

# Assessing The Effectiveness Of Clinical Disease Surveillance Of Cattle In Great Britain In Detecting New Epidemic Strains Of Salmonella

## AUTHORS AND DETAILS:

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## ABSTRACT

*Salmonella* is an important human and animal pathogen. Taking into account under-reporting, there were likely over 36,000 cases of human Salmonellosis in 2006 in England and Wales (HPA, 2008, FSA, 2000). New and emerging strains of *Salmonella* could be introduced into Great Britain (GB), with potentially unknown zoonotic consequences. Early detection of these strains could help to restrict their spread and prevent them becoming endemic in GB. However, it is currently unknown how quickly and effectively current surveillance techniques in GB will identify a new *Salmonella* strain.

Therefore, we have developed a mathematical model to assess the time-dependent likelihood of detection for the emergence of a new *Salmonella* strain in the livestock population. The model is made up of three components: a within-herd transmission model, a between-herd transmission model and a surveillance model.

New *Salmonella* strains that are likely to be of concern will display certain characteristics. In discussion with microbiological experts, we investigated the following scenarios: increased transmission, increased virulence, lower infectious dose, increased shedding in cattle faeces, enhanced environmental survival and a combination of increased transmission and decreased virulence.

Strains with increased transmission lowered the time to detection, but more farms were infected. Increased transmission combined with lower virulence increased the number of holdings affected. However, the time for detection was significantly slower than for those strains with higher transmission alone. It is therefore likely any new epidemic strain would possess a combination of factors that would make detection unlikely before it had spread significantly in the cattle population.

Keywords: Salmonella, surveillance, transmission modelling, cattle

## INTRODUCTION

Outbreaks of *Salmonella* amongst the human population are common in GB (HPA, 2008) and have been attributed to many sources with consumption of beef as one potential source of human *Salmonella* infection (Hald *et al.* (2004), Havelaar, *et al.* (2008)). Further, it is well known that many strains of *Salmonella* are endemic in GB beef herds (VLA, 2007) and several of these endemic strains are virulent to cattle and can cause clinical disease, or salmonellosis in cattle.

As well as the current endemic strains, new and emerging strains of *Salmonella* could be introduced into GB with potentially unknown zoonotic consequences. Early detection of these new and emerging strains could help to restrict their spread and prevent them becoming endemic in GB, as is the case with *Salmonella* Dublin and was historically observed for *Salmonella* Typhimurium DT104. However, it is currently unknown how quickly and effectively current surveillance techniques in GB will identify a new *Salmonella* strain. This paper aims to use mathematical methods to quantify the probability of detecting *Salmonella* within GB beef herds and estimate the duration of time between initial infection and detection. This information can assist in estimating the likelihood of new strains entering GB being detected before they become endemic.

## MAIN TEXT

The model simulates the *Salmonella* transmission process both within and between beef farms. In the within-farm model, suckler calves mature and, when old enough, become an adult suckler cow or move to a finishing herd. This simulation process was followed over a four year period. For the purposes of this model, the farm consisted of both a suckler and finishing herd. Between farm transmission was simulated in this model by determining whether animals leaving the within-farm model were infected and whether they will

introduce infection into the herd to which they are moved. The model also includes surveillance techniques that estimate when a farmer thinks he has a disease problem on his farm and decides to call a veterinarian. Isolations of *Salmonella* from livestock are reportable under the Zoonoses Order 1989 in GB. We assume that if a vet is called to a disease outbreak on a beef farm, diagnostic samples would be taken and tested at a laboratory and if *Salmonella* was isolated this would be reported to Defra. However, it should be noted that full test results would be likely to take around 14 days from submission. Thus, the model determines the time from the initial seeding of infection to detection of *Salmonella*, which we assume to be when the farmer calls the veterinarian.

A new and emerging strain of *Salmonella* might have different characteristics than other strains, such as an increased likelihood of causing disease or the ability to survive longer in the environment. To investigate the effect of these different characteristics we develop a baseline model (i.e. a baseline strain of *Salmonella* with particular characteristics) and then perform different scenario analyses to represent different strains of *Salmonella*, where we change particular characteristics of the baseline strain, in order to observe the predicted effect on spread and detection. To model the effect of new and emerging strains of *Salmonella* within the model framework, we modify a selection of *Salmonella* dependent parameters to simulate different characteristics. We have modelled 5 strains, each with different characteristics: high transmission (Increase probability of transmission), high virulence (Increase probability of infection resulting in clinical signs), lower infectious dose (lower the dose-response, so that animals are more easily infected), increased shedding (increased level of *Salmonella* to be shed in the faeces of asymptomatic cattle), enhanced survival (Increased *Salmonella* survival time in the environment) and a combination of high transmission and low virulence.

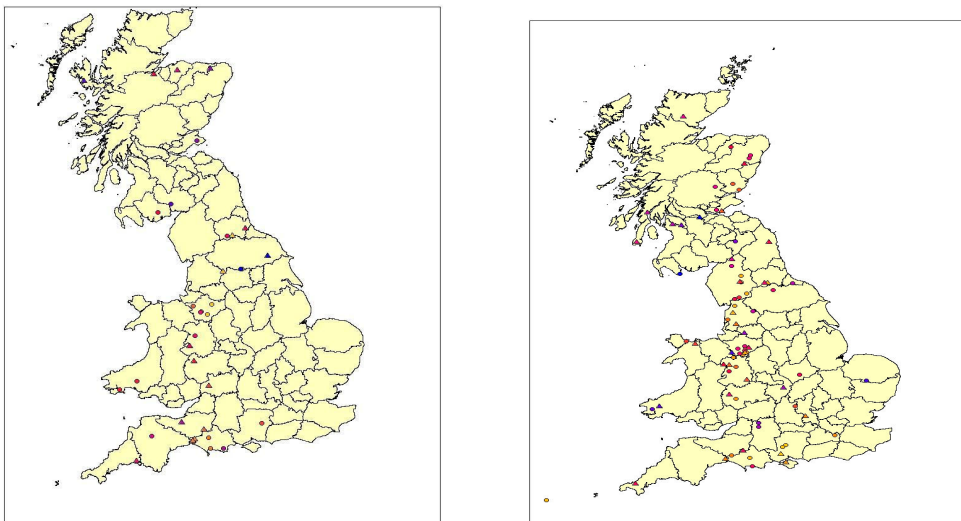
For each scenario, the baseline model is adapted and a simulation run for 5000 iterations. Each iteration represents an initial infection, on a primary farm, of one animal with the scenario strain. The model is then run over 730 days during which time the strain may spread to secondary farms and/or be detected by surveillance techniques. The primary farm for each iteration differs to encompass the variability in types of management practices (e.g. herd size, number and date of cattle movements) employed in GB.

The results of the scenario analysis are shown in Table 1. It can be seen that the characteristics that have the biggest effect on both between farm spread and the probability of detection (i.e. veterinarian being called), compared to the baseline model, are transmission and virulence (i.e. probability of developing clinical signs). In both cases if the parameters relating to these characteristics are increased then the probability of between-farm spread from the primary farm and the probability of calling the veterinarian are increased. It can also be seen that for high virulence the average time to detection (i.e. calling the vet) decreases from the baseline, as would be expected due to the increased probability of clinical symptoms. It is interesting to observe that the scenario with high transmission but low virulence shows an increase in between-farm spread and probability of detection but a smaller decrease in time to detection. This is likely due to the lower proportion of animals showing clinical signs, making it harder for the farmer to be aware that there is *Salmonella* on the farm and therefore less likely to call the vet (given the current model assumptions). The last row of Table 1 shows that for the high transmission and high virulence strains that is a greater chance of *Salmonella* spreading to a secondary farm before it is detected on the primary farm.

**Table 1: Scenario analysis results: each scenario consists of a run of 5000 farms**

	<i>Baseline</i>	<i>Enhanced survival</i>	<i>High transmission / low Virulence</i>	<i>High transmission</i>	<i>High virulence</i>	<i>Increased shedding</i>	<i>Low dose</i>
% farms with secondary spread	0.32%	0.44%	3.04%	2.82%	0.50%	0.38%	0.40%
Prob. vet call on primary farm	4.42%	6.66%	26.78%	28.06%	10.12%	5.14%	5.14%
mean days until detection	17.55	18.94	20.88	22.43	14.64	18.67	19.20
% farms where secondary spread occurs before detection	0	0	0.08	0.04	0.02	0	0

Figure 1 shows the spread of infection between farms over time for the baseline and high virulence strains. It can be seen for the baseline strain that only a small number of initial infections result in secondary spread to other farms. When secondary spread does occur, the number of secondary farms infected is small and is generally geographically localised. However for the high virulence strain it can be seen that secondary spread occurs more often than for the baseline strain. Also more secondary farms can be infected resulting in wider geographical spread.



**Figure 1: Maps showing spread of infection for the baseline (left) and high virulence (right) strains. Triangles represent primary farms, circles secondary infections and different colours represent different 'outbreaks'.**

## CONCLUSION

The model discussed in this paper aims to describe the transmission of *Salmonella* both within and between farms and investigate the comparative spread and detection of strains of *Salmonella* with different characteristics. Infection was seeded into one adult suckler cow on a primary farm and the model was run for 730 days to investigate the within-farm spread and the spread of infection to secondary farms. Using this approach it was estimated that, on average, 2.01% of finishing cattle, 1.68% of calves and 1.41% of suckler adults were infected, which is consistent with data from a United Kingdom abattoir study which found the prevalence of *Salmonella* faecal carriage to be 1.4% (Milnes *et al.* 2008). It was estimated that between-farm spread would occur from 0.32% of primary farms and 4.42% of primary farms would call the vet to investigate their cattle. The average time until the vet was called was 17.55 days. A scenario analysis showed that strains of *Salmonella* with higher transmission or virulence would be detected more often and in almost half the time, but would still cause a larger amount of between-farm transmission.

## REFERENCES

- Hald, T., Vose, D., Wegener, H.C., Koupeev, T. (2004). A Bayesian approach to quantify the contribution of animal-food sources to human salmonellosis. *Risk Analysis*, 24(1), 255-269.
- Havelaar, A.H., Galindo, A.V., Kurowicka, D., Cook, R. (2008). Attribution of Foodborne Pathogens Using Structured Expert Elicitation, *Foodborne pathogens and disease*. 5(5), 649-659.
- HPA, (2008). *Salmonella* in humans, England and Wales, 1981 – 2006. [http://www.hpa.org.uk/webw/HPAweb&HPAwebStandard/HPAweb\\_C/1195733760280?p=1191942172078](http://www.hpa.org.uk/webw/HPAweb&HPAwebStandard/HPAweb_C/1195733760280?p=1191942172078).
- FSA, (2000). A report of the study of infectious intestinal disease in England. The Stationery Office, London.
- Milnes, A.S., Stewart, I., Clifton-Hadley, F.A., Davies, R.H., Newell, D.G., Sayers, A.R., Cheasty, T., Cassar, C., Ridley, A., Cook, A.J., Evans, S.J., Teale, C.J., Smith, R.P., McNally, A., Toszeghy, M., Futter, R., Kay, A., and Paiba, G.A. (2008). Intestinal carriage of verocytotoxigenic *Escherichia coli* O157, *Salmonella*, thermophilic *Campylobacter* and *Yersinia enterocolitica*, in cattle, sheep and pigs at slaughter in Great Britain during 2003. *Epidemiology and Infection*, 136, 739-51.
- VLA, (2007). *Salmonella* in livestock production in GB, 2006, defra. ISBN 1 8995 1329 3.

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