

# A stochastic model for investigating factors affecting the within-herd prevalence of *E. coli* O157 within beef cattle

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## Abstract

To investigate control measures for reducing the within-herd prevalence of *E. coli* O157 within beef cattle herds, it is important to gain an understanding of the influential factors affecting transmission within the herd. This has been achieved through the development of a stochastic model that aims to simulate transmission of *E. coli* O157 within an autumn calving beef herd. The model accounts for two main infection routes namely, direct contact between animals and contact with the contaminated environment. In addition, the model accounts for the impact of varying management practices throughout the year on the transmission dynamics (i.e. summer grazing versus winter housing) by modifying the spatial structure of the herd.

Using sensitivity analysis it is observed that, during the summer, contact between the animals is an important factor whereas during winter housing it is contact with the environment that has an impact on *E. coli* O157 transmission. This finding has been used as a focus for identifying the key factors affecting the transmission dynamics. For example, by modifying the model, the impact of increasing the frequency that the housing environment is cleaned out, reducing contact with the environment, and increasing the herd size has on *E. coli* O157 transmission was explored. Based on this research, it is concluded that *E. coli* O157 is most effectively managed by reducing the number of animals managed in a single unit and reducing contact with *E. coli* O157 in the environment.

## Introduction

Modelling transmission of infectious disease has become common tool within both the veterinary and public health fields for providing insight into the dynamics of pathogens within a population (see for example Ferguson *et al.*, 2001). In relation to *E. coli* O157, this approach has been used to explore the transmission dynamics within dairy cattle (Wood, 2002, Turner *et al.*, 2003) and cattle herds (Matthews *et al.*, 2006; Liu *et al.*, 2005). Using these previously developed models as a basis, particularly the former models, a stochastic simulation model was developed to describe the transmission of *E. coli* O157 within a typical beef herd in GB.

The model simulates the transmission process within a beef herd by following a group of adults from 3-months prior to the birth of their calves to the time the calves are weaned and ready for fattening. During this time period, animals are either on pasture (summer) or in housing (winter). In the former situation, animals have the opportunity to mix homogeneously whereas during winter housing, animals are usually housed in small groups, limiting the contact that they have with each other. This change in the group structure of the herd is addressed by assuming that the herd mixes on a single pasture during the summer month whereas in the winter, the herd is divided into 4 pens (two pens for the calves and two pens for the adults). This set up is used as an illustration of the differences in the dynamics between summer and winter rather than being representative of a specific farm. Regardless of season, however, it is assumed that the transmission dynamics of *E. coli* O157 within a random beef suckler herd are the same.

## Materials and methods

Current understanding of *E. coli* O157 infection within beef herds suggests animals are either susceptible (S) or infected (I) at any time. Infected animals are those with the bacteria present in

their gastro-intestinal tract. The colonisation process of cattle is thought to occur more frequently in young stock than older stock and they also have higher excretion rates (Robinson *et al.*, 2003). In view of these important differences, the herd is divided into the young stock (u) and adult cattle (a). Infected cattle excrete *E. coli* O157 into the environment in the faeces whereby it serves as a reservoir for maintaining infection within the herd. This environmental pool of bacteria (E) is incorporated into the model and represents the Colony Forming Units (CFU) excreted onto the pasture during the summer grazing period or excreted into the housing environment during winter.

The susceptible-infected-susceptible (SIS) process is described by a continuous-time semi-Markov process. Using this approach, the time between all but one state change is a random variable with a memory-less distribution. Due to the fact that colonised animals may intermittently excrete the bacteria, leading to a highly variable distribution of recovery times (Robinson *et al.*, 2004), it was considered that this time period was best described by an empirical distribution, rather than a memory-less distribution (e.g. exponential). It is assumed that infection may occur via three routes: direct contact with infected animals of the same age group, direct contact with infected animals of a different age group and consumption of VTEC O157 from the environment. To model these routes of infection, two interacting processes are considered: animal processes (e.g. infection, death, birth) and environmental processes (e.g. death, excretion).

The simulation model contains several parameters, some of which are uncertain due to a lack of scientific understanding and data. To understand which parameter estimates have a significant impact on the final output, a sensitivity analysis was undertaken. Seven key parameters for which there was no information were selected for analysis. To analyse the effect of these seven key parameters and to detect interactions between the parameters, a two-level factorial experimental design approach was adopted (Gardiner & Gettinby, 1998). Using this approach, a high and low level value for each factor was tested with a high and low value for every other factor resulting in  $2^7$  treatment combinations (design points) to be tested (Law & Kelton, 2000).

## Results

Assuming that 2% of adults are infected at  $t=0$ , by the end of the grazing period ( $t=183$ ), this proportion increases to 4% [0, 5%]. The mean proportion of calves infected at  $t=183$  is 5% [0, 14%]. By the end of housing ( $t=365$ ), the proportion of infected adults decreases slightly to 3% [0, 5%] whilst the proportion of infected calves increases to 32% [0, 69%]. At the herd level at this time, the proportion of infected animals is 12% [0, 27%]. After the winter period, the animals are turned out to grass for a second grazing period. Immediately prior to the assumed removal of the young animals to a fattening herd ( $t=454$ ) the proportion of infected animals within the herd decreases to 2% [0, 6%].

Regardless of time period, the transmission between adults is the most important effect. Differences in ranks of the seven factors are, however, noted between summer grazing and winter housing. In particular, it was concluded that during the summer grazing period, transmission between the animals has the most influential effect on the output, whilst during winter housing it is the parameters associated with contact with the environment that are of importance.

## Discussion

The stochastic simulation model aims to capture the main contributors to VTEC O157 infection as currently agreed upon in the scientific field (i.e. variable excretion of VTEC O157 over time, age-specific recovery and excretion patterns, and non-constant contact with VTEC O157 in the environment). Using this modelling approach, specific insights into the influential routes of transmission at different times of year (housing versus summer grazing) were observed. In

particular, the transmission dynamics are most influenced by animal-to-animal contact during the summer grazing period and by contact with the environment during the housing period. Based on the findings from this research, therefore, it is important to reduce contact with the environment during the winter and turn cattle out onto clean pasture in order to observe a reduction in the prevalence of *E. coli* O157 within the herd.

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