

A farm transmission model for Salmonella in pigs for individual EU Member States

Hill, A. 1*

Simons, R. 1, Swart, A. 2, Kelly, L. 1, Hald, T. 3, Snary, E. 1

1 Veterinary Laboratories Agency, Woodham Lane, New Haw, Surrey, UK

2 National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands.

3 National Food Institute, Technical University of Denmark, Søborg, Denmark.

* Veterinary Laboratories Agency, Woodham Lane, New Haw, Surrey, KT15 3NB, United Kingdom.

e-mail: a.hill@vla.defra.gsi.gov.uk; fax: +44 (0) 1932 357 445

Abstract

The burden of Salmonella entering pig slaughterhouses across the European Union (EU) is considered to be of public health significance. Therefore, targets will be set for each EU Member State (MS) to reduce the prevalence of Salmonella in pigs at slaughter. As part of the evidence base for the development of National Control Plans (NCPs), a Quantitative Microbiological Risk Assessment (QMRA) was funded to support the scientific opinion required by the EC from the European Food Safety Authority, and subsequently adopted by the BIOHAZ panel. We present the farm transmission model component of the QMRA, which was used to model the transmission of infection between pigs and investigate the effect of on-farm interventions in reducing human salmonellosis attributable to EU pig meat consumption.

The magnitude of Salmonella shedding by the sow was a good predictor of eventual batch prevalence in slaughter pigs, as the subsequently infected piglets became a large source of Salmonella once mixed during weaning. As a direct result of this effect, it was concluded that MSs with high breeding herd prevalence (i.e. > 10-15% of breeding herds are infected with Salmonella) must tackle the breeding herd as part of any NCP in order to achieve a significant reduction in national slaughter pig prevalence. Conversely, it was predicted that MSs with low breeding herd prevalence would benefit most from controls on feed contamination, as this becomes relatively more important as a route of transmission of Salmonella when the sow is rarely a source of infection.

Introduction

The burden of Salmonella entering pig slaughterhouses across the EU is considered a primary food safety concern. Therefore, through EU legislation, targets are being set for each MS to reduce the prevalence of Salmonella infection in pigs at slaughter (probably as measured by infection of the ileo-caecal lymph node). These targets will be based on scientific studies commissioned by the EC/EFSA, including a QMRA. The primary aim of the QMRA was to assess the effectiveness of on-farm and abattoir interventions in reducing Salmonella levels in pigs and/or humans. In this paper we discuss in detail the Farm model, which describes the transmission of Salmonella within pig herds, and which can be used to investigate interventions that may reduce prevalence in pigs at slaughter.

Infectious disease transmission models have been developed for a variety of animal diseases, including Salmonella in pigs (Hill et al. 2008; Lurette et al. 2008) and are now often used within a full farm-to-consumption QMRA in order to predict the impact of on-farm interventions on public health (e.g. Simons et al. In Preparation). Typically these models have become more detailed over time and in the case of a recent study the traditional use of "general" transmission parameters was replaced by specifically modelling the environmental transfer of Salmonella via the faecal-oral route (Lurette et al. 2008). A transmission parameter is essentially a "black-box", which encompasses many different factors, including the resistance of the pig to infection and the level of contamination in the environment. However, in order to investigate interventions (such as cleaning and disinfection, vaccination etc...) it is necessary to differentiate between those factors that increase/reduce the level of contamination in the environment and those factors that affect the resistance of the pig to infection. The farm model was designed to be generic and can be parameterised (given relevant and available data) to represent any EU MS. In this paper the results from two case study MSs are described (one "low-prevalence" MS (MS1) and one "high-prevalence" MS (MS2)).

Material and Methods

The farm model is an individual-based stochastic Susceptible-Infected-Susceptible (SIS) model, therefore considering the infection status of every individual pig on a farm. The model is implemented using Monte-Carlo simulation and run for 1000 iterations, where each iteration represents production from one farm over a 500 day period, incorporating farrowing, weaning, and grower and finisher production. Management factors (for example flooring, feed type used) were used to define farm types. Farm types were allocated proportionally to the 1000 farms to represent the national structure of the pig herd within a particular MS, based on data from the EFSA breeding pig survey (EFSA, 2009). Over the 500-day cycle of production batches of pigs are sent to slaughter on a weekly basis. Two outputs are generated for each batch of pigs sent to slaughter: the prevalence of lymph-node infection and a distribution for the concentration of Salmonella shed within the faeces of infected pigs.

For each iteration there are a large number of spatial and temporal events that can occur at random, including the seeding of infection into the farm, the response to exposure (in terms of whether or not infection occurs given exposure to a particular dose) and subsequently the shedding rate. All farms are set to be Salmonella-negative at the start of an iteration (day 1). There are four assumed sources of infection: sows, feed, wildlife and the introduction of new infected stock. Following initial infection of the herd, which can occur at any time, transmission is described by an individual-based environmental infection model, which tracks i) the shedding and inactivation/movement of Salmonella in the environment and ii) the dose-response of pigs exposed to environmental contamination (see Figure 1). The schematic is appropriate for all rearing stages: farrowing, weaning, growing and finishing.

More detail on the methods and data used to parameterise the model can be found in the full QMRA report (EFSA, 2010).

Results

The average within-batch prevalence of lymph-node positive pigs at slaughter age was estimated to be 0.007 (5th percentile 0, 95th percentile 0.031) for MS1, and 0.176 (0, 0.813) for MS2. The percentage of positive batches for MS1 and MS2 were estimated to be 38.0% and 62.9% respectively. Comparing the percentage of positive batches with the average within-batch prevalence shows that the majority of batches are infected at low levels, even in "high"-prevalence MSs such as MS2.

Figure 2 summarises the impact of each source of infection (sow, feed, external contamination including wildlife) in determining the slaughter pig prevalence within the two case study MSs. Within MS2 reducing breeding herd prevalence to zero (i.e. $p_{\text{breedingherd}} = 0$) removes the vast majority of infections at depopulation; conversely, removing feed or external contamination as sources does little to change the national pig prevalence. This result suggests that the sow is a major source of infection; only when sow infection is rare (as in MS1), does feed play an important role in determining slaughter pig prevalence.

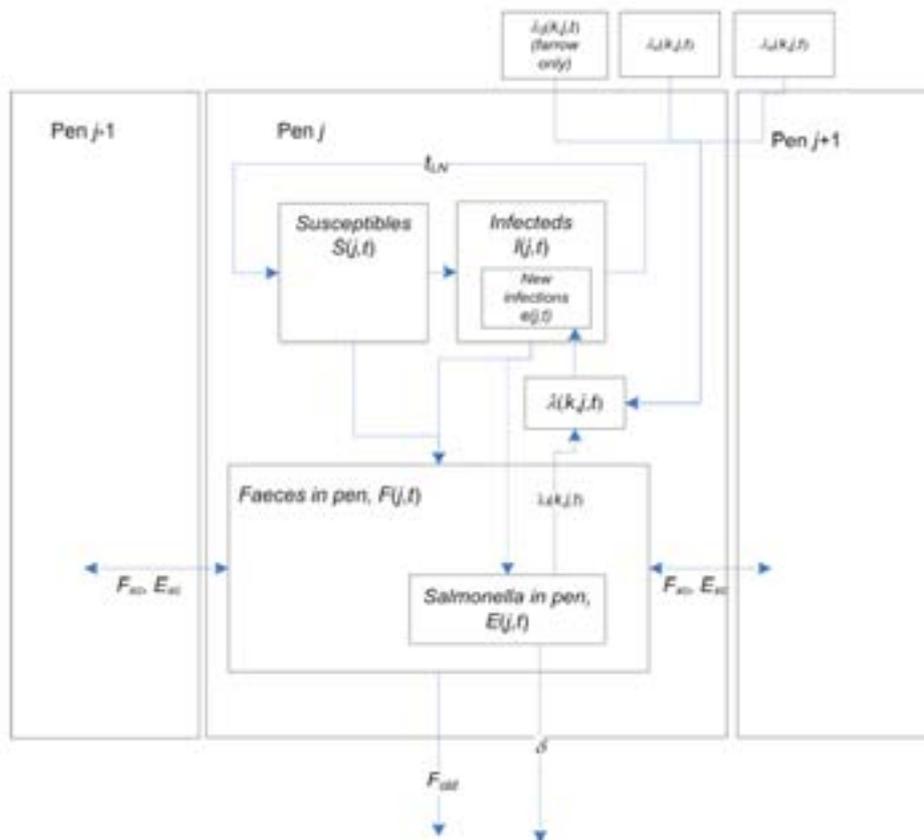


Figure 1: Schematic diagram of transmission model. Only the interactions associated with pen(j) are shown. The total faecal material in the pen, $F(j,t)$, is added to each day by Susceptibles ($S(j,t)$), Infecteds ($I(j,t)$) and cross-contamination from other pens (F_{xc}) while it is simultaneously reduced each day via cross-contamination (F_{xc}) or removal (F_{dt}). This faecal material contains $E(j,t)$ salmonellas, which are added to each day from the infected group via shedding in their faeces and reduced each day as a result of decay, λ , and cross-contamination E_{xc} . Each pig k ingests λ_1 organisms per day via the amount in the faeces, λ_2 via feed and λ_3 via the environment and $\lambda_3 = 0$ unless pig k is a piglet in farrowing). This process results in $e(j,t)$ new infections according to the dose ingested and the dose-response relationship applied.

Discussion

Analysis of the model pointed to one overwhelming conclusion: the level of infection within a MS's breeding herd largely determines the slaughter pig prevalence for that MS. However, in low prevalence MSs of which MS1 is typical, infection of the sow is relatively rare and the proportion of initial infections of a piglet, weaner etc. via either feed or external contamination are relatively much higher. This result of breeding herd prevalence determining slaughter pig prevalence is supported by data from the EFSA Salmonella in pig surveys; breeding herd prevalence was correlated with slaughter pig prevalence (EFSA 2008, 2009).

Conclusion

In summary, breeding herd prevalence is likely to be a strong predictor of national pig prevalence and feed only becomes an important source of infection once contamination of the environment by sows or other slaughter pigs is reduced to low levels.

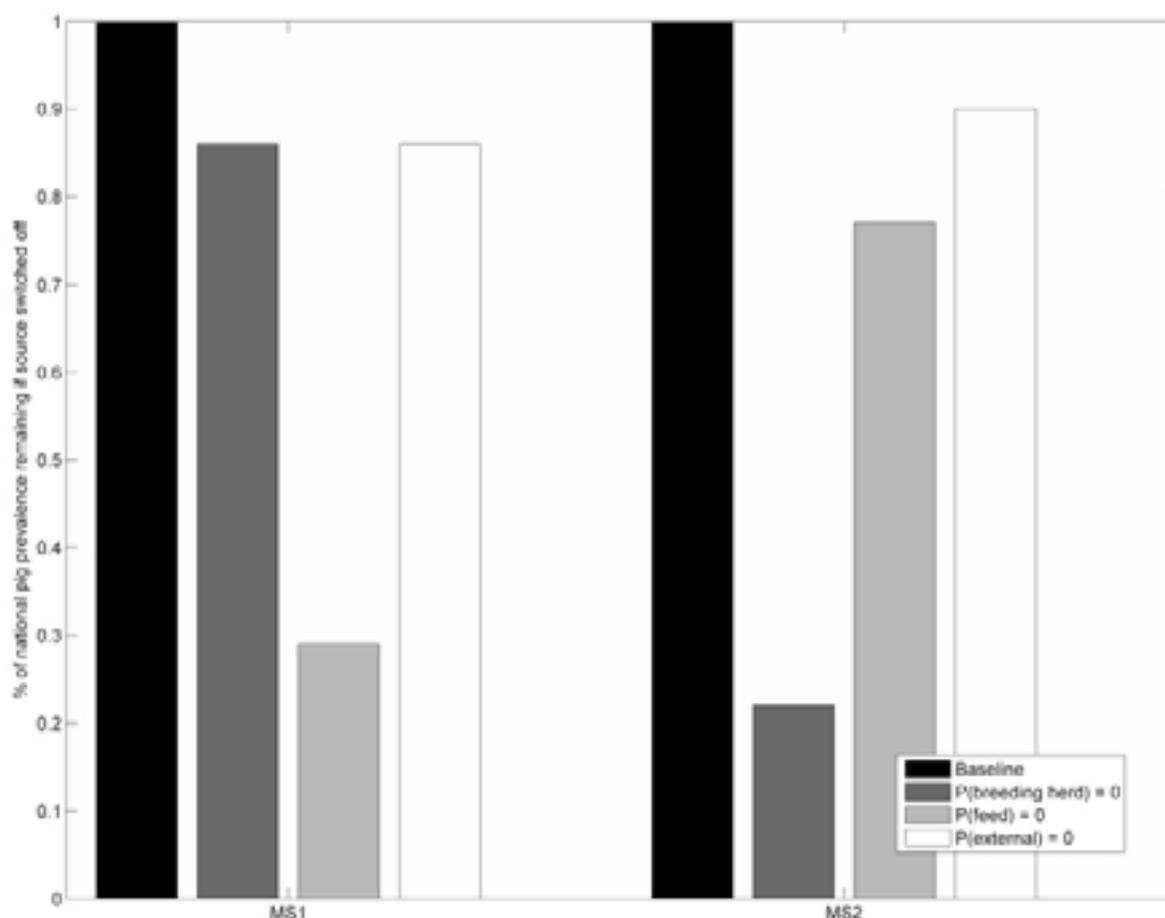


Figure 2: Relative impact on national pig prevalence for MS1 and MS2 if each source of infection is set to zero. Baseline (black), breeding herds all negative (dark grey), feed all negative (light grey), no external contamination events (white).

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