrub areas. This is no exception for Karamea. Run-off blocks are rougher than home dairy farms and both young stock and older dry cows can spend prolonged periods there.

Stock water

All properties in Karamea or on the West Coast are likely to provide stock with access to groundwater at some point throughout the year.

Of 11 herds that had access to water in troughs only, 5 were infected, compared with 0 out of 8 herds that had access to natural waterways ($p = 0.04$).

Where culls are slaughtered

Some farmers believe some slaughter premises find more TB than others. During the farm survey interviews, farmers indicated that they preferentially sent culls to the North Island for two reasons. First they attract a better price and second they believed TB was less likely to be found if present. However, analysis of slaughter-house data from Karamea herds indicates no significant difference in the detection rate between North Island and West Coast slaughter premises.

Carry-over cows

Carry-over cows are milking stock that fail to conceive and the farmer chooses (for reasons of pasture management, genetic gain or sentimentality) to keep a non-productive cow until the following season in the hope that she will conceive and produce milk again. These animals may represent a risk of continuous infection as they tend to be grazed in marginal productive areas usually in close proximately to bush and scrub. Longstanding infected herds were less likely to keep carry-overs (54%) than herds that have not remained infected (67%). Fifty per cent of herds that became infected prior to the last aerial control operation routinely carried cows over to the next season, compared with 78% that were not infected during that period. Of the case-study farms only 50% routinely kept carry-overs compared with 85% of control herds, but this may have been a recent choice as a result of becoming infected. The practice of keeping carry-over cows does not appear to be associated with any greater risk of movement restrictions due to TB infection (based on this small sample of properties). Some farmers with an infected status herd may have made the decision not to retain carry-over cattle because of a perceived risk.

5.3.2 Milk production/ herd health/disease fallacy

Herds suffering stress as a result of feed deprivation or other stressors (as a result of flooding, drought, or neglect) and exposed to *M. bovis* can experience 'blow out' numbers of TB animals at a herd breakdown. The origin of the infection may be from infectious cattle or a tuberculous possum. Once the infection establishes in the herd it can then spread from susceptible animal to susceptible animal. The dissemination of the infection can be amplified by close contact and confinement, such as dairy cows in a dairy shed twice a day. Some farmers suggested that the productivity (or health) of the herd is actually a factor in the initial or repeat infection of a herd. Data on total stock numbers, milk solids per hectare, and milk solids per cow were therefore obtained for each of the study farms and plotted against the various response variables identified above (Figure7a, b, c).

Regardless of how infection was classified, the total stock numbers (size of herds) tended to be larger for the infected herds than the control herds, but not significantly so. The productivity per effective hectare also did not differ between case-study and control farms, and if anything tended to be higher, rather than lower, on infected farms. Similarly, milk solids per cow were not significantly different between case-study and control herds.

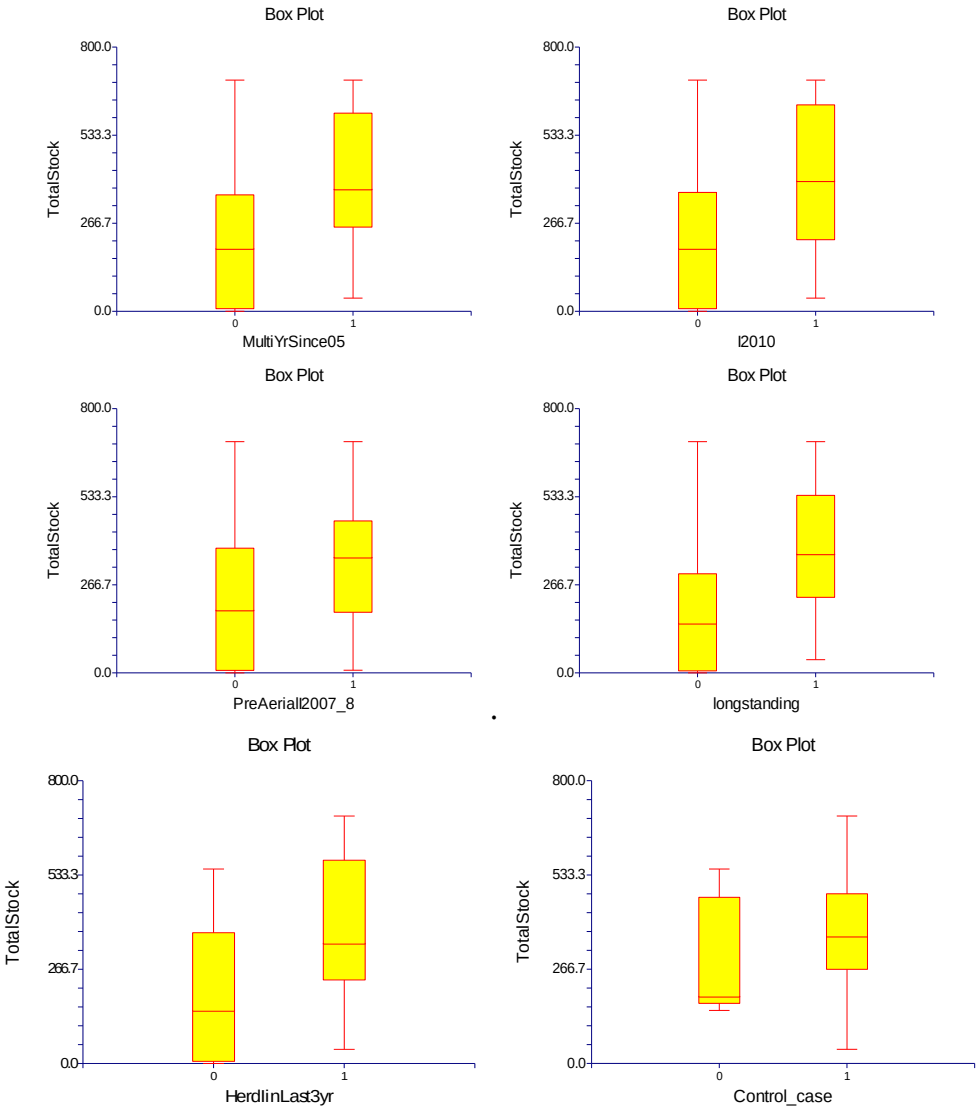

Figure 7(a) Boxplots of herd size for each response variable. 1 = those herds having that characteristic, and 0 = those not having that characteristic. MultiYrSince05 = herds with multiple years of infection from 2005; I2010 = herds with an infected status in 2010; PreAerial2007_8 = herds between 2007 and 2008; Longstanding = herds continuously for 10 years or greater; HerdinLast3yr = herds with infection since last aerial control (i.e. 2009–2011); Control_case = case (1) and control (0) herds selected as part of this project.

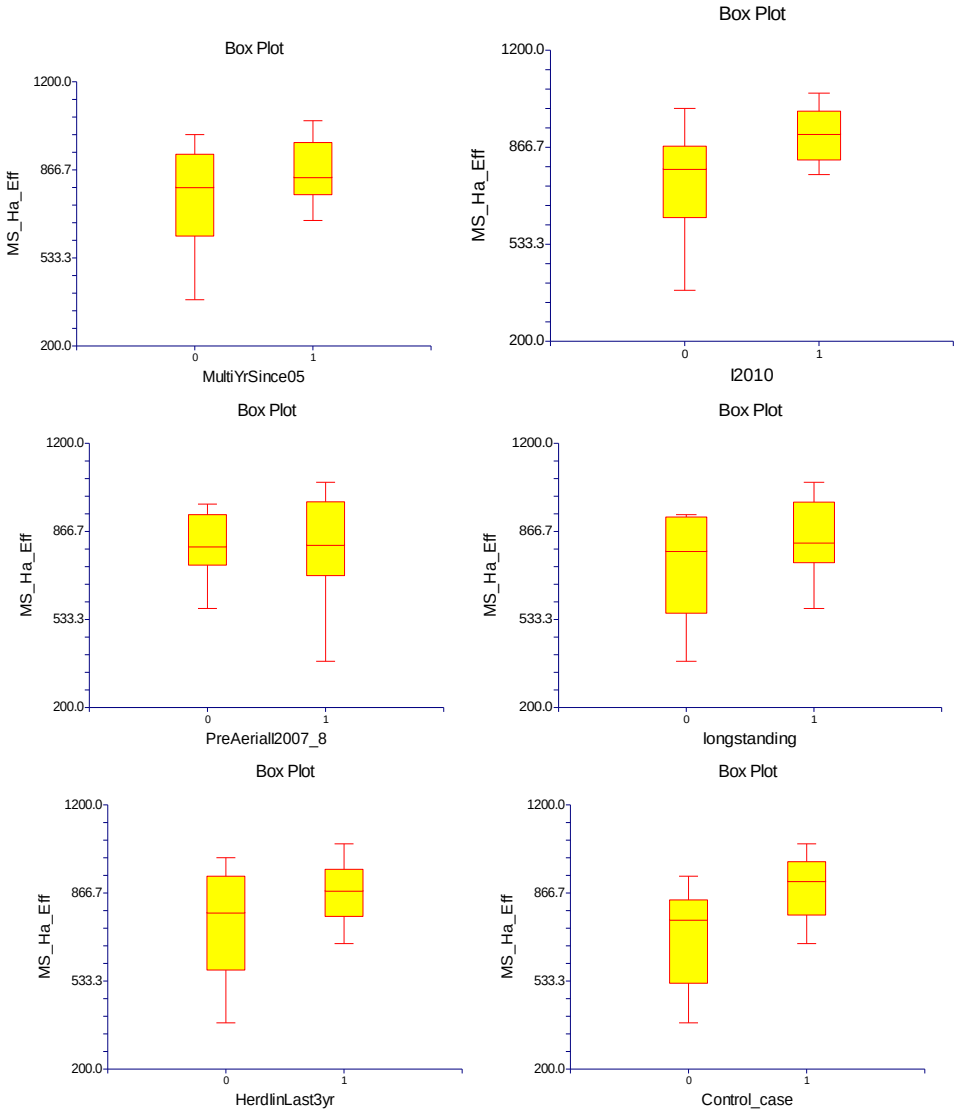

Figure 7(b) Boxplots of milk solids per effective hectare for each response variable. Variables same as for Figure 7(a).

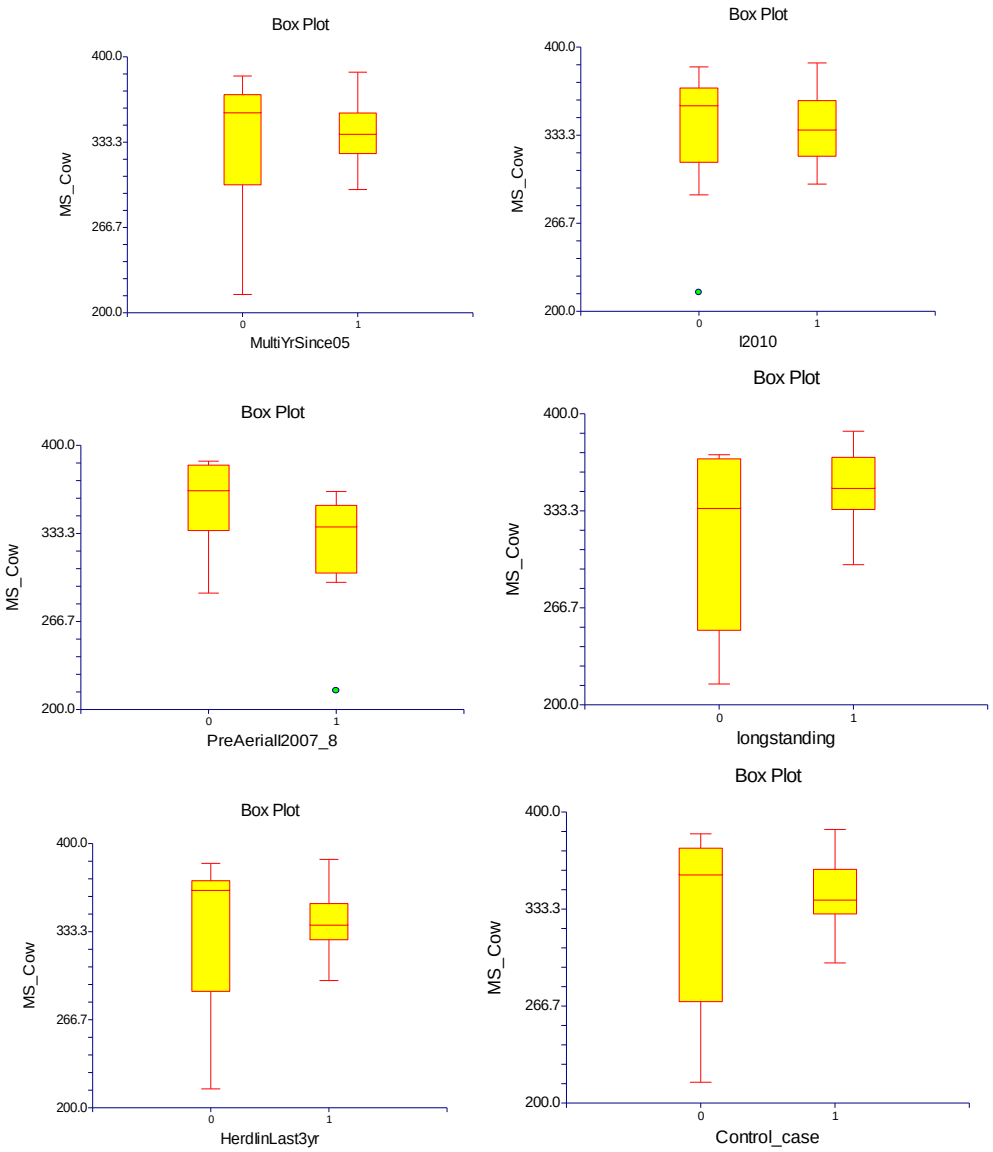

Figure 7(c) Boxplots of milk solids per cow for each response variable. Variables same as for Figure 7(a).

5.4 Possum control history

Possum control was first undertaken in the Karamea district in the 1970s, initially managed by the New Zealand Forest Service, then by the West Coast Pest Destruction Board from about 1978 to 1989, and by the West Coast Regional Council from 1989 onwards. When the contractor-based control industry was developed in 1996, control operations had objectives to reduce possums uniformly to below an RTC of 5%. By the early 2000s control targets were reduced to a mean RTC of 2% with no line catching more than two possums (B. Petrie pers. comm.), but because of the presence of weka, all traps had to be raised on leaning boards. These initial operations were carried out as performance contracts with payment dependent on an independent RTC monitor showing the target RTC had been achieved. After 2008, input-based contracts were carried out using traps and brodifacoum, cholecalciferol, and

Feratox. Although some of the performance-based operations failed to meet their control targets, most did so. Nevertheless, because infection rates in herds remained high there was concern that control had not been applied intensively enough or not uniformly enough, especially in areas of swamp lands (i.e. Kongahu swamp). As a result of this concern, an extensive control/survey was carried out in 2006 that placed traps and WaxTags® in every piece of potential possum habitat. This resulted in 16 788 sites being selected and trapped for at least six nights over a 7-month period (see Appendix 6 for an example of sites). This survey followed a conventional control operation that had been completed in 2005.

In late 2007 and early 2008 another extensive ground control operation was carried out on the farmland, and then in the winter of 2008 all forest adjacent to Karamea farmland from Blue Duck creek in the south to Kohaihai in the north and extending 5 km into the forest interior was aerial sown with 1080 baits. A trend monitor carried out in 2009 showed the RTC was below 1% and indicated the aerial operation had reduced the possum population to very low numbers. There were, however, exclusion zones (e.g. on both sides of the Karamea River) required as part of the 1080 consent, although these were treated, to various extents, by subsequent ground control.

5.5 Possum abundance and patchiness

5.5.1 Abundance

The only data available suitable for estimating total possum numbers were obtained from the intensive survey carried out in 2006 (Appendix 6). However, this survey followed a control operation so the numbers estimated will underrepresent what was there prior to control. Nevertheless the extensive 2006 survey resulted in 249 possums being trapped from 100 728 trap-nights, representing an overall catch rate of 0.24%. Just taking the captures on the first three nights (roughly equivalent to an RTC survey) there were 187 possums caught from 50 364 trap-nights (0.37% RTC equivalent).

When possum captures in all traps were grouped into nightly captures (1–6), the captures on each successive night declined linearly (Figure 8). The total population was estimated to be 347 (95% CI = 311– 407) derived from a WinBugs simulation that for each night used the number of possums caught (n[i]) as having a binomial distribution from the number remaining with probability p (i.e. the number remaining is the initial population size (N) minus the cumulative number caught until that time period (x[i])). This estimate was based on assumptions that trapping effort stayed constant for each night, all habitat/possums were exposed to the trapping effort, and the population was closed.

Although this trap-out estimate of total numbers is ‘crude’, it is likely to be in the right ‘ballpark’.

The total area of potential possum habitat in the Karamea district is about 3719 ha including the area of potential possum habitat on the Karamea farms plus a 100-m strip of forest boundary. In 2006 the estimated pre-survey density of possums in this habitat was therefore about 0.1 possums/ha (i.e. 347/3719) or as a worst case 0.11 possums/ha (i.e. 407/3719). Subtracting the number of possums killed, these results suggest a post-control population of about 100 possums (0.03/ha), a ~70% reduction.

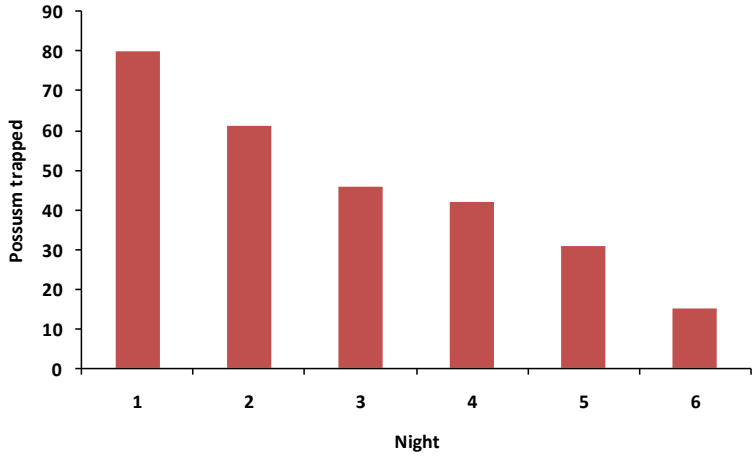

Figure 8 Possums captured on successive nights during the 2006 intensive survey.

Following the 2006 survey, further ground control was carried out in late 2007 – early 2008 (prior to the aerial operation in the adjacent forest), and a further 329 possums were trapped primarily along the farm–forest edge (see Appendix 7 for location of these possums). Assuming that trapping was for three nights, and (from Figure 8) that about two-thirds of the possums captured in the 2006 survey were caught in the first three nights, we estimate that this operation will have accounted for only half (48%) of the population – if so, these calculations suggest the total population had increased from 100 in 2007 to more than 600 about 18 months later. The resident survivors will have produced substantially fewer than 100 recruits, suggesting the arrival of ~400 immigrant possums from the adjacent forest (accepting assumptions).

Surveys subsequent to the 2008 aerial 1080 operation of the adjacent forest indicated low possum densities based on chewcard detections. The first survey (Dec. 2009) had an interference rate of 5.4% (98/1810), which declined by 80% to 1.1% (24/2121) in mid-2010 after a contractor (EPRO) had carried out ground control. In mid-2011 the interference rate was 2.8% (192/6789) along the forest–pasture margin, 2.6 times higher after just 12 months.

Using the 6-times multiplier suggested for converting conventional RTCI values into 7-day CCIs by Nugent et al. (2012) (based on a calibration within central North Island forest) this suggests RTCIs of 0.9% in late 2009, 0.2% in mid-2010, and 0.5% in mid-2011.

Further, assuming that an RTCI of 5% equates to a possum density of about 1 possum/ha, this suggests, even when accepting the highest likely average density of 0.2 possum/ha, the total number of possums present in late 2009 was ~700 (i.e. 0.18 × 3719 ha), ~100 in mid-2010, and ~350 in mid-2011. Again, these rough calculations suggest annual immigration of some hundreds of possums.

5.5.2 Patchiness

Although possum numbers were low, possums did not occur uniformly across all habitat. Comparing the mean distance between closest sites where neighbouring possums were trapped with the mean distance between closest neighbours when the same number of possums were distributed at random between all trap sites shows possum distribution was significantly aggregated (Figures 9 and 10).

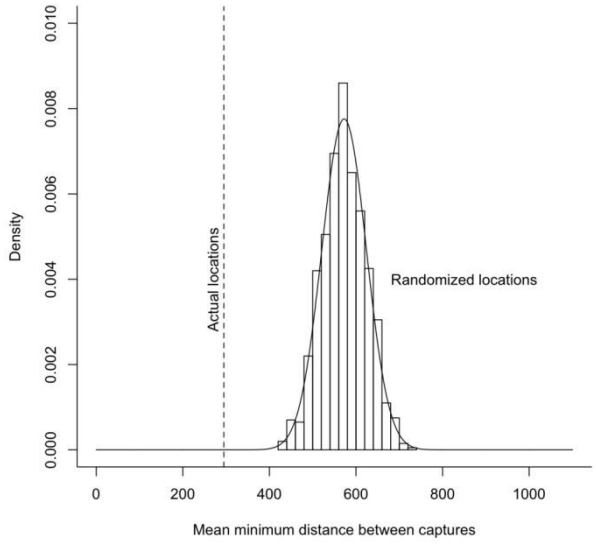

Figure 9 Mean minimum distance between actual capture locations (vertical line) and distribution of mean minimum distances if possums were randomly distributed (histogram). Data from 2009 detection survey.

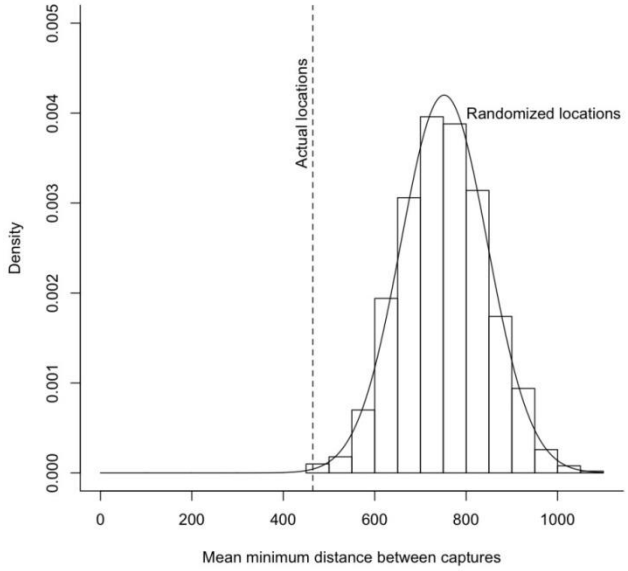

Figure 10 Mean minimum distance between actual capture locations (vertical line) and distribution of mean minimum distances if possums were randomly distributed (histogram). Data from 2011 detection survey.

Some patches of possums were found in similar places over subsequent surveys, suggesting particular areas were either favoured by possums or were geographically-defined sinks for immigrant possums (e.g. at top of Aripito Valley – bottom of Karamea Gorge) (Figures 11 and 12). See Appendix 2 for maps of all detection surveys carried out.

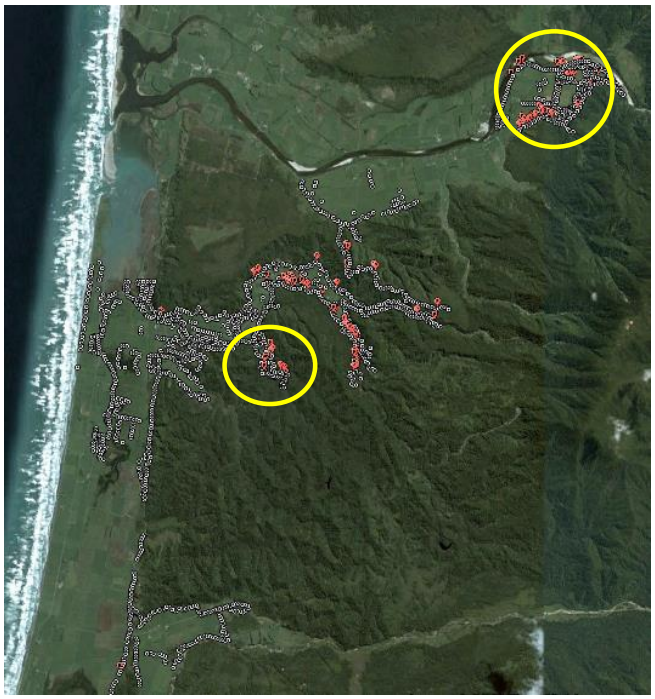

Figure 11 Chewcard (white dots) and possum detections (red balloons) identified during the 2009 survey. River at top of image is the Karamea (Arapito Valley).

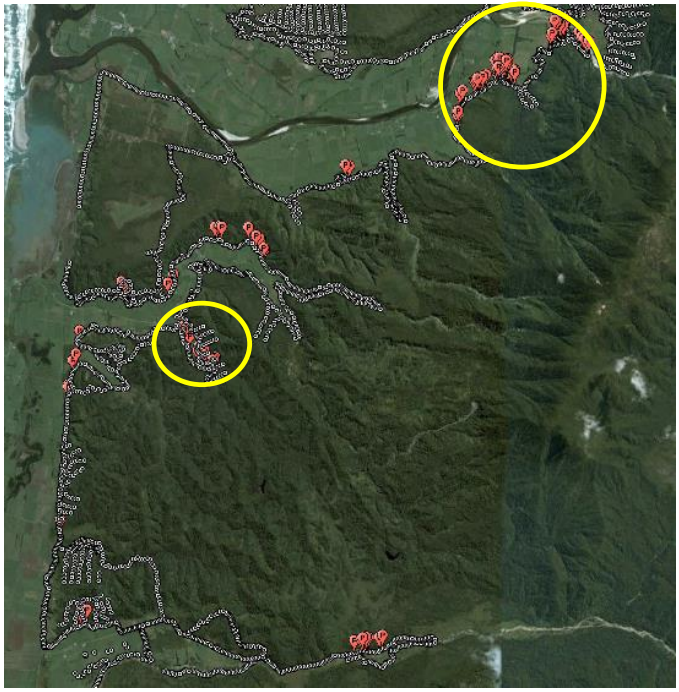

Figure 12 Chewcard (white dots) and possum detections (red balloons) identified during the 2011 survey.

Modelling of TB persistence (Barron & Warburton 2010) predicts that where there is either an average of 10 possums present within a single hectare, or 10 possums present over 10 ha (1 possum/ha) there is a 1 in 20 chance that TB might still be present after 5 years solely as a result of local transmission. However, the accuracy of this prediction is unknown.

To assess if such clusters of possums might be present at Karamea, we used positive chewcard detections (from the 2009 survey) and possum 'captures' (Figures 13 and 14) to determine possible clusters of possums. Around each positive chewcard site, we considered a 10-ha circular area, and determined if the detection rate of possums was greater than 20% on all other chewcards within that area (we assumed that 20% detection with linear sampling represented at least 1 possum/ha even though 30% CCI (i.e. 5% RTC) would be expected if sampling was applied in a more 2D design). Six possible 'clusters' of possums were identified, two at the top of the Arapito Valley and four in Granite Creek (Figure 15). Thus, even if all six of these clusters were infected, the 1 in 20 chance that TB could still be present suggests little chance of infection persisting more than 5 years in one of these sites. However, given that TB-infected possums have been detected at only one location since 2006 (in 2012; see below) despite an apparent 50–80% reduction of possums in 2007/08 and 2010/11 that would have provided surveillance sensitivities of 35–60%, the probability that all six clusters were infected in 2009 is very small.

Figure 13 Possum captures from an EPRO contract (Jan–Feb 2010) and from Landcare Research shooting (June 2010) at prefed bait stations (bait stations were located at positive chewcard detections).

Figure 14 Possums trapped during an AHB survey/control operation during 2011.

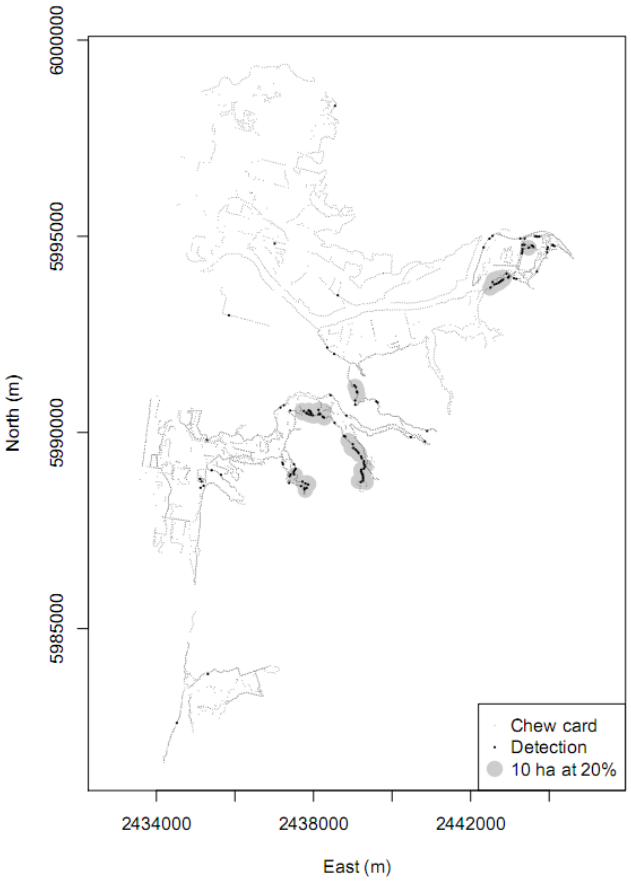

Figure 15 Potential clusters of possums where TB could persist based on positive chewcard detection sites. The very small dots represent all chewcard locations.

5.6 TB prevalence in possums and risk to cattle

The first TB-infected possum reported from the Karamea district was found on the south side of the Kohaihai Bridge along the Heaphy Track in about Sep.–Oct. 1974 (P. Livingstone pers. comm.). A second one was then found on the coast side of the Little Wanganui River in 1975.

In 2006 four TB-infected possums were identified from at least three widely spaced locations (see Appendix 6). The four infected possums came from a sample of 249 possums captured, necropsied, and cultured (i.e. 1.6% prevalence).

Between 2007 and 2011, a further 386 possums (317 from routine control mainly in late 2007 – early 2008, 35 from an AHB 2011 survey, and 34 from EPRO and Landcare Research) have been sampled. The 317 from 2007/08 were necropsied only, but the EPRO and Landcare Research samples were also cultured. No infected possums were detected in these samples. Overall, since 2006, 635 possums have been examined with 4 infected (i.e. 0.6% prevalence). Given the low sensitivity of necropsy alone (~75%), this will be an underestimate, but since no TB lesions were found in the 317 possums from 2007/08 that were cultured, any bias will be small.

The 2006 survey indicates the prevalence of TB is typical of most areas were TB has been or still is present in possums. Based on observed prevalence and the estimates of population size above, we calculate prevalence was 1.6% in 2006, equating to six infected possums before control, and two remaining afterward.

In 2007/08, the observed prevalence was zero. Assuming from above that half the possum population was necropsied, and allowing for low sensitivity (~75%) from necropsy alone, survey surveillance sensitivity was possibly 37%. If so, we can be 95% confident that there were fewer than six infected possums present before control, and four or fewer after control.

In 2010/11 the observed prevalence was again zero. Because only an apparently small proportion of the possums killed were examined for TB, this provides little useful insight into likely numbers of infected possums – except to say that if the sample represented 11% of the population (79/700), we can be 95% confident that there were fewer than 25 infected possums present before control and fewer than six afterward (assuming an 80% reduction of a population of 700 possums).

That high estimate aside, the two most complete possum TB surveys (2006, and 2007/08) suggest that there have only been 2–6 infected possums present at any one time on or near Karamea farmland since (and including) 2006 – an average of about 4. Including the high estimate would increase the average to a worst case of about 8.

Recent research (Nugent et al. in press) suggests possums die on average about 6 months after becoming infected, faster than previously thought (Ramsey & Cowan 2003; Norton et al. Corner 2005). If so, then the total numbers of infected possums present each year would be double the average numbers present at any one time; a best estimate of 8 and a worst-case estimate of about 16.

If infected possums are the main driver of TB infection in Karamea cattle herds, then there must be sufficient infected possums to enable the transfer of infection to cattle. Where a herd is exposed to an infected possum, we assume at least some tens of cattle are individually

exposed (in the sense of being in the vicinity of, or occupying the same range as an infected possum). If so, the probability of an individual animal becoming infected with TB must be low, otherwise the number of infected cattle per breakdown would be higher than observed.

Nationwide, the number of TB cases confirmed for each breakdown in cattle is usually low. Using nationwide data (supplied by T. Ryan), Nugent et al. (2006) identified 524 short-lived breakdowns that (1) were isolated from previous or subsequent breakdowns by at least 2 years and (2) were attributed to a wildlife source. Of those herds, 85% involved a single TB case, 9% two cases, and 2% involved three cases, which strongly suggests that there are many instances in which TB-infected possums are present, but no TB cases result. Using a probability simulation model, Nugent et al. (2006) estimated that only about one in four infected possums resulted in a TB breakdown in cattle.

Over the past seven years, the average number of herds on movement control at Karamea was ten, and each year the average number of new herds on movement control was five. If just the five newly infected herds were caused by possums, and if four infected possums were required (on average) to produce a breakdown, the logic above suggests that at least 20 possums with TB must be present annually, far more than even our worst-case estimates.

This disparity suggests either possums are not the primary cause of TB breakdowns in cattle or the 'one-in-four' estimate is not appropriate for Karamea. One indication of the latter would be a larger number of TB cases per new breakdown at Karamea than nationally, but this is not the case, with most breakdowns comprising only one or two animals.

5.7 Immigrant possums

Because the Karamea farmland is an elongated stretch of land sandwiched between the sea and forest, it has a long (c. 38 km) farm–forest boundary subject to high immigration pressure from forest possums. The possum population on farmland after control in 2006 was estimated to be about 100 individuals but 18 months later to be more than 600, suggesting numbers of immigrant possums must have been high (i.e. in excess of 300 per annum). However, aerial control carried out in 2008 over 34 000 ha immediately behind the Karamea farmland reduced the adjacent forest possum population to an RTCI of less than 1%, and modelling suggested that this reduced the numbers of immigrant possums to less than 150 per annum. This scenario is supported by the much lower numbers of possums detected and caught in 2009–2011 on the farmland and along the forest–pasture margin. However, the aerial operation had exclusion zones (of several hundred hectares) that were treated later and to unknown effectiveness by ground control. These areas could have been an additional source of immigrant possums, but given the small percentage of the area affected this will have been modest.

Based on the known kill figures and population estimates above, we suggest at least 300 possums arrived annually in 2006–2008, and an average of fewer than 150 in 2009–2011, about 1200 in total, or 200 per annum on average. If so, and if every infected immigrant caused a TB breakdown in cattle, about 2–3% of immigrants would need to have been infected to account for five breakdowns per annum, which is not an unreasonable expectation. However, if each new infection required on average four infected possums, then 8–12% of immigrants would need to be infected.

The possum model provides another approach to estimating immigration. Accepting model assumptions of carrying capacity, TB prevalence, and dispersal parameter values, the model predicts the number of infected immigrant possums arriving on the adjacent farmland in a 12-month period was one per 10 km, which equates to 3–4 for the full length of Karamea farmland. The model predicted 50 uninfected possums arrived for each infected possum, or 150–200 in total (based on 2% prevalence, and infected and uninfected animals having similar patterns of movement). Obviously, the numbers of infected immigrants would have been significantly higher pre-2008 before the 5-km buffer was put in place. If infected possums (i.e. prior to becoming infectious) disperse in random directions and also settle in habitat at random (as simulated in the possum model) then, over time, the model predicts all farms would have a chance of becoming infected (everything else being equal). However, the spatial distribution of infected and clear farms (Figure16) and the fact that clear/infected status has often persisted for ≥10 years, suggest either (1) infection for some farms is not possum related, and/or (2) dispersing possums (infected and uninfected) have dispersal and settlement rules that are not random, resulting in some properties being much more frequently used than others as transit and/or settlement sites. Additionally, given the current prevalence of TB in possums (c. 1%), for every infected immigrant arriving on a farm there should also be about 100 uninfected possums if not arriving simultaneously then on average over time. Farmers and control contractors are not seeing or killing these numbers of possums.

To summarise the above, if possums are causing infection on c.5 farms annually, then our estimates of numbers of resident and immigrant possums suggest most TB-infected possums must be infecting cattle, and (1) some TB possums are somehow infecting multiple properties; and/or (2) there is an unusually high prevalence of infection amongst the 100–300 immigrants arriving annually (most of which may not be detected because the infected animals die soon after arrival); and/or (3) immigrants are preferentially settling at particular locations, sometimes resulting in clusters of possums large enough for 3–4 ‘residents’ or fellow immigrants to become infected.

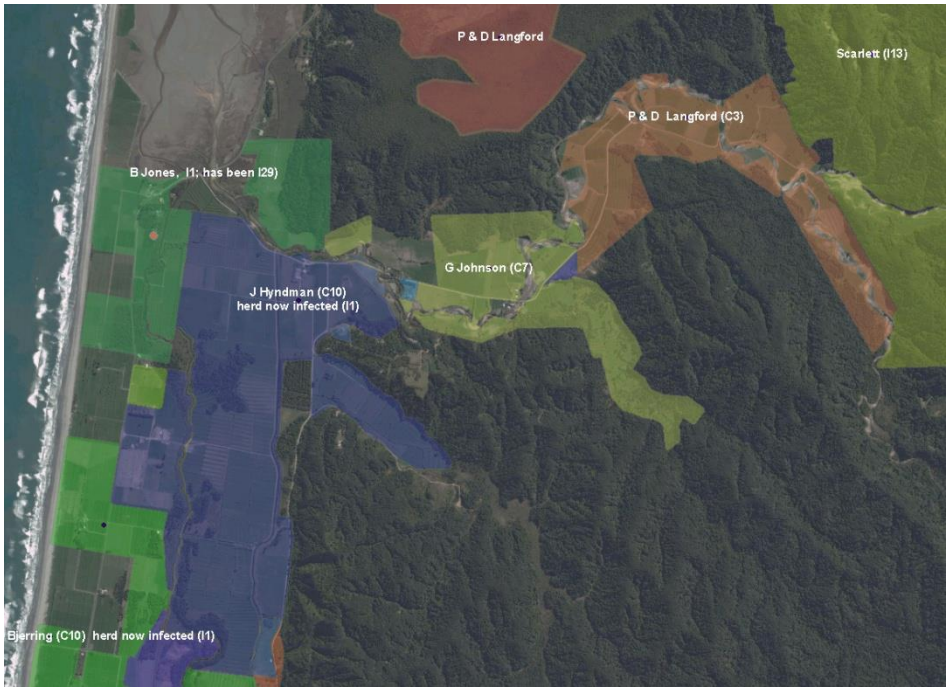

Figure 16 Adjacent farms centred on Granite Creek that have had persistent I and C herd status over many years. Note two of the C10 herds have now shifted to an I status.

5.8 Other species as potential wildlife TB vectors

Stoats, ship rats, Norway rats (*Rattus norvegicus*), hedgehogs (*Erinaceous europaeus*) and NZ fur seals have all been suggested as possible alternative sources of TB infection in the Karamea district. Red deer (*Cervus elaphus*) also frequent the adjoining forest, but ferrets (*Mustela furo*) and feral pigs are absent from the area. Red deer are harvested by helicopter for commercial recovery and such animals are inspected for TB infection. To date there have been two TB-infected deer reported (in 2009/10), one from the Ugly and one from the interior end of the Karamea Gorge. Rates of infection obtained from abattoir inspection could be underestimated if infected animals are identified in the field, the carcass discarded, and the infection not reported, but this bias will be small, as easily detectable generalised infection is rare in West Coast deer.

In 2006, 187 stoats were trapped from 14 030 trap nights (from 1403 trap sites) (i.e. a 1.3% trap rate), and two were confirmed with TB (c. 1.1% prevalence) (see Appendix 8 for locations). No other species has been recorded with TB at Karamea but there has been very little survey effort. Stoats probably pick up the disease from scavenging as do ferrets, and they appear unable to maintain the disease in the absence of reinfection from possums or some other source. Given the lack of evidence that stoats have a significant role in TB transmission in other parts of New Zealand it is unlikely this species plays a significant role in maintaining disease in cattle herds in Karamea.

Rats (laboratory rats – typically *Rattus norvegicus*) are known to be highly resistant to TB and TB infection has not been found in wild rats in New Zealand (P. Livingstone pers. comm.). Although NZ fur seals have been identified with *Mycobacterium pinnepedii* there are no reported cases of seals with *M. bovis*. For both these species very few, if any, surveys have been carried out to assess the prevalence of *M. bovis*.

5.9 Risk analysis

Over 9 years (2003–2011) 77 cattle herds were tested, 144 469 animal testings were conducted, and 123 animals were deemed to be TB positive. Of these TB-positive animals, 107 were from ‘wet’ dairy herds, 13 from beef breeding, 3 from beef dry, and 0 from dairy dry herds.

We identified that seven different testing protocols had been used for testing cattle in the Karamea district. The mean sensitivities of these protocols ranged from 0.438 to 0.650 (Table 2) (see Appendix 3 for details). Of particular interest here, given they are the sources of most TB-infected animals, are the dairy herds with a recent history of infection (Protocol 2), where testing sensitivity is 0.65. While blood tests are conducted on all animals (apparent parallel testing), not all animals with positive skin tests are declared infected, which would represent true parallel testing. Consequently, only 55% of infected animals that were skin-test positive will be identified as TB-infected.

Summary statistics (Table 5) showed high variation of covariate values used in risk analysis modelling. Collinearity among covariates was low ($r < 0.30$), with the exception of *ForestExpose* and *ProportionHabitat* in which $r = 0.59$. Consequently, explored models were allowed to contain one of the correlated variables but not both.

Table 5 Summary statistics (Median, 2.5th and 97.5th percentiles) of covariates used in modelling. Covariates were subsequently scaled to have mean 0 and standard deviation 1

Covariate	Median	2.5th percentile	97.5th percentile
ForestExpose	3.11	0.00	50.47
ForestExpose08	1.01	0.00	50.47
ProportionHabitat	0.24	0.00	0.74
Excl09	2.96	0.05	10.16
ExposeInfectedWildlife06	0.02	0.00	0.19
RiverExpose	1.57	0.00	10.02
CoastExpose	0.03	0.00	0.30
StockingDensity	1.32	0.13	5.35
*PrevRisk**	-7.57	-8.37	-5.56

*Mean values estimated in modelling (λ_{ijt-1}; Eqn 6)

We explored 22 different models varying from simple intercept-only models to multi-covariate models (Tables 6–9). Fitting a separate intercept for each herd type facilitated the convergence of the Markov Chain Monte Carlo (MCMC), and generally resulted in models with greater explanatory power than when a single intercept was fitted. Using the Deviance Information Criterion (ΔDIC) to rank models, the most explanatory model included parameters for each herd type for the *Intercept, ForestExpose08, PrevRisk,* and *Excl09* (model 1 in Table 6). This model also had a p-value closest to 0.5 and the highest Area Under the Curve (AUC). The top 12 models included covariates related to exposure to forest habitat (either on-farm or main-forest-block forest) or previous risk of infection (*PrevRisk*). Multi-covariate models were explored using covariates from those uni-covariate models that performed better than the intercept-only models (models 13 and 15). However, we included *RiverExpose* in two multi-covariate models (models 11 and 14) because we were particularly interested in the hypothesis that possums may be using waterways as corridors. The finding that the uni-covariate models with *ForestExpose* and *ProportionHabitat* (models 5 and 8) performed better than the corresponding multi-covariate models with *RiverExpose* indicates that waterways did not substantially increase the risk of infection.

The best of the models explored, as indicated by ΔDIC, p-value and AUC, had positive parameter estimates for *ForestExpose08* in beef breeding and wet dairy herds (Table 6). This indicates that the risk of an infected livestock animal generally increased with increasing exposure to forest habitat up to and including 2008. *ForestExpose08* parameters overlapped zero for beef dry and dairy dry herds. Surprisingly, the risk of infection decreased for wet dairy herds with increasing exposure to forest zones that were excluded from the 2008 aerial toxin application (*Excl09*), but which underwent subsequent ground control operations. While the parameter estimates for *PrevRisk* in model 1 overlapped zero for all herd types, it is biased positive for wet dairy herds (Table 7) and this is consistent with the *PrevRisk* uni-covariate model in which the positive parameter estimate does not overlap zero (Table 8). Further evidence for the important influence of *PrevRisk* is found by comparing the models with and without *PrevRisk* that contain habitat-related covariates (Table 6). The explanatory strength increased substantially when *PrevRisk* was added in the following model pairs: models 1 and 4; models 3 and 6; and models 7 and 8. Evaluation of the most explanatory model (model 1, Table 7) demonstrates that exposure to uncontrolled forested habitat

increased the risk of infection and its effect was relatively strong compared to the effect of *PrevRisk*.

Similarly, the risk of infection in a cow in a wet dairy herd increased with increasing proportion of forest habitat on a farm (model 7 in Table 6; Table 9). The *ProportionHabitat* parameter for the other herd types overlapped zero, and this was consistent with all other models with this covariate, including the uni-covariate model of *ProportionHabitat* (model 8 in Table 6).

Table 6 Models were ranked using *Δ*DIC, where relatively low values indicate better fit to the data than models with relatively high values. We used Bayesian p-values and AUC (including 95% credible intervals) to assess goodness of fit. Bayesian p-values approaching 0.50 indicate that the model fits the data very well, whereas values near 0 or 1 suggest very poor fit. The AUC values vary from 0.5 (random predictions) to 1.0 (perfect prediction). When the Intercept or a covariate was preceded by *Herd*, such as *Herd:Intercept + Herd:Forest Expose*, a separate parameter was fitted for each of the four herd types

Model	*Δ*DIC	p-value	AUC (95% CI)
1) *Herd:Intercept + Herd:ForestExpose08 + Herd:PrevRisk + Herd:Excl09*	0	0.59	0.71 (0.68-0.75)
2) *Intercept + Herd:ForestExpose + Herd:Prev Risk*	28.26	0.61	0.69 (0.65-0.73)
3) *Herd:Intercept + Herd:ForestExpose + Herd:Prev Risk*	29.67	0.63	0. 70 (0.67-0.75)
4) *Herd:Intercept + Herd:ForestExpose08 + Herd:Excl09*	40.11	0.63	0.70 (0.67-0.71)
5) *Herd:Intercept + Herd:ForestExpose*	40.34	0.68	0.68 (0.65-0.69)
6) *Intercept + Herd:ForestExpose*	43.67	0.68	0.66 (0.64-0.67)
7) *Herd:Intercept + Herd:ProportionHabitat + Herd:PrevRisk*	47.65	0.61	0.70 (0.66-0.75)
8) *Herd:Intercept + Herd:ProportionHabitat*	52.90	0.64	0.67 (0.65-0.68)
9) *Herd:Intercept + Herd:PrevRisk*	53.42	0.65	0.68 (0.64-0.71)
10) *Intercept + Herd:ProportionHabitat + Herd:PrevRisk*	55.01	0.60	0.68 (0.64-0.73)
11) *Herd:Intercept + Herd:ForestExpose + Herd:RiverRisk*	55.39	0.67	0.69 (0.67-0.70)
12) *Herd:Intercept + Herd:ForestExpose08 + Herd:PrevRisk09*	57.23	0.67	0.69 (0.67-0.70)
13) *Intercept*	64.13	0.70	NA
14) *Herd:Intercept + Herd:ExposeRiver + Herd:ProportionHabitat*	67.94	0.63	0.67 (0.64-0.69)
15) *Herd:Intercept*	68.26	0.66	0.63 (0.60-0.65)
16) *Herd:Intercept + Herd:ExposeCoast*	73.33	0.69	0.64 (0.61-0.65)
17) *Herd:Intercept + Herd:ExposeRiver*	74.43	0.68	0.63 (0.60-0.65)
18) *Herd:Intercept + Herd:SkinTestPosPrevYear*	78.38	0.66	0.63 (0.61-0.64)
19) *Intercept + Herd:PrevRisk*	104.03	0.67	0.66 (0.58-0.72)
20) *Intercept + Herd:ForestExpose08 + Herd:PrevRisk + Herd:Excl09*	170.48	0.64	0.69 (0.67-0.74)
21) *Herd:Intercept + Herd:ExposeInfectedWildlife06*	272.11	0.67	0.63 (0.59-0.65)
22) *Herd:Intercept + StockingDensity*	279.21	0.71	0.64 (0.63-0.65)

Table 7 Summary statistics (median, and 2.5th and 97.5th percentiles) of posterior parameter distributions of model 1 (Table 6). The 95% credible intervals of parameters in bold do not overlap zero. Model variance cannot overlap zero. The mean and variance parameters for *Intercept*, *ForestExpose08*, *PrevRisk* and *Excl09* are not shown here

Parameters	Median	2.5th percentile	97.5th percentile
Intercept – Beef breeding	−6.43	−7.06	−5.76
Intercept – Beef dry	−7.16	−8.35	−6.10
Intercept – Dairy dry	−8.19	−11.00	−7.00
Intercept – Dairy herd	−7.40	−7.73	−7.13
ForestExpose08 – Beef breeding	0.97	0.27	1.86
ForestExpose08 – Beef dry	0.38	−1.58	1.72
ForestExpose08 – Dairy dry	0.98	−0.26	4.46
ForestExpose08 – Dairy herd	0.33	0.21	0.44
PrevRisk – Beef breeding	−0.01	−0.69	0.54
PrevRisk – Beef dry	0.07	−0.85	0.90
PrevRisk – Dairy dry	0.06	−0.59	0.69
PrevRisk – Dairy herd	0.12	−0.32	0.48
Excl09 – Beef breeding	0.17	−0.99	2.03
Excl09 – Beef dry	0.52	−0.74	4.89
Excl09 – Dairy dry	0.34	−1.00	4.25
Excl09 – Dairy herd	−0.39	−0.73	−0.07
Model variance	1.21	0.76	1.89

Table 8 Summary statistics (median, and 2.5th and 97.5th percentiles) of posterior parameter distributions of model 9 (Table 6). The 95% credible intervals of parameters in bold do not overlap zero. Model variance cannot overlap zero

Parameters	Median	2.5th percentile	97.5th percentile
Intercept – Beef breeding	−6.64	−7.30	−5.95
Intercept – Beef dry	−7.59	−8.55	−6.69
Intercept – Dairy dry	−8.68	−11.00	−7.54
Intercept – Dairy herd	−7.65	−7.96	−7.37
PrevRisk – Beef breeding	0.14	−0.50	0.71
PrevRisk – Beef dry	0.37	−0.77	0.99
PrevRisk – Dairy dry	0.19	−0.52	0.85
PrevRisk – Dairy herd	0.43	0.10	0.70
Model variance	1.99	1.33	2.73

Table 9 Summary statistics (median, and 2.5th and 97.5th percentiles) on posterior parameter distributions of model 7 (Table 6). The 95% credible intervals of parameters in bold do not overlap zero. Model variance cannot overlap zero. The mean and variance parameters for *Intercept*, *ProportionHabitat* and *PrevRisk* are not shown here

Parameters	Median	2.5th percentile	97.5th percentile
Intercept – Beef breeding	−6.37	−7.02	−5.72
Intercept – Beef dry	−7.40	−8.57	−6.40
Intercept – Dairy dry	−8.58	−12.00	−7.26
Intercept – Dairy herd	−7.47	−7.79	−7.18
ProportionHabitat – Beef breeding	−0.03	−0.67	0.47
ProportionHabitat – Beef dry	0.15	−0.51	0.71
ProportionHabitat – Dairy dry	0.38	−0.33	1.20
ProportionHabitat – Dairy herd	0.33	0.16	0.50
PrevRisk – Beef breeding	0.04	−0.60	0.60
PrevRisk – Beef dry	0.21	−0.88	0.96
PrevRisk – Dairy dry	0.12	−0.55	0.79
PrevRisk – Dairy herd	0.36	−0.08	0.67
Model variance	1.44	0.93	2.14

5.10 Probability of TB freedom in possums

Despite no evidence of TB in possums since 2006, the surveillance in 2010 and 2011 was insufficient to declare freedom of disease in the central area of Karamea (Table 10). Following the 2010 and 2011 surveys, the median probabilities of disease eradication were 0.74 and 0.78, respectively. Further, the CIVs of 0.025 and 0.04 were well below the target 0.90. The survey data had little influence on the CIV values because much of the land was improved pasture, which was not surveyed by the detection devices used.

Table 10 Results of modelling the probability of TB eradication (POF) and surveillance sensitivity (SSe) from possums in the central area of Karamea. The median and 95% credible intervals (CI) are presented for the POF and SSe. The credible interval value (CIV) is the proportion of the posterior distribution of the probability of eradication that is greater than 0.90. A target CIV of 0.90 would be regarded as successful eradication

Year	POF Median	POF Low CI	POF High CI	POF CIV	SSe Median	SSe High CI	SSe Low CI
2010	0.744	0.542	0.896	0.025	0.365	0.363	0.367
2011	0.782	0.605	0.91	0.04	0.288	0.286	0.29

6 Discussion

The persistence of infection in 20–30% of Karamea herds since about 2000 suggests current herd testing and possum control programmes are missing a significant source of infection.

If the disease is persisting in the cattle herds without a sustained wildlife source, there must be some form of inter-generational spread (horizontal, pseudo-vertical or vertical) that occurs despite regular disease control activities (testing and cull post-mortem inspection).

The long duration of infection in some herds (up to 29 years for one herd), and the almost equally long freedom of infection in others (even properties neighbouring infected herds), is suggestive of within-herd transmission. However, it is difficult to reconcile persistence of infection with the fact that simple skin-test-and-cull-only protocols have been sufficient to rapidly clear infection in many situations globally where no wildlife reservoir was involved.

Surveys of farmers with case-study and control herds indicated that the only significant risk factor was the use of run-off blocks and that fact agreed with the modelling, which indicated exposure to forest and thus to wildlife was an important risk.

In line with possum control carried out in vector risk areas throughout New Zealand, contractor-based possum control has been carried out over Karamea farmland since the mid-1990s, with RTC targets generally being met. Nevertheless, there has been particular concern about the quality of this control because of the continuing level of herd infection. Results from an intensive WaxTag® and trapping survey in 2006, and chewcard detection surveys carried in 2009 and 2010, indicated that possum numbers are, on average, very low with RTC values at or below 1%. Modelling indicates that such level of control is sufficient to eliminate TB from possums within less than 10 years (Barron 2012 submitted). However, possum abundance is not uniformly low and residual possums are aggregated across the landscape. Whether such aggregation or the number of individual possums within each aggregation is sufficient to maintain TB without immigration is unknown, although Barron (2012) modelled aggregation effects and found they had little effect on TB persistence under the scenarios explored.

By the end of this study, all the TB-infected possums that had been identified (n = 4) were from the 2006 survey, although many of the 635 possum samples were only examined for gross lesions and therefore prevalence would have been underestimated. De Lisle et al. (2009) showed from surveying four possum populations that necropsy and inspection for gross lesions detected from 20% to 80% of infected animals, and suggested that relying on searches for gross lesions will be inadequate for detecting presence of TB in some populations. In the winter of 2012 an AHB control operation recovered 50 possums (up to the date of this report) from the Arapito Valley, four of which were confirmed with TB although there is some possibility of contamination for two of these. Nevertheless the two absolute infections confirm that TB is still present in the possums at Karamea.

Karamea farmland is ‘squashed’ between the sea and Kahurangi National Park, an extensive area of indigenous forest that provides a significant source of immigrant possums, and is understood to have infected possums. The risk that infected immigrant possums pose to ongoing herd infection of Karamea herds has been acknowledged for many years and was the main justification for carrying out the extensive aerial control operation in 2008 when 1080 bait was applied to a 5-km-wide buffer of forest adjacent to the farmland. However, contrary

to expectations, this operation did not result in a greater or more persistent decrease in herd infection than was achieved with the earlier, less intensive aerial control operations. This suggests (1) at least some infection remains resident within the farmland, (2) exclusion zones were sufficiently numerous and not subsequently controlled adequately enough to stop potential infected immigrants, and/or (3) even a 5-km buffer is not sufficient to stop infected immigrant possums. However, accepting the parameter values used in the possum model, the model did predict that even with a 5-km buffer there could be at least 3–4 infected possums migrating from the forest onto farmland annually. The question is whether this number of infected immigrants is realistic and sufficient to drive the current level of herd infection?

Both modelling and empirical data show that to eliminate TB from possums (assuming no immigration), populations of possums must be maintained below a density generally indexed at about a 5% RTC (Ramsey & Efford 2005). However, if the prevalence of TB in the area is 2%, then for every infected possum there must be, on average, 50 uninfected possums. For TB to persist, Barron and Warburton (2010) suggested that for a 5% probability that TB would persist for at least 5 years there needs to be at least 10 possums per 'patch', some of which need to have overlapping home ranges (note, this could be 10 possums in one hectare or 1 possum/ha over 10 ha). For Karamea, given the overall density of possums appears to be below the required 5% RTC (and even below the commonly required 2% RTC), then for TB to persist (without infected immigrants) would require the possums present to be aggregated sufficiently and for aggregations to persist over time. Analysis of the chewcard data indicated that some clusters were of a size that might enable TB to persist (Figure 15). However, even if there are infected possums present, there needs to be sufficient infected possums to generate a 'force of infection' for the disease to transfer to cattle. If only a quarter of infected possums sympatric with livestock pass on TB that is detectable by livestock testing, then for every new herd infection there needs to be 3–4 infected possums. In Karamea there might be some factor (e.g. large numbers of weka that scavenge dead possums and open them up for increased transmission of disease from possums to livestock) that influences the dynamics of this transmission process so the number of infected possums needed to infect a herd might be less than that derived from analysing herds nationwide. Nevertheless, even if every infected possum results in an infected herd, each newly infected herd must have at least 50 (if prevalence is 2%) uninfected possums within a home range of the herd. All the data suggest it is unlikely such numbers of possums (when taken as an average across the Karamea district) are associated with the infected farms.

The risk-modelling results suggest that TB infection in Karamea livestock was mostly influenced by wildlife factors, and that previous risk of infection in a herd was of secondary importance. Much of the variance in the number of infected animals (Y_{jt}) that was explained by *PrevRisk* in the uni-covariate model (model 9; Table 6) in which the parameter estimate for *dairy herd* was significant (i.e. did not overlap zero) could be attributed to exposure to forest (*ForestExpose08* and *Excl09*) in the multi-covariate model 1. *PrevRisk* made an important contribution to model 1, yet its parameter estimates for all herd types overlapped zero. This suggests that forest exposure presents ongoing risks for herds by causing repeated disease transmission events, but the statistical importance of *PrevRisk* indicates that there is likely within-herd persistence of infection. The negative *dairy herd* parameter estimate for *Excl09* indicates that ground control in the exclusion zones was effective at reducing the risk of infection from wildlife.

Wildlife factors seem to be the most important, but our measures were indirect and therefore we cannot confirm that the risk comes from possums. While the Proof of Freedom analysis

did not demonstrate high confidence that possums are free of TB, this could be because surveillance was insufficient and not because TB is definitely still in the population, despite the recent confirmed TB-possum presence.

A priori, we expected that once a herd became infected (with or without detection) it would have an increased risk of remaining infected due to imperfect surveillance techniques, or the presence of anergic or non-reactive infected animals. While surveillance can always be improved, our results did not indicate the current testing protocols were ineffective at indentifying infection and clearing herds. We did find evidence that previous herd infection was a risk factor and although not as strong as the risk posed by wildlife, should still be considered as important.

Applying the Proof of Freedom utility to the chewcard data obtained from 2010 and 2011 (given no evidence of TB in possums since 2006) showed that the median probabilities of disease eradication were 0.74 and 0.78 for 2010 and 2011, respectively. Further, the CIVs of 0.025 and 0.04 were well below the target 0.90. Given the subsequent control programme has identified at least two infected possums, the POF utility correctly indicated that possums were not free of TB (at a 0.95 level of acceptance).

Four lines of evidence (i.e. use of run-offs, exposure to forest, likely immigrant infected possums, and actual TB-possums present) support the case that wildlife (most likely possums) are the main cause of continuing infection in herds at Karamea.

If it is accepted that possums cause most of the observed infection, our estimates of possum population size, TB prevalence, and immigration rate over the last six years suggest the following:

1 It is unlikely that self-sustaining infection in resident possums is the cause, leaving immigrants as the only likely possum option. The distribution of infection in livestock is widespread throughout Karamea, which would require infected possums at many locations (because there is no evidence that infectious possums range widely). For those all to be maintained by self-sustaining infection in resident possums would require numerous separate foci of continuous infection, and despite its moderate sensitivity the 2007–2011 surveys would have detected at least some of those.

2 Assuming immigrants are the cause, the highly non-random pattern of infection in cattle implies non-random dispersal and settlement of immigrants. Cowan (2001) showed that movements of translocated possums were not influenced by landscape features, although it is accepted that large rivers do influence movement.

3 However, the total number of possums, the maximum likely numbers of immigrants, and the low (<1%) prevalence observed, together suggest too few TB-infected immigrants are arriving to cause the numbers of infected cattle observed, especially if multiple possums are required to produce each new or ongoing outbreak event in cattle. Transmission to cattle may occur more readily at Karamea than elsewhere – although the one indication that that is the case (i.e. there should be on average more TB cases involved in each new outbreak on a previously clear farm) does not appear to occur. However, even if every TB-possum causes infection in cattle, the number of immigrants is still too low if the TB prevalence in immigrants is the same as that observed among on-farm possums.

4 Prevalence may be higher (much higher) in immigrants, but not detected because (1) TB-infected immigrants die within a few months of arrival, so are available to be sampled for only a fraction of the time of surviving TB-free immigrants; and (2) such recently-arrived immigrants comprise only a fraction of the population sampled (the bulk being TB-free residents or immigrants that arrived in previous years or survived in situ). This hypothesis appears unlikely, but high TB prevalence in possums of up to 60% has been recorded elsewhere on the West Coast. Such pulses of infected immigrants could be tested by surveying deep-forest possums and over an extended period of time (especially during the autumn peak of dispersal).

5 Alternatively, the number of TB-infected immigrants may be low, in line with model predictions, but because of a strongly non-random pattern of dispersal and settlement (driven by local geography and habitat), immigrants are much more likely to pass through and/or settle in the same location as previous residents, and are therefore more likely to encounter clusters of previously immigrant possums, control survivors and their descendants, to which they are able to transmit TB, causing a short-lived outbreak in TB in possums that soon dies out (as observed in Orongorongo Valley; Arthur et al. 2004). Such short-lived outbreaks could easily have been missed by the TB-possum surveillance conducted since 2006 (whereas – as noted above – long-lived foci of infections are likely to have been detected if they were numerous).

In summary, while considering that within-herd infection is still contributing to the situation at Karamea, we conclude that a wildlife source is the most likely cause of most infection in cattle at Karamea. We suggest that immigrant possums are most likely to be the ultimate wildlife source, but only if (1) possum behaviour at Karamea results in a greater risk to cattle than is the national norm, (2) possum dispersal from deep forest and settlement on farmland is strongly non-random, and (3) either TB prevalence in recent immigrants is much higher than in residents or TB transmission between possums on Karamea farmland is higher than usual.

7 Conclusions

- The period prevalence of infected herds at Karamea was as high as 40% in the early 1990s, but even with ground-based on-farm control and aerial control of the adjacent forest over a number of years, the period prevalence has not been reduced below 20%.
- Parallel blood testing has been used, but it has not been as effective for resolving problem herds as in other areas of New Zealand.
- All case and control herds were essentially closed herds, therefore posing very low risk of introducing new infection from outside the area.
- Based on chewcard detection surveys in 2009 and 2010, possum abundance was low (i.e. less than 1% equivalent RTC), and therefore met the AHB operational requirements.
- Although average abundance of possums was low, those present were not distributed randomly and some sites may have had sufficient numbers of possums to enable TB to persist.
- The apparent rapid recovery of possum numbers between 2006 and 2007 (from numbers of possums killed in control operations) suggests immigration rates of

possums from the adjacent forest onto the farmland were very high, but since the 2008 aerial control of the forest, immigration is likely to be low (i.e. as indicated by the possum model).

- Karamea geography (long strip of farmland sandwiched between the forest and coast) lends itself to be a sink (i.e. an area for migrating possums to settle in) for a large number of immigrant possums, and this appears likely to have played a significant role in maintaining TB prior to the 2008 aerial control operation.
- Prevalence of TB in possums is low (surveys up until 2011 suggested a prevalence of about 1%), although this estimate will be an underestimate because most possums were only examined for gross lessions. Recent surveillance using possums recovered during 2012 control operations has identified two confirmed infected possums (and possibly four) from a sample of 50.
- Although other wildlife species are present (e.g. rats, stoats, hedgehogs, seals, deer), there is nothing to suggest they play a greater role in TB persistence in herds at Karamea than the generally negligible role they appear to play elsewhere.
- The likely presence of non-specificity, recrudescence, and anergy will contribute to decreasing the sensitivity of the different testing protocols.
- Some farms (e.g. Meidema's) are likely to be exposed to a higher risk of immigrant infected possums than others more distant from aerial exclusion areas or from likely 'corridors' for dispersal.
- Examining each possible risk factor in a balance of probability approach suggests wildlife (i.e. possums) is the main cause of ongoing infection. Specifically:

    1 The testing and slaughter programme carried out in Karamea, if not different from elsewhere in NZ should eliminate most infection if it is primarily in-herd, but because this has not happened then it indicates continuing wildlife infection.

    2 Because run-off blocks were the only factor identified as a risk factor from the survey of case/control herds indicates herd proximity to forest (and therefore presumably possums) is critical.

    3 The risk modelling identified proximity to forest edge as a significant risk factor (and therefore possums).

    4 The geography of the Karamea (i.e. a narrow strip of farmland between forest and sea) lends itself to be a sink for immigrant possums but one in which they will accumulate more rapidly than elsewhere because continual spread west is prevented by the sea

    5 Even with a 5-km control buffer, the possum model suggested there could still be at least 3-4 infected possums immigrating onto the farmland annually.

    6 At least two infected possums were recovered in 2012.

- However, although the weight of evidence implicates possums several factors also indicate that we do not fully understand the dynamics of the disease in this area. This includes:

1. The long-term persistence of infection on some farms, but not on their immediate neighbours, suggesting that either wildlife is not the main cause of infection or infected wildlife movement and settlement is not random.
2. Given a 2% prevalence of TB in possums and the potential number of infected possums needed for each new herd infection (i.e. 3.5), then there needs to be at least 150 possums sympatric with several farms for at least one of them to become newly infected. Given the apparent low abundance of possums, it seems unlikely that possums are driving infection in all herds.
3. The sensitivity of the range of herd testing protocols used at Karamea is relatively low (0.43–0.65) suggesting a high risk of allowing TB to persist in herds.

8 Recommendations

- Parallel testing should be used to increase test sensitivity on those farms where there is uncertainty regarding the relative importance of wildlife or in-herd infection.
- Current skin testing protocols should be evaluated to ensure skin test sensitivity is maximised, and staff should be trained in best practice.
- Use of run-offs should be viewed as a high risk factor, and strategic herd testing of stock that use run–offs should be implemented (i.e. consider a combination of pre-movement and timing of subsequent whole herd testing (90 – 120 days after animals return from a run-off).
- Contracted possum control should continue as planned, with all device locations recorded by GPS and possums collected for necropsy and culture. This will help identify any persistent 'hotspots' of TB in possums and enable their treatment with more focused control effort. Locations where TB possums are found should be immediately trapped to extinction, over about a radius of 500–1000 m, both to eliminate the focus and begin to characterise the absolute local possum densities at which TB is occurring.
- Research should be undertaken to better understand:
    - the influence that patchiness of possum distribution has on TB persistence even if average RTC levels are low
    - if possum abundance changes seasonally and increases significantly at expected times of seasonal dispersal (i.e. Feb.–April) by monitoring possum abundance monthly or bimonthly on two or three selected farms (e.g. Jones, Meidema)
    - the extent to which immigrant infected possums are contributing to the ongoing infection in livestock, by (1) measuring TB prevalence and possum abundance at the most likely source (behind the control buffer); (2) over 2 years, using DNA genotyping of possums, surveyed during control, to determine the likely rate of immigration.
- A farmer self-help programme should be developed that aims to reduce abundance of possums on their farms by establishing permanent bait-stations that are rat and weka proof (i.e. Weka-proof Sentry bait-stations). This approach is to ensure any infected possums (immigrant or resident) have the minimum time to interact with livestock.

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Appendix 1 – Questionnaire used to interview farmers on farm and herd management

Karamea Project 2010

TB has been present in wildlife and livestock in the Karamea for decades. The disease has persisted in the area despite control efforts and varying intensity of surveillance testing of livestock (test and slaughter programme). A project is underway to better understand the reasons for persistence of this disease.

It is likely to be that the persistence of infection is a combination of infection from interactions between infected wildlife and undetected infection within herds which can continue to cycle within the herd.

A map of farm to be taken out to interview: Show – sheds used for stock, boundaries, fenced off bush, calf shed & grazing, cattle yards, feed pads, dairy shed (where applicable), riparian areas, location of offal pit, possum sightings (if any), deer sightings.

HOME FARM

Herd composition:

	Predominant stock type	Numbers by stock type present
Beef (purebred) / Beef cross		
Beef (dairy) (dairy-beef cross)		
Dairy herd		
Dairy grazing		

Herd makeup:

Sex	>2 years (breeding)	>2 years (fattening)	R2	R1
Female				
Male				

Detailed demographic (age breakdown of current herd, if possible):

Age (yrs)	3	4	5	6	7	8	9	10+
Number								
The oldest cow in the herd is								years old
Where are culls routinely sent?								

Approximately how many culls in a year?				
Are stock regularly bought / brought in?			**Yes**	**No**
If Yes, from where?				
Karamea	**West Coast**	**Canterbury**	**North Island**	**Other (detail below)**
Other:				
Have stock been bought in during last 18 months?			**Yes**	**No**
Are ASDs available for these stock?			**Yes**	**No**
Details:				

GRAZING MANAGEMENT:

Are cattle grazed along the bush-pasture margin (BPM) at night?	**Yes**	**No**
If Yes, then:		
Are all patches of bush only fenced off?	**Yes**	**No**
Is the bush edge only fenced off?	**Yes**	**No**
Do cattle have access to graze along BPM at any time?	**Yes**	**No**

If yes, how often would this happen?

Rarely / occasionally	**Commonly / weekly**	**Frequently / daily**

When mustering for procedures such as drenching, Tb testing, etc., how complete are the musters of cattle (give percentage)	%

Stock water		
Water troughs only	**Natural waterways only**	**Both**

Outer boundary fence type:							
5 wire	**7 wire**	**Deer fenced**	**Netting**	**Hot wire/tape**	**Other**	**Permanent**	**Temporary**
Condition of fences (outer boundary)?							
Excellent			**Average**			**Needs work**	
Comments (outer boundary fences):							

Is there an Offal pit?	**Yes**	**No**
If Yes, is it:	**Open**	**Closed**
Where is the offal pit located? (show on map)		
Co-ordinates (NZ Map Grid / Transverse Mercator):	Easting (x)	Northing (y)

FARM DEVELOPMENT STAGE (refers to bushed areas):

1	Actively developing (cutting bush to make more arable land)	**Yes**	**No**
2	Plans to develop further	**Yes**	**No**
	If Yes, when?		
3	No further development planned.	**Yes**	**No**
4	Are cleared areas grazed during development?	**Yes**	**No**
	If Yes, by what?		

FARM MANAGEMENT PRACTICES:

Stock feed:

Does the farmer make own:	**Silage**	**Bailage**	**Hay**	**Straw**
Does the farmer grow winter crops:	**Yes**		**No**	
If Yes, what type(s):				
Further details:				

Shed type (Dairy):

Herringbone	**Rotary –(heads out)**	**Rotary (heads in)**	**Walk through**

Are supplements fed?:

During season?	**Yes**	**No**
If Yes, type(s):		
During dry period?	**Yes**	**No**
If Yes, type(s):		
Facility for feeding supplements in shed?	**Yes**	**No**
Description:		

When are supplements fed? And what supplements? (circle month(s) and write in cells below)												
When	**JAN**	**FEB**	**MAR**	**APR**	**MAY**	**JUN**	**JUL**	**AUG**	**SEP**	**OCT**	**NOV**	**DEC**
What												

Milking arrangements:

Milking herd size:			(for this current season)
Are the yards big enough to hold the entire herd at once?		**Yes**	**No**
How long does milking take?		Hours (at peak production)	
Predominant milking pattern?			
Once a day	**Twice a day**	**16 hours**	**Other**
If Other, give details:			
If a combination, give details:			

Production (optional):

Milk solids last season year	Kg	
Number of cows milked last season	Head	
Dry off date last year		
Size of milking platform	Ha	
Was last year an average year?	**Yes**	**No**

Carry-overs (Dairy):

Are 'Carry-overs' routinely kept?	**Yes**	**No**
Were animals 'carried over' this last year?	**Yes**	**No**
Where are 'carryovers' kept / run?		

Calf shed (Dairy/rearing):

Location of calf shed				
Proximity to milking sheds				Metres
Proximity to bush pasture margin				Approximate metres
How long do calves spend in the shed?				
The decision on removal is based on:				
Weight	**Age**	**Management**	**Numbers**	**Other**
If Other, give details:				
Calf feeding method:				
Calfeteria	**Bucket**		**Open troughs**	
Is calf meal fed?			**Yes**	**No**
Describe calf shed construction (e.g. pole shed, old piggery, purpose built, etc.):				
When calves move out of shed where are they grazed?				
Alongside or near shed:			**Yes**	**No**
Or moved off property immediately:			**Yes**	**No**
If moved off property immediately, to where?				
Or elsewhere than above options:			**Yes**	**No**
If Elsewhere, to where?				
Calves grazed with bush interface			**Yes**	**No**

Same place every year	**Yes**	**No**
If the same place, describe:		

RUN-OFFS:

Are run-offs used?			**Yes**	**No**
If Yes, give details:				
Is it a separate block from the home farm (i.e. not adjacent)			**Yes**	**No**
Is it under a separate herd number?			**Yes**	**No**
If Yes, what is the herd number?				
Is the run-off under day-to-day control of:		**Farmer**	**Separate manager**	
If Separate manager, give details:				
What are the run-off(s) used for?				
Stock classes	**Calves**	**Heifers**	**Dry Cows**	**Bulls**
Management	**Platform grazing**	**Winter grazing**	**Seasonal grazing**	
Is the use the same each year?			**Yes**	**No**
If No, give details:				
For winter grazing of milking herds, indicate where the grazing occurs:				
Home farm	**Run-off**	**Commercial grazing - Canterbury**	**Commercial grazing – West Coast**	
Give details for grazing blocks and run-offs used for winter grazing:				

How are stock moved to run offs?:

Trucking firm	Own truck	Walk using roads	Other
If Other, give details:			

Run-off management practices:

Are cattle roadside grazed?	**Yes**	**No**

Are cattle grazed along BPM at night?	**Yes**	**No**
If Yes, then:		
Are all patches of internal bush only fenced off?	**Yes**	**No**
Is the bush edge only fenced off?	**Yes**	**No**

Do cattle have access to graze along bush pasture margin at any time?	**Yes**	**No**
If yes, how often would this happen?		

Rarely / occasionally	**Commonly / weekly**	**Frequently / daily**

Fencing:

Run-off fencing:	**Adequate back fence**	**Geographic boundary (e.g. river, cliff)**					
Is boundary bush fenced off?	**All**	**Some**	**None**				
Outer boundary fence type (of run-off):							
5 wire	**7 wire**	**Deer fenced**	**Netting**	**Hot wire/tape**	**Other**	**Permanent**	**Temporary**
Condition of fences (outer boundary)?							
Excellent	**Average**	**Needs work**					
Comments (outer boundary fences):							

Stock water		
Water troughs only	**Natural waterways only**	**Both**

Run-off development stage (refers to bushed areas):

1	Actively developing (cutting bush to make more arable land)	**Yes**	**No**
2	Plans to develop further	**Yes**	**No**
	If Yes, when?		
3	No further development planned.	**Yes**	**No**

4	Are cleared areas grazed during development?	**Yes**	**No**
	If Yes, by what?		

Stock feed:

Does the farmer make own:	**Silage**	**Bailage**	**Hay**	**Straw**
Does the farmer grow winter crops:	**Yes**		**No**	
If Yes, what type(s):				
Further details:				

PEST CONTROL

Does the farmer:	Home farm		Run-off	
Carry out own possum control?	**Yes**	**No**	**Yes**	**No**
Allow hunters on farm?	**Yes**	**No**	**Yes**	**No**
If Yes, for what species?				
If Yes, When?				
Employ private contractors?	**Yes**	**No**	**Yes**	**No**
If Yes, for what species?				
If Yes, When?				

Pest control (other than official programmes), if carried out:

Frequency of pest control:				
Weekly	**Monthly**	**Annually**	**Occasionally**	**Never**
Method(s) of control used:				
Shooting	**Trapping**	**Poisoning**	**Other**	
If Other, give details:				
Species that control is targeting:				
Possums	**Rats**	**Deer**	**Stoats**	**Pigs**	**Other**
If Other, give details:					

Details of captures / kills:					
Species:	**Possums**	**Stoats**	**Wild deer**	**Pigs**	**Wild cattle**
Interval:					
Wildlife seen (farmer's assessment of abundance):					
Possums	**Stoats**	**Wild deer**	**Pigs**	**Wild cattle**	**Other**
[The above to be a measure of population size & absolute number (rate as Low / Medium / High)]					
If Other, give details:					
When was the last feral animal seen?					
Possums	**Stoats**	**Wild deer**	**Pigs**	**Wild cattle**	**Other**

Pest control – official programme assessment:

Farmer's opinion of overall official operational work (includes everything):				
Poor	**Fair**	**Average**	**Good**	**Excellent**
Farmer's opinion of contractor effort (just the perceived amount of effort):				
Poor	**Fair**	**Average**	**Good**	**Excellent**
Farmer's opinion on frequency of official pest control work:				
Insufficient		**Ideal**		**Excessive**

FARMER'S GENERAL COMMENTS:

Appendix 2 – Detection sites 2009–2011

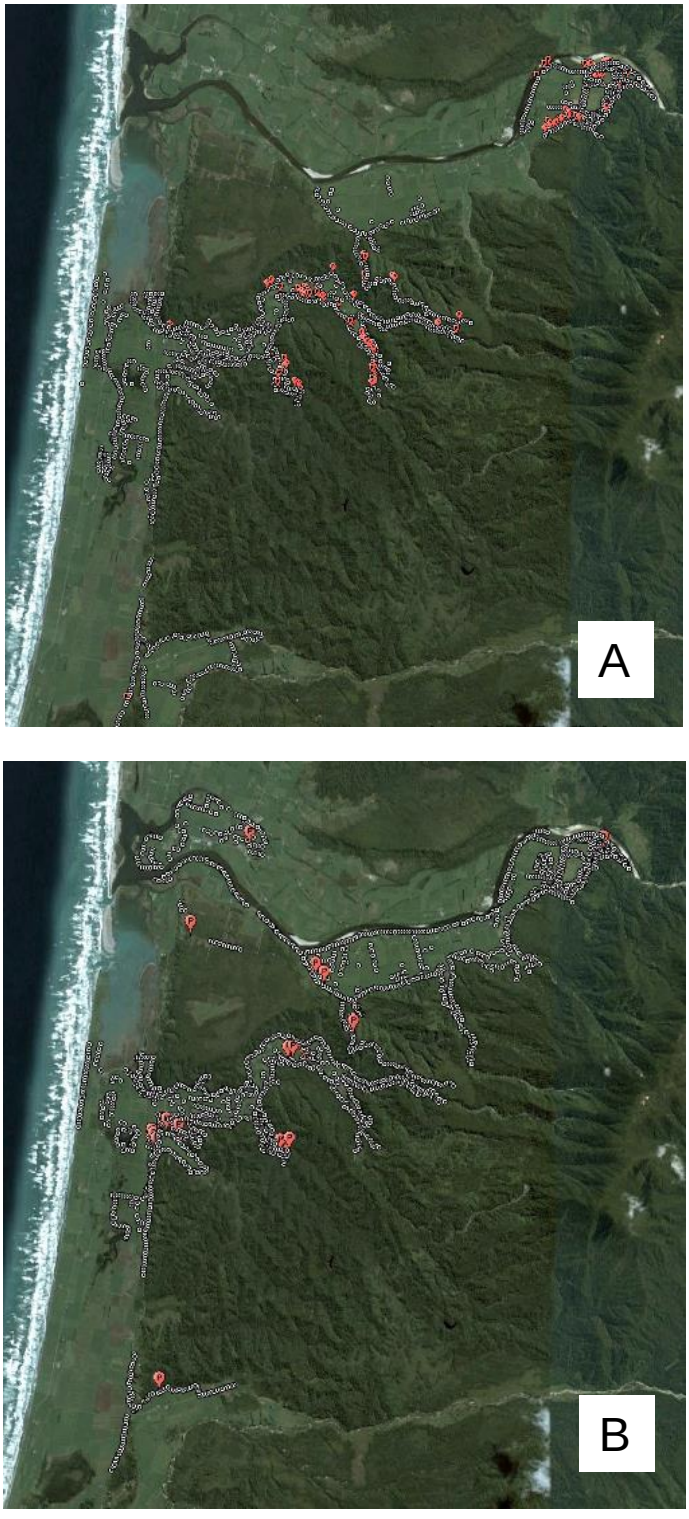


Figure 17 Detection sites (white dots) and positive detections (red balloons) from:
(A) 2009 pre-Epro control; (B) 2010 post-Epro control.

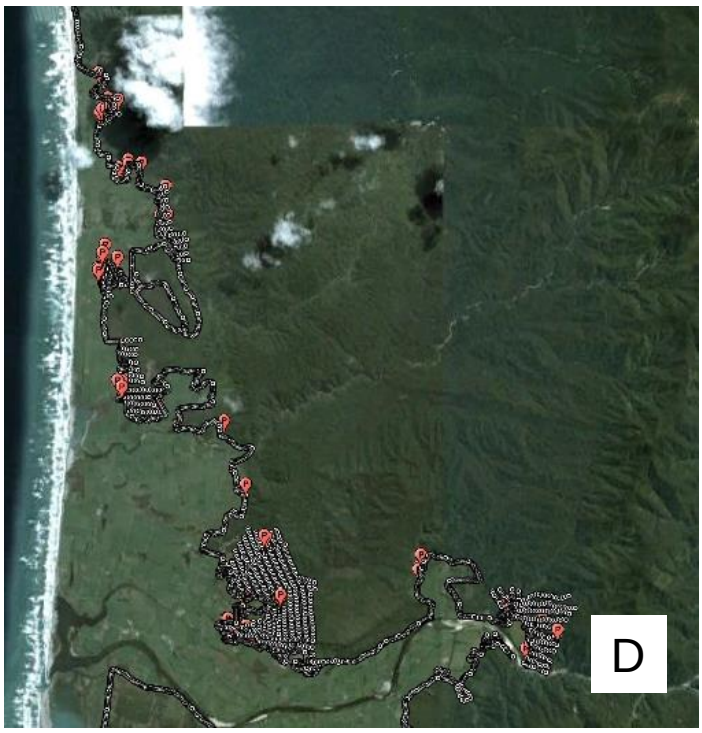


Figure 17 (cont.) Detection sites (white dots) and positive detections (red balloons) from: (C) 2010 June north of Karamea River; (D) 2011 Karamea North.

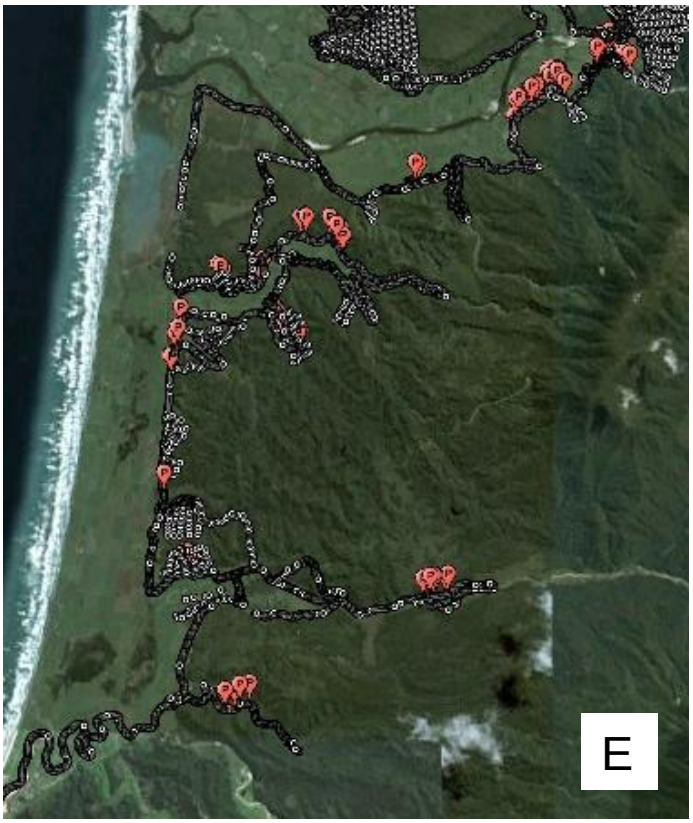


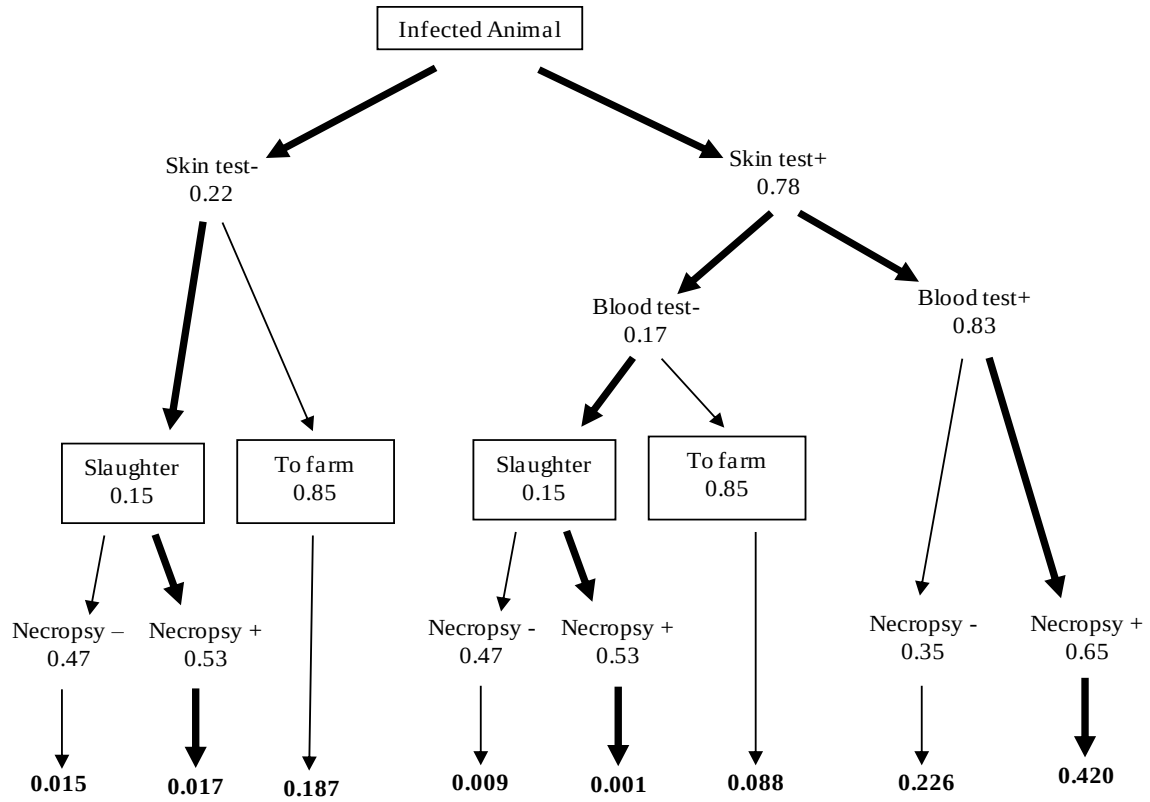
Figure 17 (cont.) Detection sites (white dots) and positive detections (red balloons) from: (E) 2011 Karamea South.

Appendix 3 – Herd-testing protocols

Branch probabilities for calculating the animal-level sensitivity, or the probability of detecting TB in an animal in the Karamea district, given that it is infected, are shown below. There are a seven testing protocols. The closed boxes represent groupings of animals and the probability that an individual animal along the associated branch will fall into that group. Each probability branching for each protocol starts with a single infected animal (*P(Infected)* = 1). The bold arrows indicate the pathways by which TB could be detected in an infected animal. The testing sensitivity is simply the sum of all the branches that result in a positive detection. The sum of all branches (detections and missed detections) equals 1.

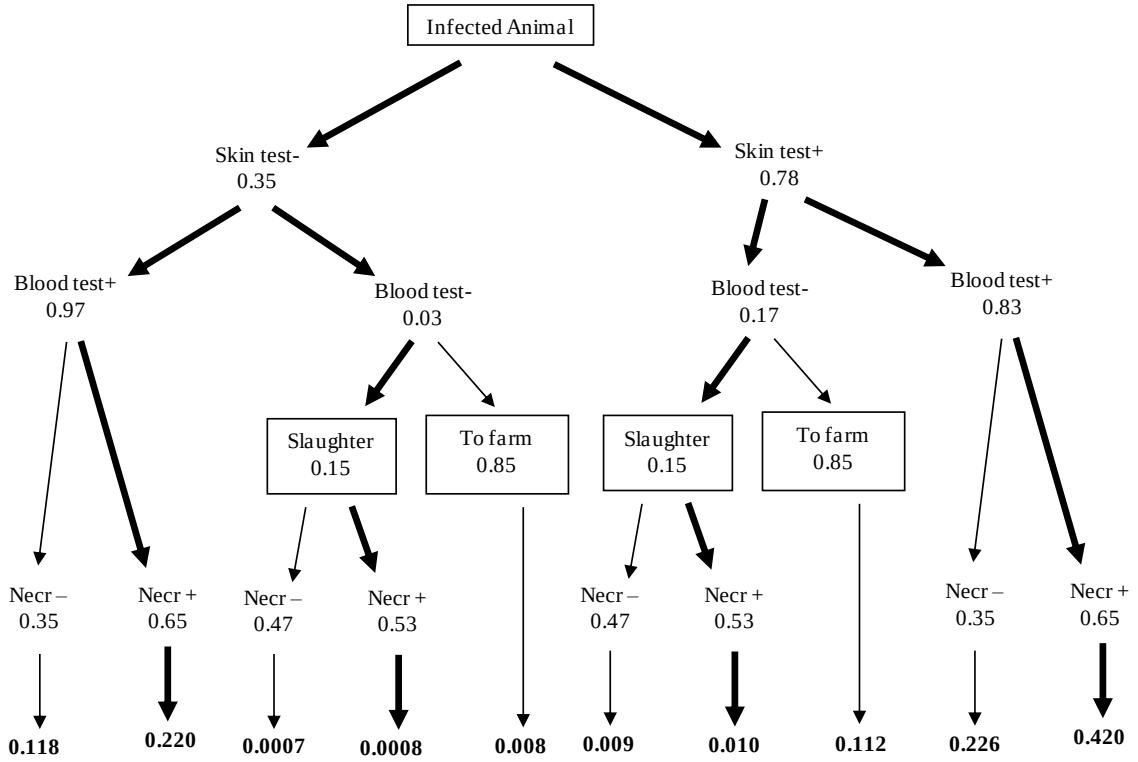
Sensitivities for each step of the diagnostic process were estimated from published data and expert opinion. The sensitivity of the subjective caudal-fold test (skin test) varies greatly in published papers. Pharo and Livingstone (1997) reported the expected range of sensitivities for the caudal-fold tuberculin test, gamma interferon blood test (g-IFN; Bovigam™) and slaughter premise post-mortem examination are 75–85%, 82–94% and 50–80% respectively. To better reflect the performance of tests carried out in field conditions, values were selected at the lower end of the ranges for the caudal-fold test, g-IFN blood test and necropsy.

Dairy testing of clear herd: Protocol 1



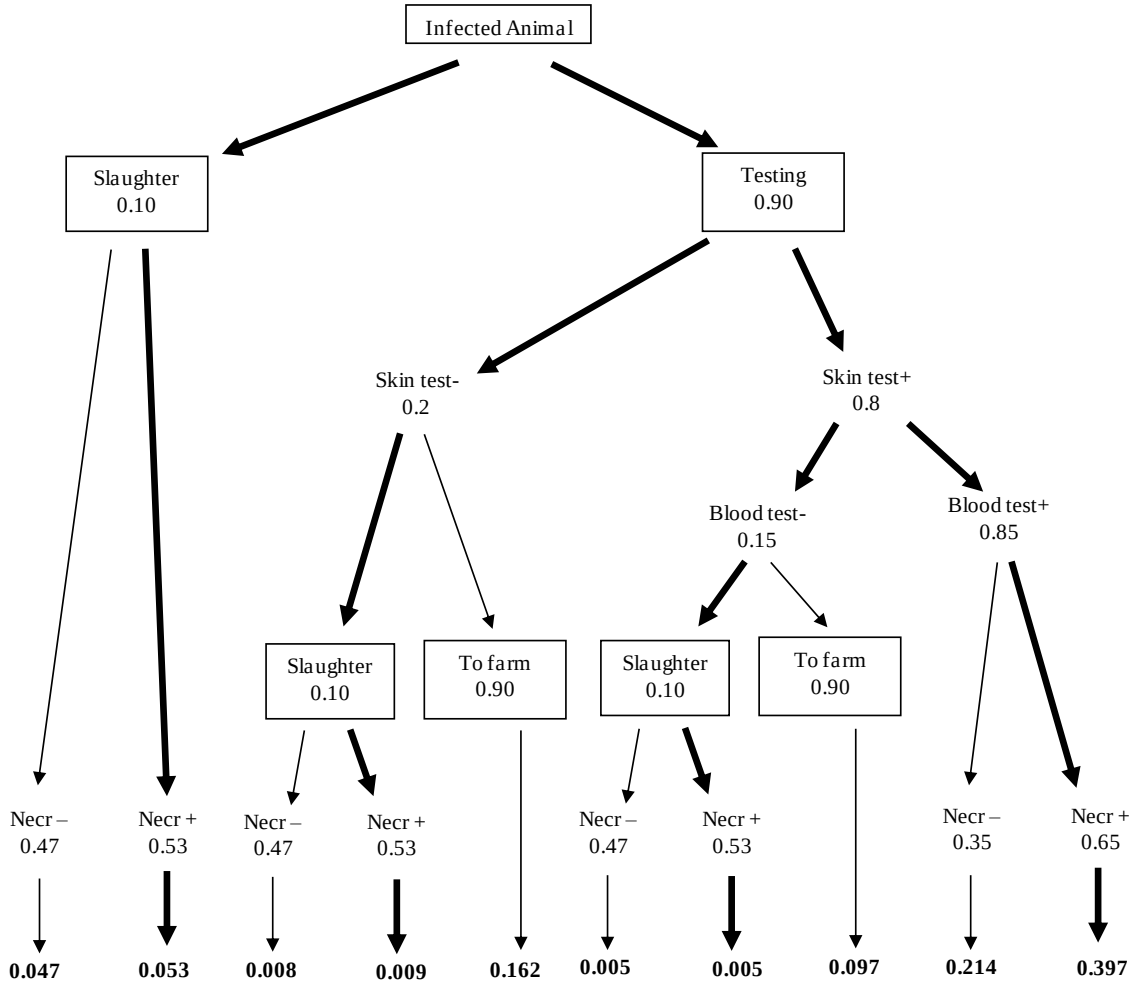
Total Sensitivity = 0.438

Dairy testing of infected herd: Protocol 2



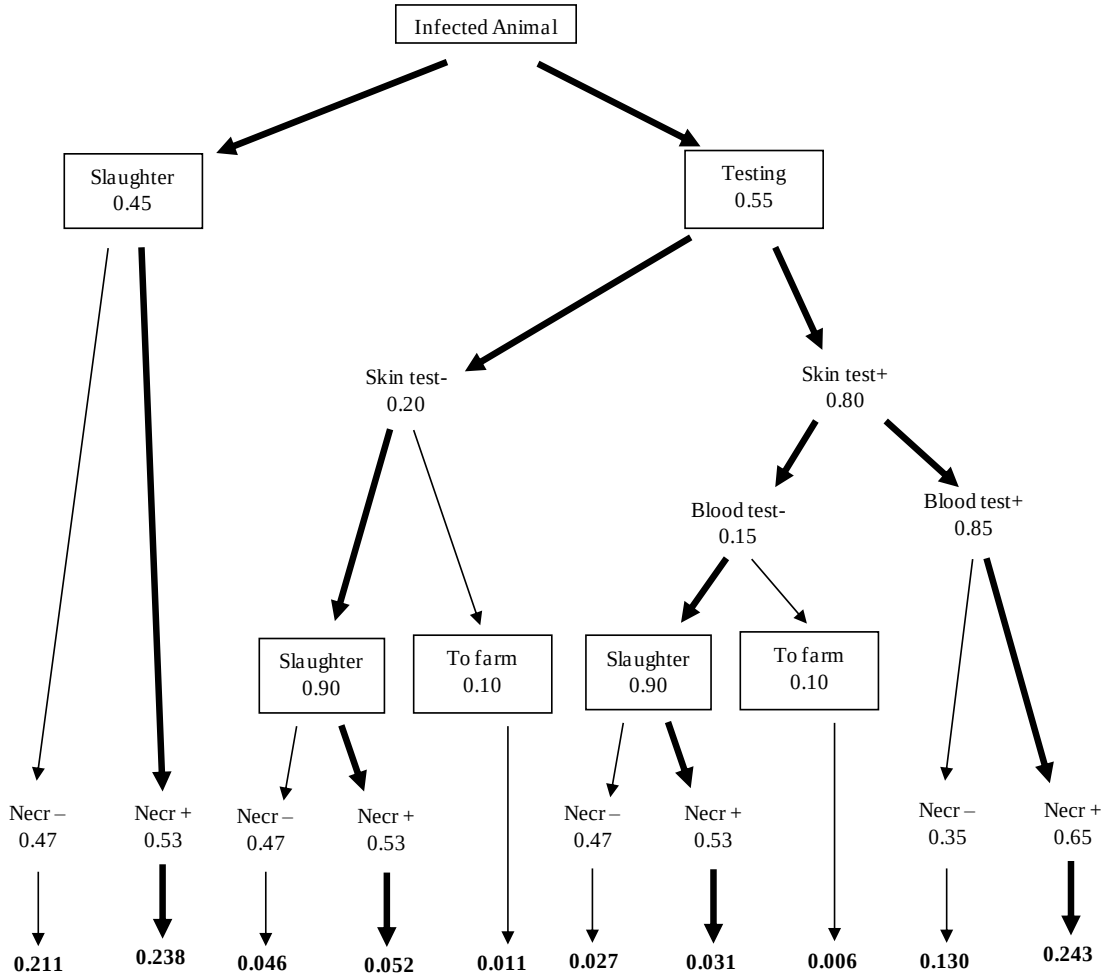
Total Sensitivity = 0.650

Beef breeding testing: Protocol 3



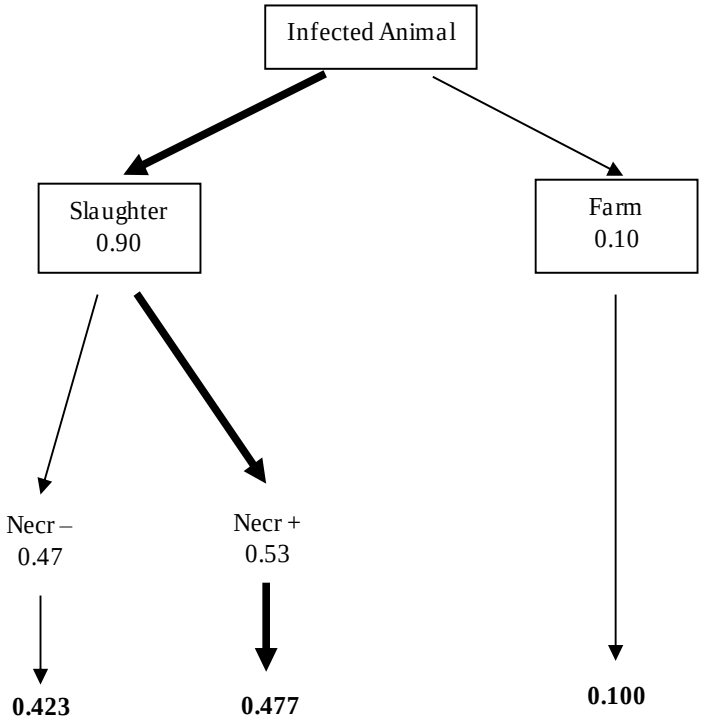
Total Sensitivity = 0.464

Beef Dry testing: Protocol 4



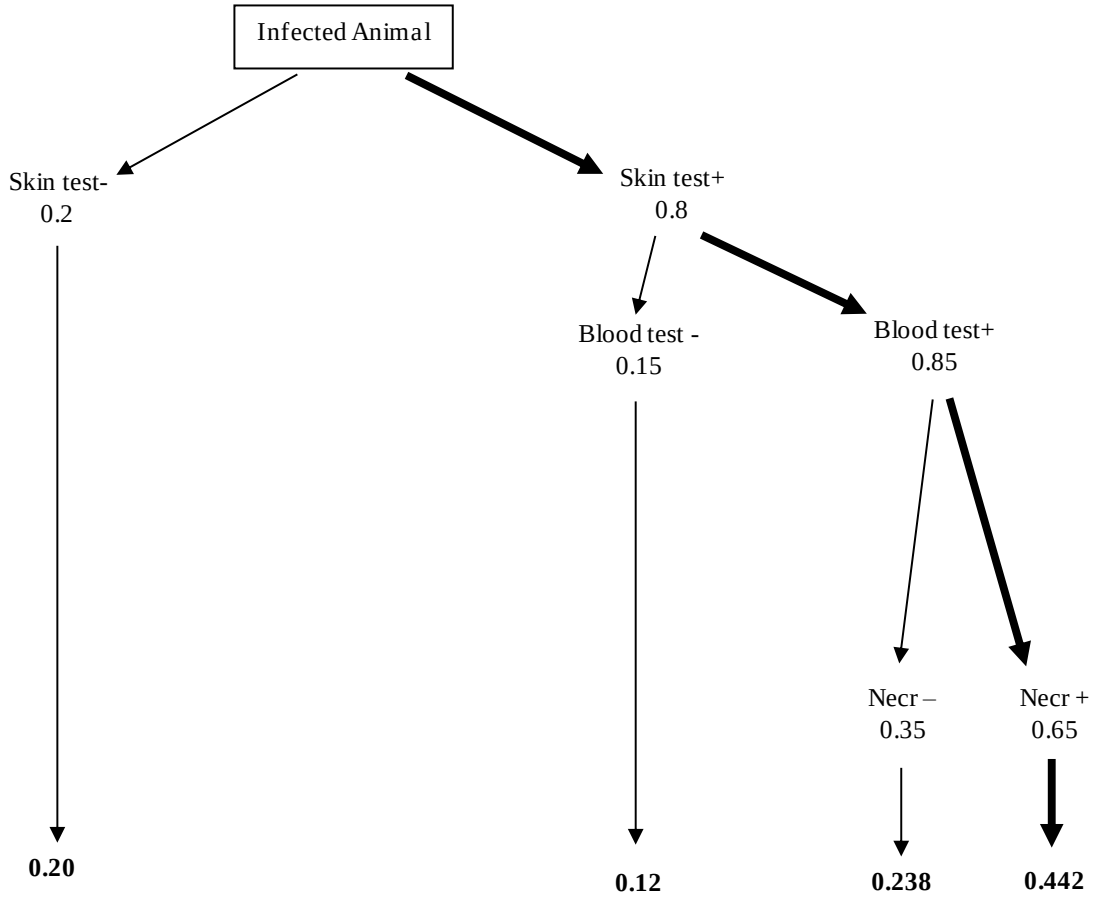
Total Sensitivity = 0564

Beef Dry work surveillance: Protocol 5



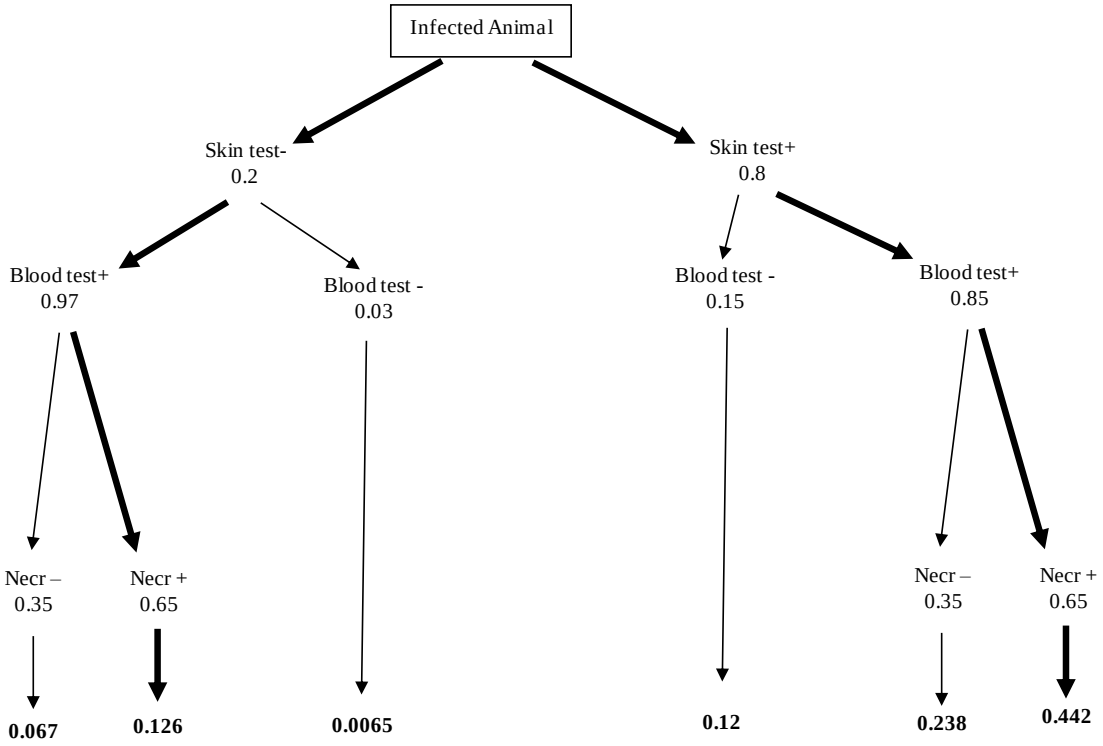
Total Sensitivity = 0.477

Movement testing 1: Protocol 6



Total Sensitivity = 0.442

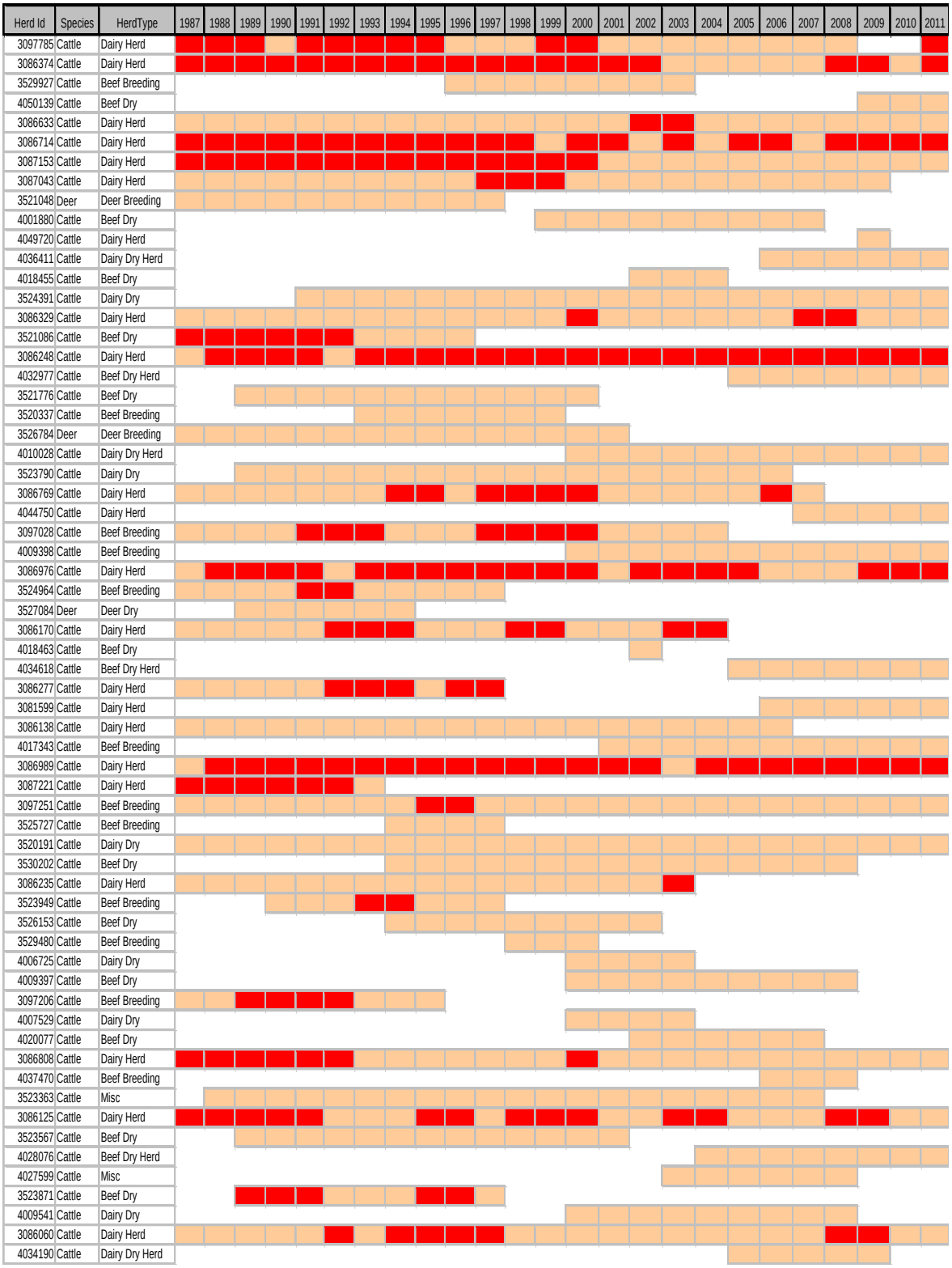
Movement testing 2: Protocol 7



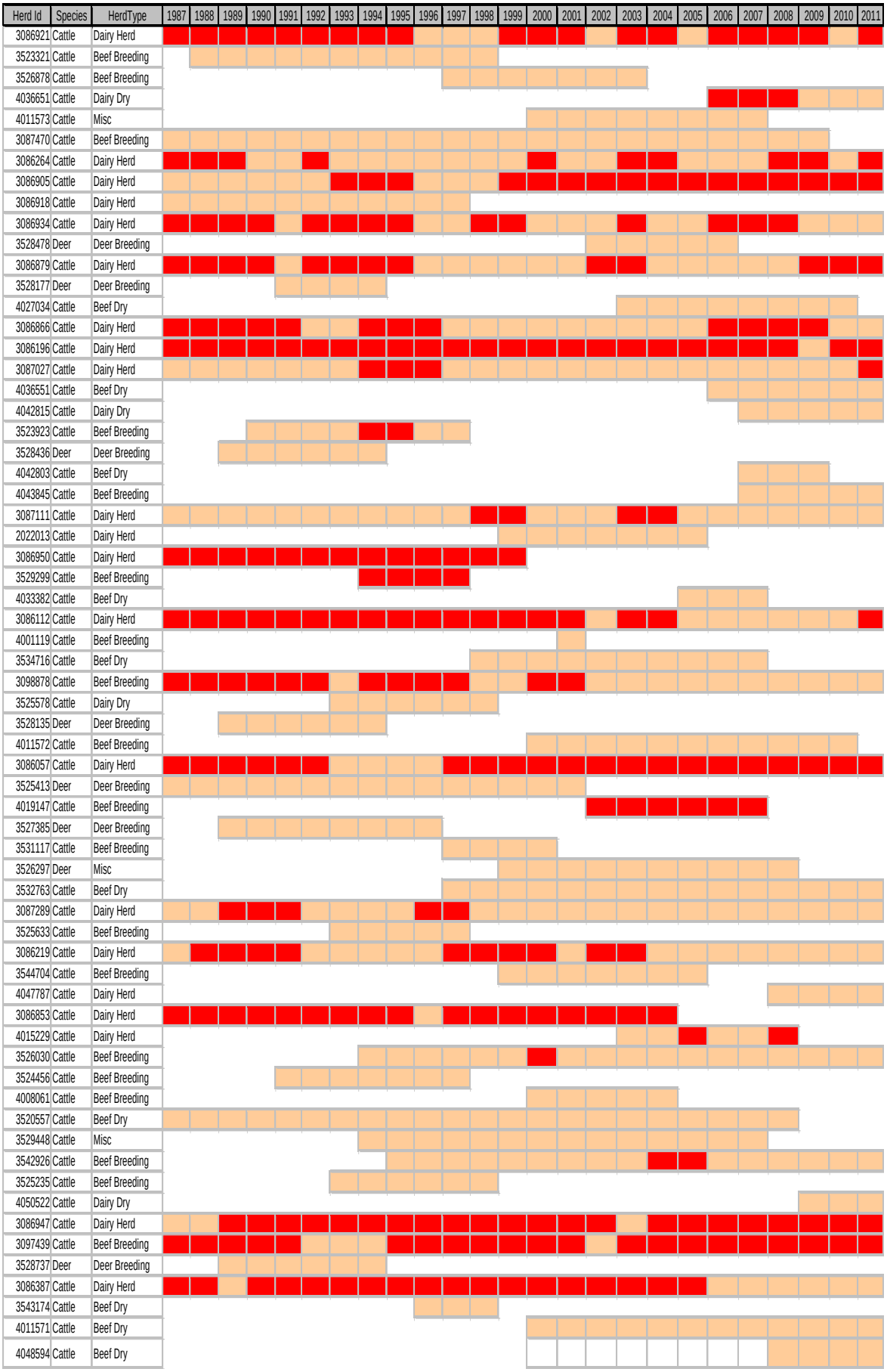
Total Sensitivity = 0.568

Appendix 4 – Herd infection status

Table 11 Years in which herds have had infected herd status (red), clear status (pink) or herd inactive/disbanded (blank). Rows are arranged in geographic order from north to south



Herd Id	Species	HerdType	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011
3097785	Cattle	Dairy Herd																									
3086374	Cattle	Dairy Herd																									
3529927	Cattle	Beef Breeding																									
4050139	Cattle	Beef Dry																									
3086633	Cattle	Dairy Herd																									
3086714	Cattle	Dairy Herd																									
3087153	Cattle	Dairy Herd																									
3087043	Cattle	Dairy Herd																									
3521048	Deer	Deer Breeding																									
4001880	Cattle	Beef Dry																									
4049720	Cattle	Dairy Herd																									
4036411	Cattle	Dairy Dry Herd																									
4018455	Cattle	Beef Dry																									
3524391	Cattle	Dairy Dry																									
3086329	Cattle	Dairy Herd																									
3521086	Cattle	Beef Dry																									
3086248	Cattle	Dairy Herd																									
4032977	Cattle	Beef Dry Herd																									
3521776	Cattle	Beef Dry																									
3520337	Cattle	Beef Breeding																									
3526784	Deer	Deer Breeding																									
4010028	Cattle	Dairy Dry Herd																									
3523790	Cattle	Dairy Dry																									
3086769	Cattle	Dairy Herd																									
4044750	Cattle	Dairy Herd																									
3097028	Cattle	Beef Breeding																									
4009398	Cattle	Beef Breeding																									
3086976	Cattle	Dairy Herd																									
3524964	Cattle	Beef Breeding																									
3527084	Deer	Deer Dry																									
3086170	Cattle	Dairy Herd																									
4018463	Cattle	Beef Dry																									
4034618	Cattle	Beef Dry Herd																									
3086277	Cattle	Dairy Herd																									
3081599	Cattle	Dairy Herd																									
3086138	Cattle	Dairy Herd																									
4017343	Cattle	Beef Breeding																									
3086989	Cattle	Dairy Herd																									
3087221	Cattle	Dairy Herd																									
3097251	Cattle	Beef Breeding																									
3525727	Cattle	Beef Breeding																									
3520191	Cattle	Dairy Dry																									
3530202	Cattle	Beef Dry																									
3086235	Cattle	Dairy Herd																									
3523949	Cattle	Beef Breeding																									
3526153	Cattle	Beef Dry																									
3529480	Cattle	Beef Breeding																									
4006725	Cattle	Dairy Dry																									
4009397	Cattle	Beef Dry																									
3097206	Cattle	Beef Breeding																									
4007529	Cattle	Dairy Dry																									
4020077	Cattle	Beef Dry																									
3086808	Cattle	Dairy Herd																									
4037470	Cattle	Beef Breeding																									
3523363	Cattle	Misc																									
3086125	Cattle	Dairy Herd																									
3523567	Cattle	Beef Dry																									
4028076	Cattle	Beef Dry Herd																									
4027599	Cattle	Misc																									
3523871	Cattle	Beef Dry																									
4009541	Cattle	Dairy Dry																									
3086060	Cattle	Dairy Herd																									
4034190	Cattle	Dairy Dry Herd																									


Herd Id
Species
HerdType
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
1997
1998
1999
2000
2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
3086921 Cattle Dairy Herd
3523321 Cattle Beef Breeding
3526878 Cattle Beef Breeding
4036651 Cattle Dairy Dry
4011573 Cattle Misc
3087470 Cattle Beef Breeding
3086264 Cattle Dairy Herd
3086905 Cattle Dairy Herd
3086918 Cattle Dairy Herd
3086934 Cattle Dairy Herd
3528478 Deer Deer Breeding
3086879 Cattle Dairy Herd
3528177 Deer Deer Breeding
4027034 Cattle Beef Dry
3086866 Cattle Dairy Herd
3086196 Cattle Dairy Herd
3087027 Cattle Dairy Herd
4036551 Cattle Beef Dry
4042815 Cattle Dairy Dry
3523923 Cattle Beef Breeding
3528436 Deer Deer Breeding
4042803 Cattle Beef Dry
4043845 Cattle Beef Breeding
3087111 Cattle Dairy Herd
2022013 Cattle Dairy Herd
3086950 Cattle Dairy Herd
3529299 Cattle Beef Breeding
4033382 Cattle Beef Dry
3086112 Cattle Dairy Herd
4001119 Cattle Beef Breeding
3534716 Cattle Beef Dry
3098878 Cattle Beef Breeding
3525578 Cattle Dairy Dry
3528135 Deer Deer Breeding
4011572 Cattle Beef Breeding
3086057 Cattle Dairy Herd
3525413 Deer Deer Breeding
4019147 Cattle Beef Breeding
3527385 Deer Deer Breeding
3531117 Cattle Beef Breeding
3526297 Deer Misc
3532763 Cattle Beef Dry
3087289 Cattle Dairy Herd
3525633 Cattle Beef Breeding
3086219 Cattle Dairy Herd
3544704 Cattle Beef Breeding
4047787 Cattle Dairy Herd
3086853 Cattle Dairy Herd
4015229 Cattle Dairy Herd
3526030 Cattle Beef Breeding
3524456 Cattle Beef Breeding
4008061 Cattle Beef Breeding
3520557 Cattle Beef Dry
3529448 Cattle Misc
3542926 Cattle Beef Breeding
3525235 Cattle Beef Breeding
4050522 Cattle Dairy Dry
3086947 Cattle Dairy Herd
3097439 Cattle Beef Breeding
3528737 Deer Deer Breeding
3086387 Cattle Dairy Herd
3543174 Cattle Beef Dry
4011571 Cattle Beef Dry
4048594 Cattle Beef Dry

Appendix 5 – Details from farmer surveys: case-study and control herds

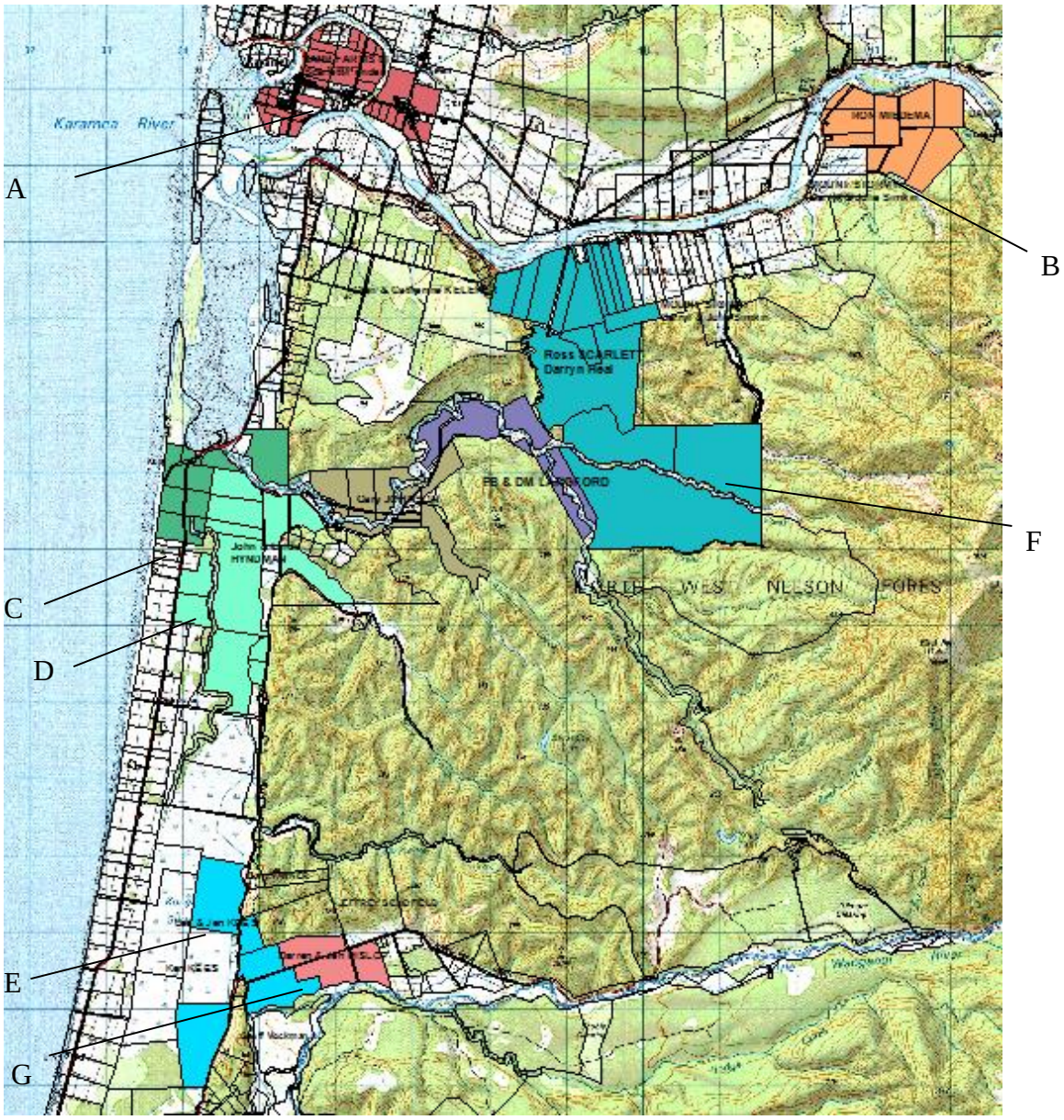


Figure 18: Original case-study herds: A = Scarlett/Pender; B = Miedema; C = Jones; D = Hyndman; E = Kees; F = Scarlett/Heal; G = Hislop (ex Dorman).

CASE-STUDY HERDS

1. Scarlett/Heal – 3086905 (F on map)

This dairy herd has the highest Infected status index of any herd on the West Coast at present (I13).

Size and location: The herd of approximately 520 animals and is the first farm encountered when entering the Arapito Valley on the true left bank (south side) of the Karamea River. The herd is closed (i.e. they do not routinely buy in or sell stock to other farmers). A herd of Jersey heifers were purchased from a C10 herd in the north Island in 2007 as numbers had to be made up following a poor breeding season.

The herd had movement control restrictions from 1993 to 1995, and then from 1999 onwards. The herd had a large number of skin-test-positive animals identified in the early 2000s. In November 2000, 45 skin-test-positives were found. From available records it appears that three were slaughtered without ancillary testing and were found to have lesions. The balance of the skin-test-positives appear to have been ancillary blood tested using the Bovigam™ test and 10 were positive (6 of these were found to have lesions at slaughter). A combination of blood testing and necropsies revealed 14 TB-infected animals. There were 52 skin-test-positives at the subsequent whole-herd test. Again a combination of blood testing and slaughter was carried out and 23 animals were found to have tuberculous lesions. While this whole-herd test was being completed, a TB-infected cull animal was found at routine slaughter through the slaughter premises.

A parallel test was carried out and it appears 4 out of 6 'risk'[2] animals had TB lesions. Regular TB testing continued and the number of animals reacting to the skin test was reduced by approximately two-thirds at the next whole-herd test. In December 2001, 16 out of 19 skin-test-positives were considered to have TB. Another parallel test was carried out and 1 out of 4 'risk' animals had lesions. Parallel tests in 2002 identified 18 further risk animals of which 7 had lesions. A clear test was achieved in late 2002 but a TB cull was identified in early 2003. Six risk animals found at a parallel test in 2003 were found to have no visible lesions at slaughter.

Testing continued at approximately 6-month intervals with the identification of skin-test-positives at virtually every whole-herd test (between 2 and 12). Small numbers of TB cases were also regularly found.

In 2008, another parallel test identified 4 risk animals that all had TB lesions. The farm manager advised, after this parallel test had been completed, that she had seen the cows earlier in the year investigating a 'dopey' live possum in a paddock when getting them in for afternoon milking.

Only three cases of TB have been found in the herd since then. These include a single R2 heifer that had grazed on the herd's run-off block (Kimberley), which is located within the bush at the end of Granite Creek Road. The farmer cut a narrow track through the bush to this

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[2] Parallel Bovigam test interpretation classifies high and medium risk animals.

block. The run-off block is predominantly used for young stock, but a proportion of the herd is often wintered there. This was the first TB case in an R2 heifer that could be identified in the available data. Another parallel test of the cows and heifers was completed in 2010 and this identified four risk animals of which one cow had a TB lesion of the mediastinal node.

The farm has two 'run-offs'; the one at Kimberley described and another at the Karamea River bridge that is used for dry stock.

Bush/scrub at the back of the farm has been progressively cleared and pasture developed during the 2000s.

Further parallel testing of the whole herd is planned to be undertaken before the herd is awarded a clear status.

From the data available for this herd, there is no evidence that animals previously cleared on ancillary blood tests have subsequently been found to have TB lesions. There is no evidence of the same animal being ancillary-blood-tested more than once. As unique lifetime animal identification has not been recorded, it is possible that the few TB cull animals that have been found may have reacted to tests before.

This herd has clearly shown evidence of persistent 'in-herd' infection and cow-to-cow spread as is seen in other areas. The difference with this herd is the temporal persistence of the infection and the constant 'dribble' of TB cases.

A herd in another area of the country with a similar degree of infection would have achieved a clear status more quickly. The average interval from issuing of Movement Restriction to revocation for herds in New Zealand is 315 days (5% percentile, 205 days, 95% percentile, 803 days) in herds infected between 1 July 2006 and 1 November 2010 (Kara Dawson, unpublished). Calculations based on West Coast data (John Edington, unpublished) for the same period show an average interval from issue to revocation of restrictions of 406 days for all herd types. The median interval for 'herds by type' is shown in the Table 12.

Table 12 Median interval between issuing and revocation of restrictions for West Coast herds

Herd type	Median interval from issue to revocation of restricted place notices (in days)	Source of data
All West Coast Herds	406	John Edington
West Coast Dairy Herds	433	John Edington
West Coast Beef Breeding Herds	407	John Edington
West Coast Dairy Dry Herds	289	John Edington
West Coast Beef Dry Herds	280	John Edington
All herd types in NZ	312	Kara Dawson

Subsequent TB cases are not unexpected from a herd with the same initial disease prevalence, but the number of cases and the period over which they have been seen is not typical when compared to similar herds in other areas.

Few of the cows present at the 'explosive' breakdown in 2001 are still in the herd at present.

Reactor Rate[3] = 0.015

Lesioned Reactor Rate[4] = 0.60

Average skin-test-positives per test = 5.4 (range 0–52)

(calculated across entire period; 1982–2011)

A graph of the skin-test-positives (STPs) and the confirmed TB cases identified in this herd over time is shown in Figure 19.

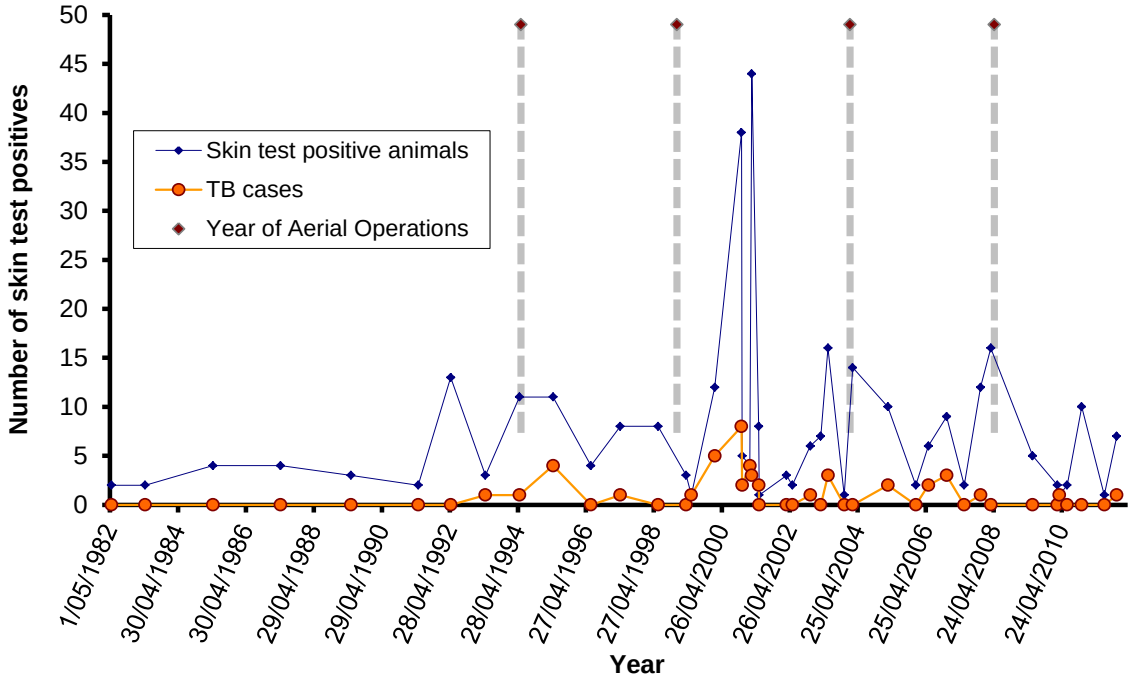

Figure 19 Scarlett /Heal Arapito herd skin-test-positive and TB-lesioned animals. Graph also shows the years in which aerial operations were undertaken.

Considering when the aerial possum control operations took place, the number of skin-test-positive animals subsequently dropped following both the 2004/05 operation and the 2008/09 operation. This herd experienced a serious disease event in 2000. This occurred within one year of the 1999 aerial operation. The operation was not prefed and used carrot bait, which was distributed by fixed-wing aircraft.

---

3 Proportion of animals destined for slaughter as reactors (positive Blood test or as determined by a DDCM) that are confirmed to have Bovine Tuberculosis[bTB] (by typical histology or culture)

4 Proportion of the animals slaughtered as reactors that are found to have bTB lesions

2. Scarlett/Pender 3086989 (A on map)

This dairy herd is located close to the Market Cross township (main township of Karamea). The farm paddocks actually break up the township into small clusters of buildings and dwellings surrounded by the dairy farm (Figure 20). There is virtually no traditional possum habitat on the property itself.

The herd used to be approximately 600 animals but has downsized since the new manager took over (in 2011).

Figure 20 Market Cross Scarlett herd showing the low coverage of possum habitat.

The herd is owned by the same farmer as the previously mentioned property. The owner has stated that there has been no transfer of stock between the two herds or properties. The sharemilker on the farm at the time of the survey owned the cows (he had purchased the original Jersey herd on the property). He sold most of the animals back to the owner when he left). TB is exclusively found in the older cows as reactors or culls often with extensive lesions, but two parallel blood tests have failed to identify a single risk-animal. The test following the last whole-herd parallel test identified a reactor with a large tracheobronchial node lesion.

The previous sharemilker took 126 young cows and calves with him to Hari Hari. These animals have been through two post-movement tests and no reactors have been identified. Other than the animals leaving with the previous sharemilker, the herd is considered to be ‘closed’.

Previous history of movement control restrictions:

November 1988 – June 2000

September 2001 – June 2002

May 2005 – December 2008

June 2009 – July 2010

Reactor Rate = 0.003

Lesioned Reactor Rate = 0.44

Average skin-test-positives per test = 2.49 (range 0–21)

3. Miedema 3086921 (B on map)

This herd is located at the end of the Arapito Valley. It is the last dairy herd in the valley and is exposed to the bush where the Karamea Gorge opens out onto farmland. The Karamea River curves around the block following the extent of the property on almost three sides. This is a multi-generational family farm. Ron Miedema's parents now live in Oxford, North Canterbury, so the young stock are sent there for grazing (until they are ready to join the milking herd). No bovine TB has been identified in young stock while away at grazing at Oxford.

There are approximately 300 animals in the herd (including young stock). This is a closed herd. The only animals entering the herd are their own young stock returning from grazing in Oxford.

Previous history of movement control restrictions:

October 1987 – July 1995

August 1999 – December 2001

July 2003 – December 2004

May 2006 – February 2008

April 2008 – June 2009

February 2011 to date

TB lesions have been identified sporadically in this herd and usually only involve a single animal at a time (either a cull or a reactor). Of the eight TB cases identified since 2003, five were found to have lesions at routine slaughter and three reacted to TB skin testing.

The herd broke down in May of 2003 as a result of a TB cull. Young stock were skin tested. There were five skin-test-positive animals and all returned a negative ancillary blood test result. A parallel blood test was undertaken on a subset of the tested calves and the results were all negative. It is assumed that these tests were carried out to allow the calves to travel to Oxford with white movement-control tags.

A whole-herd skin test in November 2003 identified three skin-test-positive animals (two were blood tested and one animal was sent straight to slaughter). One of the blood test results was positive. It appears all three animals were killed and one of the three had a TB lesion. A clear whole-herd test was completed in April 2004 (no skin-test-positives) followed by a second clear test in November 2004 at which a single skin-test-positive animal was blood tested with negative result. The status was changed to clear.

A TB cull in April 2006 put the herd back on movement control restrictions. A whole herd test in May 2006 identified 10 skin test positives, of which one was blood test positive and found to have lesions at slaughter. A part herd parallel test was carried out and 1 animal was slaughter but had no visible lesions.

A clear whole-herd test was completed in July 2006 with no skin-test-positive animals identified.

The next whole-herd test in late 2006 – early 2007 returned only two skin-test-positives. It appears that the two animals were to be blood tested but missed the window for testing so were skin tested again 3 months later and blood tested. Both returned negative blood test results. Another TB cull animal was identified at routine slaughter in April 2007. The animal had active lesions and the carcass was condemned.

Two clear whole-herd skin tests were completed (in 2007) after a handful of skin-test-positive animals returned negative blood test results and the status was reset to clear.

Another two culls were identified a month apart at routine slaughter in April and May 2008. The next test identified seven skin-test-positive animals and two were blood-test-positive. At slaughter, neither animal had visibly detectable lesions. The following herd test 6 months later found a single skin-test-positive animal. As there was some difficulty getting the reactor away to slaughter, the farmer asked if the animal could be blood tested (animal was young). The blood test result was negative and the herd once again attained a clear status.

Two skin tests later a TB reactor was identified in the herd in January 2011. The herd has completed a clear test since this time. There was one skin-test-positive animal, which was sent straight to slaughter and found to have no visible lesions.

None of the previously skin-test-positive animals have shown up at slaughter as TB culls or as reactors at subsequent tests (as can be determined from available information).

Reactor Rate = 0.003

Lesioned Reactor Rate = 0.4

Average skin-test-positives per test = 2.0 (range 0–15)

Calves from this herd are transported to Oxford for grazing each year and return as in-calf R2 heifers.

Calves are pre-movement tested before they leave and are parallel blood tested if this is required.

4. Jones 3086196 (C on map)

Location and description: The herd is located at the beginning of Granite Creek and the property has very little bush cover on or around its boundaries. The property has a coastal boundary and the spit by the lagoon is used for grazing. The herd has been on and off movement control as a result of TB cases for many years, but has spent more time under restrictions than not. The farm has been in the family for five generations and the current manager, Brian, can remember his grandfather losing cattle to TB.

In 2006 the herd achieved a clear status, which was the first time this had happened in over 21 years. The herd has had two episodes under movement control since and is currently infected. The number of TB cases has been relatively low, usually only one or two animals at any test, though in 2003, four TB cases were identified. Parallel testing has identified modest numbers of TB cases initially, but has been less rewarding more recently. The recent TB cases have been younger animals rather than older cows, although as residual infection cannot be ruled out, this makes it less likely.

Previous history of movement restrictions:

August 1986 – August 2006

July 2007 – July 2008

June 2010 to date

Reactor Rate = 0.005

Lesioned Reactor Rate = 0.5

Average skin-test-positives per test = 2.5 (range 0–36)

Four whole-herd parallel tests have been undertaken on this herd.

2000: 5 risk animals were killed and 1 had TB lesions.

2002: 1 risk animal was killed and found to have a TB lesion.

2003: 3 risk animals were killed and 1 had a TB lesion.

2011: 1 risk animal was killed (medium risk); no visible lesions found.

Despite regular TB testing and slaughter of reactors, possum control and repeated use of parallel tests this herd still produces sporadic TB cases in animals of no particular age pattern or mob. Only a handful of animals that were present in the herd in 2000 are still present and the recent TB cases are generally younger cows.

CONTROL HERDS

1. Hyndman (Owner: McGregor) (D on map)

The herd is located off the Granite Creek Road. The status was C10 before it broke down with TB in 2011. This herd was initially identified as a 'control' herd. This herd shares a boundary with Brian Jones whose herd summary is detailed above, and is also a boundary neighbour to Gary Johnson whose herd status is currently C7. According to both farmers there have not been any occasions where their stock have been 'boxed up' together.

Previous history of movement restrictions:

August 1994 – September 1996

July 2011 to date

Reactor Rate = 0.001

Lesioned Reactor Rate = 0.5

Average skin-test-positives per test = 1.7 (range 0–17)

The owner (Stewart McGregor) of this herd lives in the North Island. The farm is closer to the bush/forest edge and has a far greater bush–pasture interface than the previously described Jones' herd. There is a 'finger-like' projection of farmland that extends into the bush.

The herd recently broke down as a result of a TB reactor that was born and bred on the property. Each of the last two TB tests since the breakdown have identified a single TB animal (the latest test included a whole-herd parallel test and the lesioned animal was only positive to the parallel blood test).

2. Kees 3086219 (E on map)

First farm heading east on the Wangapeka Road. The property includes grazing on the Kongahu Swamp (see map). The run-off for this farm is adjacent to Russell Anderson's herd that has had a solid history of TB infection. The herd's current status is C9.

Previous history of movement restrictions:

April 1988 – April 1991

June 1997 – February 2000

May 2002 – June 2003

Reactor Rate = 0.004

Lesioned Reactor Rate = 0.16

Average skin-test-positives per test = 1.9 (range 0–9)

3. Hislops 3087289 (G on map)

Second dairy farm (on the left) heading east on Wangapeka Road. The current status of the herd is C10. No infection has been identified in the herd since 1996. The previous owner of this herd believes that his last herd infection (1996–1997) related to animals that had been bought in from Volckman's and was not locally acquired.

Previous history of movement restrictions:

August 1996 – November 1997

May 1989 – April 1991

April 1984 – May 1984

Reactor Rate = 0.001

Lesioned Reactor Rate = 0.3

Average skin-test-positives per test = 0.5 (range 0–7)

Reactor rates for intervals between aerial operations

The following graphs (Figures 21–23) show the reactor rates for four consecutive periods from 1991 to 2011. The periods are split by aerial operations.

The first graph (Figure 21) shows the Scarlett/Heal herd. This herd is displayed separately as the maximum value is five times greater than the next highest value for any other herd.

The time periods are:

1: 1991–1994

2: 1995–2000

3: 2001–2004

4: 2005–2008

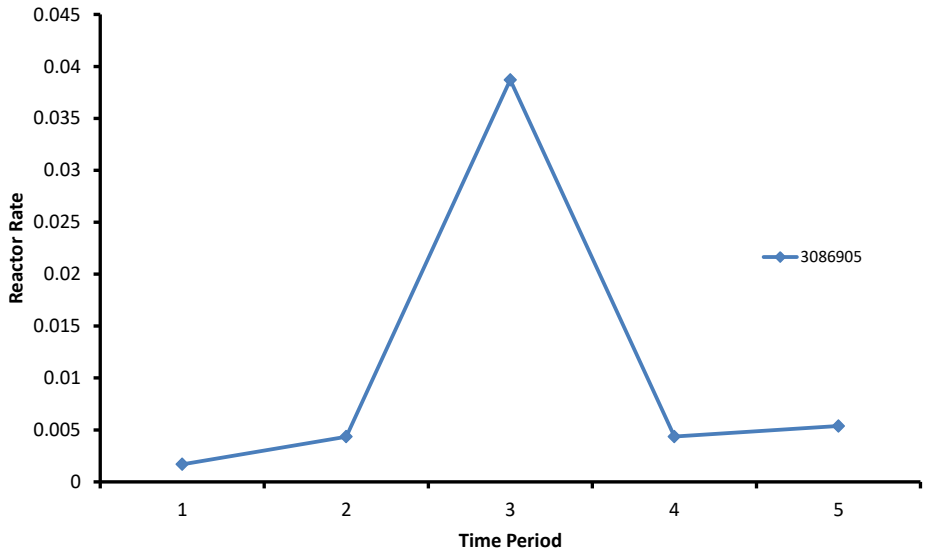

Figure 21 Reactor rate for Scarlett/Heal herd.

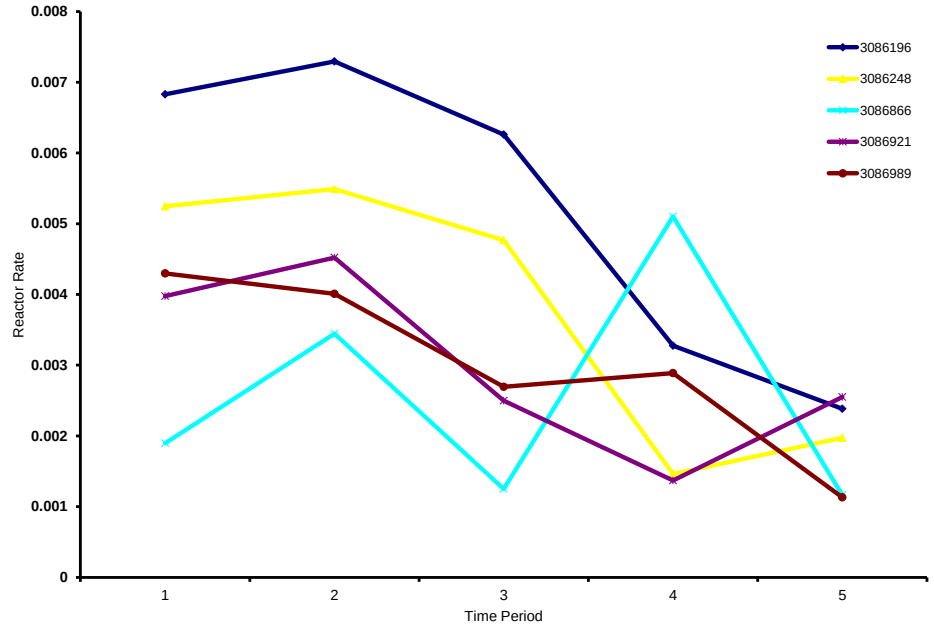

Figure 22 Reactor rates for case herds. See farm details above for farmer names and farm numbers.

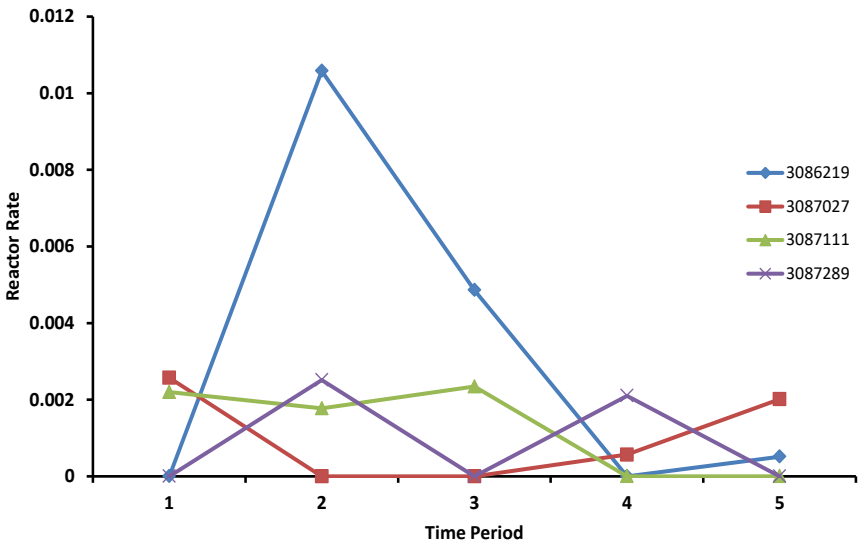

Figure 23 Control herd reactor rates (animals slaughtered as TB reactors as a function of animals tested over time). See farm details above for farmer names and farm numbers.

Appendix 6 –Trapping coverage 2006

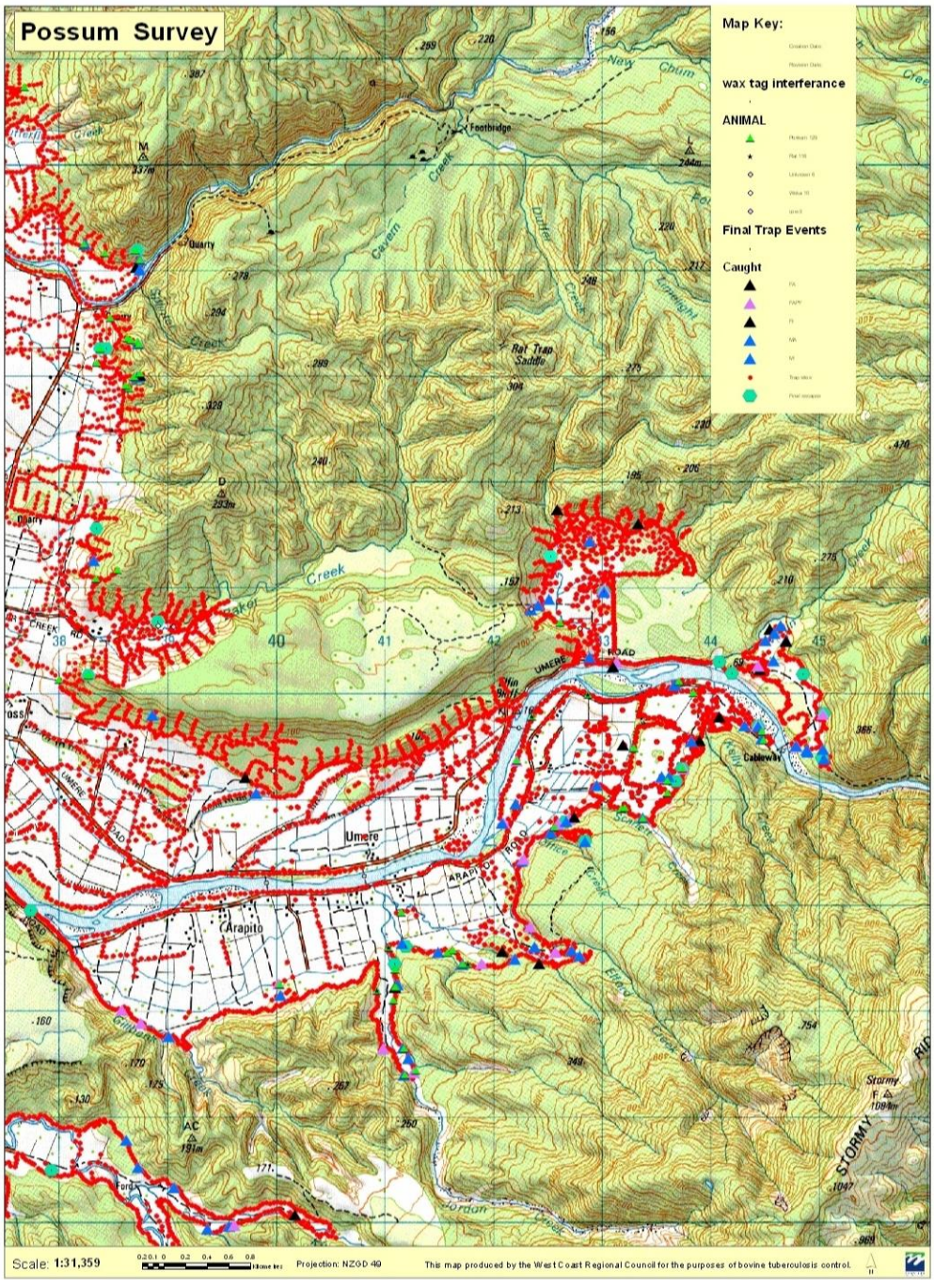

Figure 24 Trap locations from the 2006 survey in the Arapito Valley (Karamea River) and along the farm–forest edge north of Market Cross (Karamea township) showing the intensity of trap coverage. Map sourced from the AHB West Coast. Each trap location was trapped for at least six nights.

Appendix 7 – Locations of possums trapped during a control operation in December 2007 – January 2008

Figure 25 Aerial photograph showing the locations of possums trapped in the Karamea district in summer 2007/08.

Appendix 8 – Locations of TB-infected possums and stoats caught at Karamea in 2006

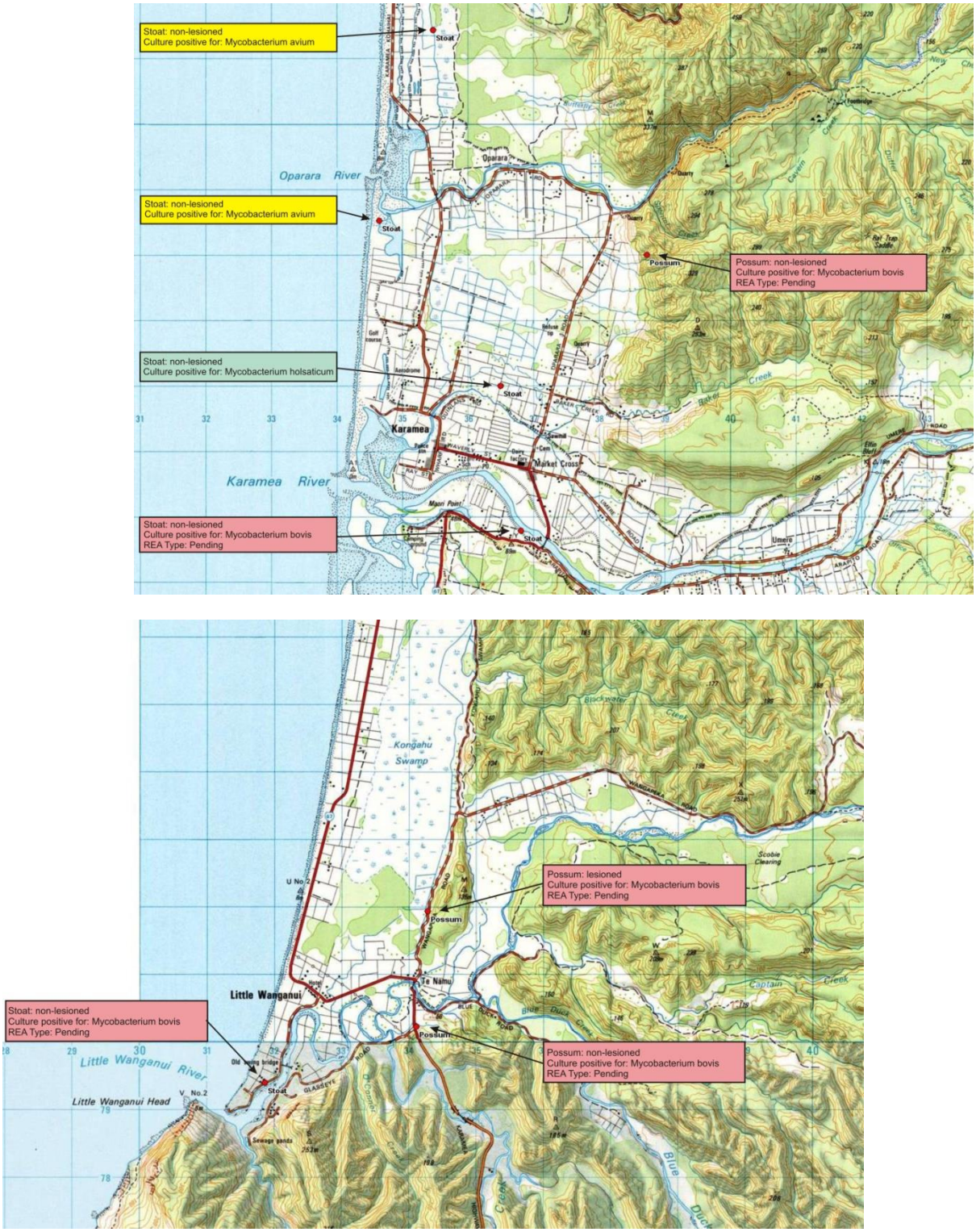

Figure 26 Locations where TB-infected possums and stoats were caught in the Karamea district in 2006.