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POSSPOP - A GEOGRAPHICAL SIMULATION MODEL OF BOVINE TUBERCULOSIS INFECTION IN A WILDLIFE POPULATION

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INTRODUCTION

In New Zealand wild populations of Australian brushtailed possums are an important reservoir of *Mycobacterium bovis* infection in 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.

MATERIALS AND METHODS

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 center 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 model has been programmed in Borland Pascal 7.0 and compiled to run as a Microsoft Windows application. Various types of model output can be generated and viewed on screen or stored in ASCII text files for further analysis. Independent random number streams have been implemented in the model so that the effect of variance reduction using antithetic and common random numbers could be evaluated.

The model contains modules representing six major aspects of possum behaviour and ecology: den site selection, reproduction, infection, survival, ageing 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 can be based on either actual locations or randomly generated locations. During the selection process a possum begins its search for a new empty den with last night's den site. If this den is occupied, it visits the den which is closest. 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 neighbouring dens for an adult male possum for mating. On finding a suitable male there is a

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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 the relevant months of the year. 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 or 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 stage. Transition from subclinical to clinical disease is controlled by probabilities varying according to season. The survival module incorporates effects which represent mortality and emigration. Separate 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. Immigration is a random process where numbers of immigrants are taken from a poisson distribution on a daily basis separately for each sex class. 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 removed from the population. Immigration probabilities vary between months of the year.

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 coordinates of den site locations were based on radio telemetry data which had been collected during the same study. The model was validated against the same dataset as no other data was available at the time. 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 of 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. Digital vegetation information for this area was used to generate random den site locations at different densities for the four significant habitat types.

RESULTS AND DISCUSSION

A series of initial simulation runs was conducted to calibrate model parameters using data from a longitudinal field study of bovine tuberculosis infection in a wild possum population. The comparison was based mainly on population size, infection prevalence and incidence. It was necessary to calibrate the parameters for survival and infection probabilities to achieve satisfactory agreement between field data and simulation output.

Given the current parameter settings it was possible to maintain endemic disease within the population in the presence of infection in immigrating possums. Simulation runs produced spatial clustering of the disease which was relatively stable in time. This is an emergent

property of the model and agrees with findings from field data. Survival analysis showed that survival of simulated possums with clinical tuberculosis compared reasonably well with the field data. Using time-series analysis it was not possible to detect long-term cycling patterns of the disease in an infected population. Spectral analysis was used to further investigate the time series patterns of tuberculosis prevalence and incidence. Prevalence of subclinically and clinically tuberculous animals did show a seasonal pattern. Incidence of infection was not seasonal.

The results of sensitivity analysis of the different transmission mechanisms show that given the current parameter settings transmission through spatial proximity controls the infection dynamics in a simulation run. Taking into account recent evidence from field data the importance of mating is underrepresented in the model. Further studies are required to obtain quantitative estimates of the parameters controlling transmission during mating.

A number of options for controlling the disease using reduction of possum population density were evaluated. The success of initial reductions by 75% depended largely on the amount of residual infection remaining in the population after control which was subject to stochastic variation. In 20% of 20 simulation runs the disease did not become extinct using a single initial reduction in population size. Amongst the control options evaluated only reduction by 75% at three yearly intervals was able to eliminate endemic infection in the presence of infection in immigrants at 5% prevalence.

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 farm boundaries and 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. Various diseases in other wildlife species could be simulated with this model by adjusting the input parameters and spatial assumptions - for example rabies in various wild animals or tuberculosis in badgers.

REFERENCES

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