Veterinary Microbiology 135 (2009) 128–133

Contents lists available at ScienceDirect

Veterinary Microbiology

journal homepage: www.elsevier.com/locate/vetmic

Epidemiological modelling of chlamydial abortion in sheep flocks

Catherine E. Milne [a,*], George J. Gunn [b], Gary Entrican [c], David Longbottom [c]

[a] Animal Health Economics Team, SAC, West Mains Road, Edinburgh EH9 3JG, UK
[b] Epidemiology Research Unit, SAC, West Mains Road, Edinburgh EH9 3JG, UK
[c] Moredun Research Institute, Pentlands Science Park, Bush Loan, Penicuik EH26 0PZ, UK

ARTICLE INFO

Keywords:
Chlamydophila abortus
EAE
Epidemiological model
Disease transmission
Sheep

ABSTRACT

Chlamydophila (*C.*) *abortus*, responsible for chlamydial abortion (commonly known as Enzootic Abortion of Ewes [EAE]), causes major financial losses to the sheep industry worldwide. There remain many uncertainties surrounding the epidemiology of EAE. The aim of this study was to construct an epidemiological model to simulate EAE based on current knowledge of the disease, and in doing so, identify knowledge gaps that need to be addressed through further research. Key parameters that impact upon the development of the disease, such as the rate of contact between naïve ewes and infected material, are defined. Sensitivity analysis was undertaken for parameter values that are unknown to explore their impact upon the pattern of disease. The simulated results show the importance of the transmission rate (i.e. contact) and the number of infected replacements introduced at the start of an outbreak. Depending upon the rate of transmission, the year in which the peak number of affected ewes occurs and the number of years over which a high number of animals are affected varies. This suggests that a better understanding of the underlying processes that drive transmission of *C. abortus* is needed. Furthermore, if infected ewes could be identified prior to parturition, when they shed the organism in large numbers, the impact of EAE on sheep flocks could be greatly reduced.

1. Introduction

Enzootic Abortion of Ewes (EAE), caused by the Gram-negative obligate intracellular bacterium *Chlamydophila* (*C.*) *abortus*, is an important production disease of sheep flocks in many countries (Buendía et al., 2001; Longbottom and Coulter, 2003; Aitken and Longbottom, 2007). The bacterium has an affinity with mucosal membranes and, following invasion of the placenta, causes disease, which takes the form of abortion, stillbirths, the birth of weakly premature lambs and seemingly normal lambs (Longbottom and Coulter, 2003). Abortions typically occur during the last 2–3 weeks of gestation. The cost of the disease to British farming has been estimated to be in the region of £6–£20 million per annum (Bennett, 2003; Wood, 1992). Infection is also zoonotic, with particularly serious consequences for pregnant women (Helm et al., 1989; Longbottom and Coulter, 2003). The implementation of effective control measures is highly desirable on economic, human health and animal welfare grounds.

As the disease is commonly transmitted between flocks by infected stock, control at the individual farm level can have benefits both for that and other flocks. Farmers will implement control measures where the cost of action is lower than the benefits. Knowledge of the costs and benefits is required in order to select these measures. Such knowledge is also useful to policy makers who may wish to promote or support the uptake of disease control strategies. A simple estimate of the costs and benefits of alternative control strategies has been made previously

* Corresponding author. Tel.: +44 131 535 4481; fax: +44 131 535 4481.
E-mail address: cath.milne@sac.ac.uk (C.E. Milne).

0378-1135/$ – see front matter © 2008 Elsevier B.V. All rights reserved.
doi:10.1016/j.vetmic.2008.09.032

using a fixed set of assumptions (Milne and Dalton, 1988/1989). More detailed estimates have not been made, in part due to a lack of data, which is a common problem associated with animal diseases. Where data are incomplete, epidemiological models can provide new insights into a disease (Graat and Frankena, 2001; Pfeiffer, 2004; Thrusfield, 2005) and into disease control choices, as has been shown for Bovine Viral Diarrhoea (Stott et al., 2003). In the case of EAE, no data are available from field studies on the number of ewes that become infected in different years. Typically, it is the ewes aborting in year 2 (the abortion 'storm') that are recorded, whereas the ewes with less severe or no clinical signs may go unrecognised and not recorded. Furthermore, there are few data on the disease incidence in other years of an outbreak. A range of values for uncertain parameters can be tested in models and by comparing simulated results with observed data, factors impacting on disease patterns can be explored (de Jong, 1995). Though not predictive, exploratory models built in this way can thus assist decision-makers.

As there remain many uncertainties surrounding the epidemiology of EAE, the aim of this study was to construct an epidemiological model to simulate EAE based on current knowledge of the disease. This will identify knowledge gaps that need to be addressed through further research. Key parameters that impact on our current understanding of disease processes are defined and, where data are not available, a range of possible values are explored. Simulated outcomes of an EAE outbreak in a flock are compared with reported field data. Finally, differences between the simulated values and those reported from the field are discussed with reference to future research needs, to enable the effective selection of control measures for EAE.

2. Methods

2.1. Theoretical background to construction of the model

Mathematical models of disease are simplified representations of a real situation (Thrusfield, 2005). While it is important to capture key processes, increasing the level of detail modelled does not necessarily improve the quality of the simulation (Humphry et al., 2005). Thus, it is recommended that simple models are constructed in the first instance with complexity added later, if necessary (Graat and Frankena, 2001). One approach that is widely used for infectious diseases is that of a SIR model as described by Graat and Frankena (2001). In this type of model, animals move between different disease states such as 'susceptible', 'infectious' and 'recovered' (hence the terms 'SIR' and 'state transition'). The transition probabilities between states can be fixed or variable depending upon certain factors, such as the number of infectious animals. It may also be necessary to include stochastic or 'random' events that can affect the spread of a disease within a population, for example, direct contact events between individual animals, as these may explain some of the observed variation in the development of a disease within a flock or herd (Graat and Frankena, 2001; Thrusfield, 2005).

2.2. EAE model construction

Three underlying features of EAE determined the general framework of the model described here. Firstly, a set of distinct disease states are identifiable, these being uninfected, latently infected, infected/diseased and immune. A state transition form was therefore appropriate and adopted for the model. Secondly, since the pattern of disease takes several years to develop (Aitken and Longbottom, 2007) the model needed to be multi-annual and a time period of 10 years was set as sufficient for the simulations required. Thirdly, and as a consequence of building a multi-annual model, it was considered necessary that the model should encompass some aspects of normal flock dynamics. These random and planned events, such as replacement of animals, are likely to affect the development of EAE in a flock. An Excel© (Microsoft Corporation) spreadsheet was used as the modelling environment allowing transparency of the mathematical relationships simulated.

The model tracks individual ewes, defined by parity and disease state, and can accommodate flocks of any size between 1 and 500 ewes. The initial distribution of parities within the flock was representative of a real flock and thereafter was determined by the annual number of replacements and losses. Each ewe encounters a series of events that occur chronologically over a year, which starts with the introduction of replacement animals in the autumn. In total eight annual events were simulated. In chronological order these were mating, mortality pre-lambing, clinical disease t_1, infection with EAE t_1, clinical disease t_2, infection with EAE t_2, mortality post-lambing and replacement. The model encompasses two time periods (t_1 and t_2) in which clinical disease could develop or infection acquired. This was necessary to simulate cases where ewes become infected and develop clinical disease within a single pregnancy (Blewett et al., 1982). Using the random number generator facility within Excel©, a Monte Carlo simulation was used to determine individual ewes that died or were replaced for reasons other than parity and all ewes that reached 5 parities were replaced.

The terms 'clinical disease' and 'clinically affected' are used in this paper to identify ewes in which *C. abortus* has invaded the placenta, resulting in either abortion, stillbirths, or the birth of weakly premature or seemingly normal lambs. With regard to the introduction of infection, it was assumed that the flock was EAE naïve in year 1 and that the source of infection was latently infected replacement ewes. This is a common source of EAE infection to naïve flocks (Philips and Clarkson, 2002; Aitken and Longbottom, 2007). The proportion of replacements that may be infected when introduced to a flock is an unknown quantity that could affect the development of disease within a flock. Within the model this parameter was therefore constructed as a user defined variable so that alternative values could be tested.

Disease transmission occurs via the oral-nasal route (Jones and Anderson, 1988). Affected ewes shed large numbers of *C. abortus* with placental material and uterine fluids at parturition (Aitken and Longbottom, 2007).