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A Geographical Simulation Model of Bovine Tuberculosis in Wild Possum Populations

Dirk U. Pfeiffer, Todd Cochrane, Mark W. Stern and Roger S. Morris

Department of Veterinary Clinical Sciences, Massey University, New Zealand

Introduction

In New Zealand wild populations of Australian brushtailed possums are an important reservoir of *Mycobacterium bovis* infection in domestic cattle and deer populations. Attempts to control the disease in possum populations over the last 20 years through localised population reduction have had only limited success. Data from a number of epidemiological field studies was analyzed to develop an understanding of the dynamics of bovine tuberculosis infection in wild possum populations (Pfeiffer 1994). This information was then used to develop a computer simulation model of the epidemiology of the disease in wild possum populations, called PossPOP. During the development process it has been possible to identify areas which need further research. The final model will be part of a decision support system which will be used by the New Zealand Ministry of Agriculture and Fisheries to evaluate alternative disease control options.

Modeling Approach

PossPOP was developed using a Monte-Carlo simulation modelling approach. The model has a modular structure and significant activities in the behaviour of individual possums are simulated on a daily basis. Spatial relationships between possums are represented on the basis of den site locations which are occupied by individual possums during a particular simulation day. Rather than interpreting these den sites as physical sleeping places they could be seen as representing the focus of a night's activity. The probabilistic events in the model are controlled by parameter settings which can be adjusted by the user. Individual probabilities can be varied on a monthly and yearly basis, so that seasonal and cyclical variation can be represented. Adjustment of the relevant parameters can be used to evaluate the effects of various methods of disease control. The simulation components of the model have been programmed and compiled in Borland Delphi. Simulation control, data management and presentation is done using Microsoft Access Version 2.0. The model runs as a Microsoft Windows application. Geographical information about an actual simulation area can be imported into the simulation system as vegetation raster maps, farm boundary and natural barrier vector maps. Model output can be displayed graphically using time series plots and maps.

Model Components

The model contains modules representing six major aspects of possum behaviour and ecology: den site selection, reproduction, infection, survival, ageing, emigration and immigration. Each simulated possum is processed by these modules on a daily basis. As a first step a possum has to select a den site location. These are based on randomly generated locations according to a pre-defined density per vegetation category. During the selection process a possum begins its search for a new empty den with the den closest to last night's den site taking into account the presence of natural barriers. If this den is occupied, it visits the den which is closest to it. Once it has found an empty den, there is a probability that it refuses to use it. If the possum does not find an empty den within a given den search distance, a counter of the days spent without a suitable den will be updated. As a next step adult, non-pregnant female possums search in neighboring dens for an adult male possum for mating. On finding a suitable male there is a probability that she becomes pregnant. If not, she searches for the next male until she has reached a maximum search distance or becomes pregnant. The mating mechanism and its components are only effective during breeding seasons. The infection module controls transition of possums between susceptible, subclinical and clinical disease stages. Infection requires direct or indirect contact between a clinically diseased and a susceptible animal. This can be through direct contact between mother and young (pseudo-vertical transmission) or between male and female during mating. Both, indirect and direct contact are represented in this module through sequential den sharing and use of a den in the vicinity of a den used by a tuberculous possum. Each of the transmission paths has its own probability for successfully transmitting infection. After successful infection a possum changes from the susceptible to the subclinical disease state. Transition from subclinical to clinical disease is controlled by probabilities varying according to season. The survival module incorporates effects which represent density-dependent and density independent mortality. Separate density independent survival mechanisms are implemented for young possums dependent on their mother, non-clinical possums, and tuberculous possums. In addition all possums resident in the population are subject to a population density-dependent survival mechanism which depends on the number of days over a given period of time a possum has been without a suitable den. The survival probabilities vary with season. Age of independence and age of sexual maturity for individual possums are both randomly sampled from appropriate distributions. Dispersal or long-distance movement of individual possums from a local population are modeled both as density-independent and independent effects taking into account age and sex of the animal. Immigration is simulated using the same mechanism as emigration but based on a static population occupying the edge habitat surrounding the main simulation area. Immigrants have a given probability of being infected. If an immigrant does not find an empty den within a given number of days, he/she will be conduct a long-distance movement. Immigration probabilities vary between months of the year.

Model Parameters, Validation and Experimentation

A baseline set of parameter settings for the model was derived from data collected during a longitudinal study of tuberculosis infection in a wild possum population (Pfeiffer and Morris 1991). The model was validated against outcome estimates for the same site, as no alternative validation data sets were available. Sensitivity analyses were conducted by varying the settings for parameters controlling transmission dynamics. Preliminary model experiments were conducted to demonstrate that the model can be used to test the effect of various strategies for reducing possum population density on the presence of tuberculosis infection in possum populations. Additional simulations were conducted using a 400 ha area in the Central North Island of New Zealand to demonstrate that the model can be used for any location in the country.

Conclusion and Further Development

In contrast to true mathematical models, PossPOP is based on a Monte-Carlo simulation modelling approach which allows a more comprehensively realistic representation of biological mechanisms in the ecology of the host and the transmission of infection. Monte-Carlo models also offer the benefit that they are much easier for non-mathematicians to understand. A major advantage of PossPOP for evaluating control of wildlife disease is that it can represent and take full account of relevant geographical features, such as possum habitat suitability derived from digital vegetation information. This allows modelling of the dynamics of *Mycobacterium bovis* infection for any chosen site in New Zealand.

The model is currently being extended to include livestock population information for each farm, so that infection in domestic stock as well as wildlife can be included. A hierarchy of models from local to regional level will be made available for policy evaluation purposes.

References

Pfeiffer,D.U. and Morris,R.S. 1991. A longitudinal study of bovine tuberculosis in possums and cattle. In R. Jackson (Editor) Proceedings of a Symposium on Tuberculosis, Publication No.132, Veterinary Continuing Education, Massey University, Palmerston North, New Zealand, 17-39.

Pfeiffer,D.U. 1994. The role of a wildlife reservoir in the epidemiology of bovine tuberculosis. Unpublished Ph.D. Thesis, Massey University, Palmerston North, New Zealand, 496pp.