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**The Role of
a Wildlife Reservoir
in the Epidemiology of
Bovine Tuberculosis**

**A thesis presented
in partial fulfilment of the requirements
for the degree of
Doctor of Philosophy
at Massey University**

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ABSTRACT

The objective of this project was to study the epidemiology of bovine tuberculosis in the presence of a wildlife reservoir species. Cross-sectional and longitudinal studies of possum populations with endemic bovine tuberculosis infection were analysed. The results were used to develop a computer simulation model of the dynamics of bovine tuberculosis infection in possum populations. A case-control study of breakdowns to tuberculosis infection in cattle herds in the Central North Island of New Zealand was conducted to identify risk factors other than exposure to tuberculosis in local possum populations.

The cross-sectional study was based on data gathered some years earlier in the Hauhungaroa Ranges from a number of traplines with a total length of 60km, hence it provided information about the epidemiology of possum tuberculosis on a large geographical scale with varying environmental conditions. The results from the study showed that disease occurrence was clustered in space with local prevalence reaching up to 20% while the overall prevalence was about 1.2%.

The longitudinal study was conducted using an area of 21 hectare of mixed pasture and bush on a sheep/beef farm. The study showed that incidence and prevalence of tuberculosis infection in possum populations has distinct spatial and temporal patterns. Environmental conditions were a major factor in determining the temporal pattern. Spatial and temporal analysis of the occurrence of different strains of *Mycobacterium bovis* allowed inferences to be made about the importance of particular transmission paths. Survival of possums depended on environmental conditions and tuberculosis disease status. Adverse weather conditions increased mortality and the incidence of clinical disease in possums. On average clinically tuberculous possums survived for about 2 to 3 months from the onset of clinical disease.

The simulation model uses a Monte-Carlo modelling approach and incorporates geographical features. Biological mechanisms which are considered important for population and infection dynamics were implemented in the model. These include mating, density-dependent and -independent mortality, pseudo-vertical transmission, transmission through spatial or temporal proximity, and transmission during mating contact. Each possum's movements and behaviour are simulated on a day-by-day basis. Simulations are conducted using a geography and possum population based on data from the longitudinal field study. For preliminary validation, model output was compared with field data from the longitudinal study. Sensitivity analyses and some initial simulation experiments were conducted to identify areas in the model structure which require the collection of additional field data. Use of the model for simulation of a possum population occupying a 400ha area in the Central North Island of New Zealand is demonstrated.

The case-control study of breakdowns to tuberculosis infection in cattle herds showed that in the Waikato area of New Zealand exposure to tuberculosis infection in local possum

populations was not the dominant cause of breakdowns when the study was conducted in 1989/90, at a time when tuberculous possums were first discovered in the region. Farmers who had breakdowns tended to follow cattle purchase and management practices which traditionally have been considered to put farms at risk of introducing tuberculosis. The results of the study indicate that there was a lack understanding among farmers about the epidemiology of tuberculosis.

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