

# An Investigation into Factors that Affect the Within-Herd Prevalence of *E. coli* O157

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## Summary

A spatially-explicit simulation model of grazing cattle has been developed to investigate factors that may affect the *E. coli* O157 infection process at the herd level. The two main infection transmission routes are modelled: environmental contact and direct animal contact. A flexible design allows the model to be applied in complex scenarios enabling methods of improving on-farm hygiene to be considered. The simulation results suggest that the most important factor in controlling the infection is the frequency of cleaning.

## Introduction/Objectives

*E. coli* O157 is a bacterium that can cause serious illness and death in humans. Cattle appear to be an important reservoir of this infection (Chapman, 1992). Experimental studies that attempt to gain an insight into the dynamics of the infection are often restricted by financial and ethical constraints and therefore, a simulation model has been developed to investigate the *E. coli* O157 infection dynamics

## Materials/Methods

The within-herd simulation model was developed and implemented via a program written using the C++ programming language. The spatially-explicit model structure allows appropriate biological information and realistic behaviour to be incorporated into the modelling of the two main routes of infection transmission: environmental contact and direct animal contact. This was achieved by discretizing the simulated field into gridsquares and then keeping track of not only the location and infection status of each cow, but also the location of *E. coli* O157 contamination within the field.

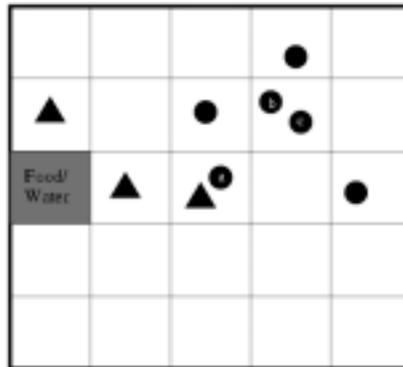


Figure 1: Cows (●) can become infected by contact with infected animals (e.g. (b) & (c) ) or contaminated gridsquares ▲ , e.g. (a)).

In order to provide a satisfactory model of the contact process between cattle, a movement mechanism based on the social dynamics of a herd was devised. Three types of movement are permissible, with the choice of move being made randomly and independently for each animal. Thus, cattle can:

- move randomly to any gridsquare,

- move to a socially-weighted gridsquare (i.e. a gridsquare towards the average location of the herd, which helps to create a cluster of animals (see Figure 2)),
- move to a source of drinking water.

The length of time between movement events is exponentially distributed.

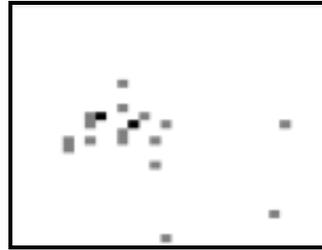


Figure 2: “Aerial view” of locations of cows within a field at one point in time. Darker levels of shading indicate multiply-occupied gridsquares.

If an uninfected animal comes into close contact (i.e. moves to the same gridsquare) with either an infected animal or contaminated pasture, infection transmission occurs with a specified probability. The probabilities of infection were estimated by comparing model output with results from the Scottish Prevalence Study (1998-2000) (Synge *et al.*, 2000)

The lengths of time for which an infected animal sheds bacteria and for which infected faecal pats define a positive force of infection are allowed to vary stochastically. Upon infection, it was assumed that following an initial 18-hour latent period, cattle shed infected faeces every 2 hours for the duration of their infection, which was randomly sampled from one of three distinct shedding patterns identified by Grauke *et al.* (2002) (see Table 1). The gridsquares into which infected faeces were shed became infected for approximately 30 days, since Kudva *et al.* (1998) found this was the average length of time that faeces remained culture-positive.

<b>Shedding Pattern</b>	1 week	1 month	>2 months
<b>Category Range</b>	3-10 days	22-38 days	56-69 days
<b>Proportion of Animals</b>	0.33	0.54	0.13

Table 1: Details of the three shedding patterns observed by Grauke *et al.* (2002)

The model design is flexible, allowing it to be applied in more complex scenarios. For instance, it is straightforward to include calves in the herd by adjusting certain parameter estimates, or alternatively, the model can be translated into an indoor setting by reducing the number of gridsquares, which increases the notional population density. Hence, the effect of these factors can be investigated.

In addition, the model can be used to explore the efficacy of potential control measures. One such method for controlling infection is to improve on-farm hygiene. The model was used to explore the efficacy of two different cleaning strategies in reducing the prevalence in housed cattle. The first strategy involves cleaning out the entire housing environment (i.e. removing bedding, cleaning area and replacing with fresh material), which was modelled by setting the environmental contamination status

of all gridsquares to zero. The second strategy involves only the targeted cleaning of key infection hotspots, such as water troughs. This was modelled by eliminating any environmental contamination in the gridsquare containing the water trough.

## Results

The model simulated the two cleaning strategies carried out at both weekly and monthly intervals in a shed housing a herd of 20 cattle in which only one animal was initially infected. The results are plotted in Figure 3.

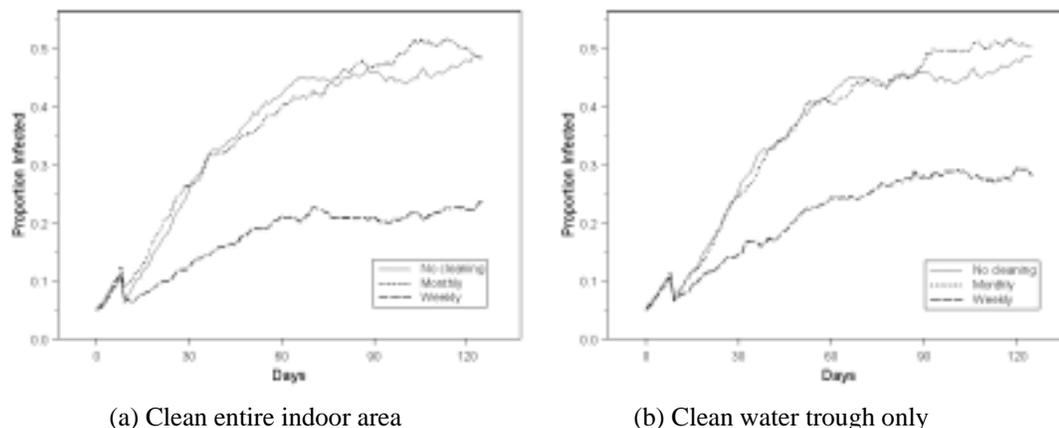


Figure 3: Comparison of the proportion of a housed herd of size 20 that is infected, over time, using different cleaning strategies at monthly and weekly frequencies.

## Discussion

The similarity of the results obtained from the two different cleaning approaches suggests that the most important factor in controlling the infection is the frequency at which these potential control measures are implemented. Furthermore, the model demonstrates that the frequent, targeted cleaning of a few key bacterial reservoirs within the herd environment is likely to be more effective than less frequent cleaning of the entire environment. Thus, the implementation of biosecurity controls, such as frequent cleaning of water troughs, could dramatically reduce the within-herd prevalence.

## References

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