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The Development of a Simulation Model for Tuberculosis in Cattle

J. M. Griffin, D. H. Williams, P.W. White and K. Towey

Introduction

In spite of its economic importance, knowledge is still very limited on some basic epidemiological features of tuberculosis in cattle. The areas of concern include the interval between an animal becoming infected and infectious, the rate of transmission of infection by an infectious animal, and other determinant factors.

Traditionally, information on the epidemiology of animal diseases has been obtained by laboratory experiments or field studies. These can be time consuming and costly, however. Bovine tuberculosis is a particularly difficult disease to study under laboratory conditions because it has such a long incubation period and the clinical phase of the disease is often prolonged. Furthermore, progression of the disease process may be interrupted as a result of an eradication programme. Apart from ethical and human health considerations, it is often impractical to infect a large number of animals to observe the progress of the disease.

An alternative approach is to use a probabilistic mathematical model to imitate as closely as possible the behaviour of an infection as it passes through a theoretical population of animals. The field of stochastic modelling of biological and ecological systems is currently undergoing considerable development as advances in computing power make the investigation of complex stochastic models by simulation methods more feasible.

Simulation models for animal disease are built using combinations of arithmetic and logical processes. Each individual animal being simulated is tracked over a period. The animal is exposed to infectious individuals and to other experiences such as calving, death, culling for other reasons, etc. The exposure of an animal to disease depends to the extent to which disease has spread among the animals with which it has contact. Consequently, this type of model can become very complex and this complexity increases as the number of individuals in the population increases. As a result, such models are normally developed through the use of computer programmes.

The aim of the present study is to develop a simulation model that will provide a better understanding of the epidemiology of tuberculosis in cattle in the Republic of Ireland. In addition, computer simulation models offer the opportunity to test control strategies and select those most likely to succeed and be cost effective. It is intended, therefore, that this simulation model will also assist in the refinement of the control programme for bovine tuberculosis in Ireland.

Objectives

1. To obtain estimates of parameters that influence the population dynamics of the herds under study and the epidemiology of *Mycobacterium bovis* infection. The relevant parameters include:

   - The mean time interval between when the animal becomes infected and when it becomes positive to a tuberculin test (the pre-allergic period).
- The mean time interval between when an animal becomes infected and when it becomes infectious (the latent period).
- The sensitivity of the Single Intradermal Comparative Tuberculin Test (SICTT).
- The specificity of the SICTT.
- The probability of transmission from an infectious to a susceptible animal, i.e. the disease transmission coefficient.

2. To predict the incidence of bovine tuberculosis at herd and animal level in a geographical area.

3. To predict the impact of new strategies on the incidence of bovine tuberculosis.

**Progress to date**

A computer programme has been designed that simulates the development of tuberculosis in a cattle herd or in a group of herds over time following the introduction of one or more *M. bovis* infected animals. Visual Basic® programming language is being used. Input and output data are displayed using the Microsoft Access® programme. The main menu window is shown in Figure 1. The model consists of two sub-models, one for the population dynamics, and the other for disease.

**Figure 1. Main menu window.**

The basic unit of the modelling procedure is an individual animal. A number of animals are aggregated into one or more herds of a pre-determined size. The size and composition of each herd is based on actual data from herds in the geographical area being simulated.

The status of each animal is evaluated on a daily basis. The fate of each animal is determined by events that occur at random, based on probability distributions, i.e. the model is stochastic. Hence, the outcome of the model for a given set of inputs can vary depending on the element of chance. This can provide a measure of how much variability could be expected between herds with similar characteristics. In so far as possible, the probability distributions are based on field as well as experimental data.

The probability of events such as calving, culling or becoming infected with *M. bovis* is entered by the programmer in the form of a daily probability between 0 and 1. Using a Monte-Carlo sampling process, the probability of a particular event is applied to each individual in turn to see whether that individual will be infected. The mechanics of the process are simple. The computer generates a random number between 0 and 1. This is compared with the daily probability, which is also a number between 0 and 1. If the random number is less than or equal to the probability, then the event happens. For example, if the
daily probability of an animal being culled is 0.01, then the animal will be culled if the random number that is generated is less or equal to 0.01; if the number generated is greater than 0.01 it will not be culled. The more complex probability distributions are incorporated into the programme by using the @Risk® computer programme (Palisade, New York, NY).

The main parameters of interest in this study are those considered to relate to the epidemiology of tuberculosis in cattle. However, the dynamics of the population at risk are also taken into account. In addition to disease parameters, therefore, the model also contains a large number of reproductive and culling parameters.

In the model, the development of tuberculosis in a herd is initiated by seeding the herd with one or more infected animals. In the current model, each animal passes through four mutually exclusive sequential stages. These are as follows:

1. Stage S - the animal is susceptible to infection,
2. Stage U - the animal is infected, it does not react to the tuberculin test and is not infectious.
3. Stage R - the animal is infected, it reacts to the tuberculin test and is not infectious, and
4. Stage I - the animal is infected, it reacts to the tuberculin test and is infectious.

The period that an animal spends in each stage is determined by probability distributions which, in turn, are based on scientific data.

The model also contains a component for the control of bovine tuberculosis. Essentially, the control measures used in the model are the same as those used in the Bovine Tuberculosis Eradication Scheme in the Republic of Ireland. The main elements of the scheme are tuberculin testing and the removal of tuberculin test-positive animals.

The computer programme allows the period of simulation to be varied in accordance with the requirements of a particular simulation. The main constraint is that the time taken by the computer to run the simulation increases as the period of simulation increases. With the computer hardware presently available, it has been possible to carry out simulations covering a 10-year period.

The main outputs of the model are those relating to herd dynamics and tuberculosis incidence. The output on tuberculosis incidence will contain information on both the actual incidence of tuberculosis in the population and the apparent incidence based on tuberculin test results.

Currently the model is at a developmental stage. Further progress will be reported on in a future edition of this publication.