Modelling the Epidemiology of Salmonella in the Pork Supply Chain

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ABSTRACT

The interest in reducing the incidence of food-borne diseases, such as salmonellosis caused by pork is increasing. All stages in the pork supply chain can take preventive and reductive measures to decrease the Salmonella prevalence. But it is necessary to have insight in the effect of these measures on the final prevalence of contaminated carcasses. In this way imposing expensive but ineffective measures can be avoided. In order to be able to obtain such evaluations, a stochastic state-transition model is designed. Five stages are included (from piglet to carcass) and two risk-profiles are formulated for each stage: high-risk and low-risk. Scenario studies with the model indicate that all stages may contribute to an increased food safety. The impact of the multiplying stage is limited, because the animals may recover during the finishing stage. Recovery after the finishing stage is not possible, although the transport and lairage can prevent further transmission. At the slaughterhouse the number of contaminated carcasses is highly determined by the prevalence of the supplied animals and the risk profile. Measures in the finishing stage are effective in the reduction of Salmonella in pork, but may be cancelled out if the following stages do not take preventive and reductive measures.

INTRODUCTION

Over the past decade food-borne diseases such as listerosis, Escherichia coli infections and salmonellosis have caused a decrease in the consumers' confidence in the safety of meat. In industrialised countries it is estimated that 5 to 30% of all cases of food-borne salmonellosis has pork as the actual source (Berends et al. 1998) and the occurrence of human salmonellosis seems to follow the presence of Salmonella in farm animals (Van Pelt et al., 1998). Prevention and control measures accompanied by improved organisation, management and information flow in the supply chain contribute to the reduction of the incidence of food-borne diseases (e.g. Van der Wolf, 1999). Up to now, decontamination of the carcasses is prohibited in the EU, so the objective is to reduce contamination in the pork chain to an acceptable level. Newly introduced regulations and prevention strategies should be based on a risk assessment to avoid too expensive or less effective measures.

In this paper the case of Salmonella (S.) in the pork supply chain is elaborated in a detailed simulation model. The purpose of the model is to analyse the epidemiological consequences of interventions designed to optimise the food safety of pork in the supply chain with respect to Salmonella. To demonstrate these effects, scenario studies were carried out in order to obtain an optimal combination of interventions in the chain to minimise the prevalence of Salmonella in pork.

MATERIALS AND METHODS

The pork supply chain

Figure 1 shows the pork supply chain which consists of 5 stages: the multiplying stage (Mu) where the piglets are produced, the finishing stage (Fi) to grow the pigs to slaughterweight, transport (Tr) to the slaughterhouse, the lairage (La) where the pigs stay for several hours before being slaughtered (Sl). Each stage contains several farms or firms with their own specific risk profile. This risk profile depends on the decisions or measures that are taken to prevent or reduce the introduction or spread of Salmonella. Besides general measures like good hygiene that are important in all stages, specific measures can be taken in each stage. In this paper two risk profiles are designed for each stage: a high-risk profile and a low-risk profile. The measures that are taken at the low-risk farms and firms are based on literature (e.g. Blaha, 2000; Van der Wolf et al., 1999; Stege et al., 2001) and the results of a recently carried out Dutch expert survey (not published yet). Table 1 shows the differences between the high-risk and the low-risk profile. Logistic supply and slaughter (implying S. free animals first) is not included in this scenario. To simulate the influence of the risk-profile of a farm or firm on the performance of the chain different combinations of contact structure are compared. To demonstrate the possibilities of the model, a selection of six different combinations are presented (see Figure 1). The first combination (path 1) indicates that the groups of pigs run through only low-risk farms and firms and in combination 6 through only high-risk farms and firms.

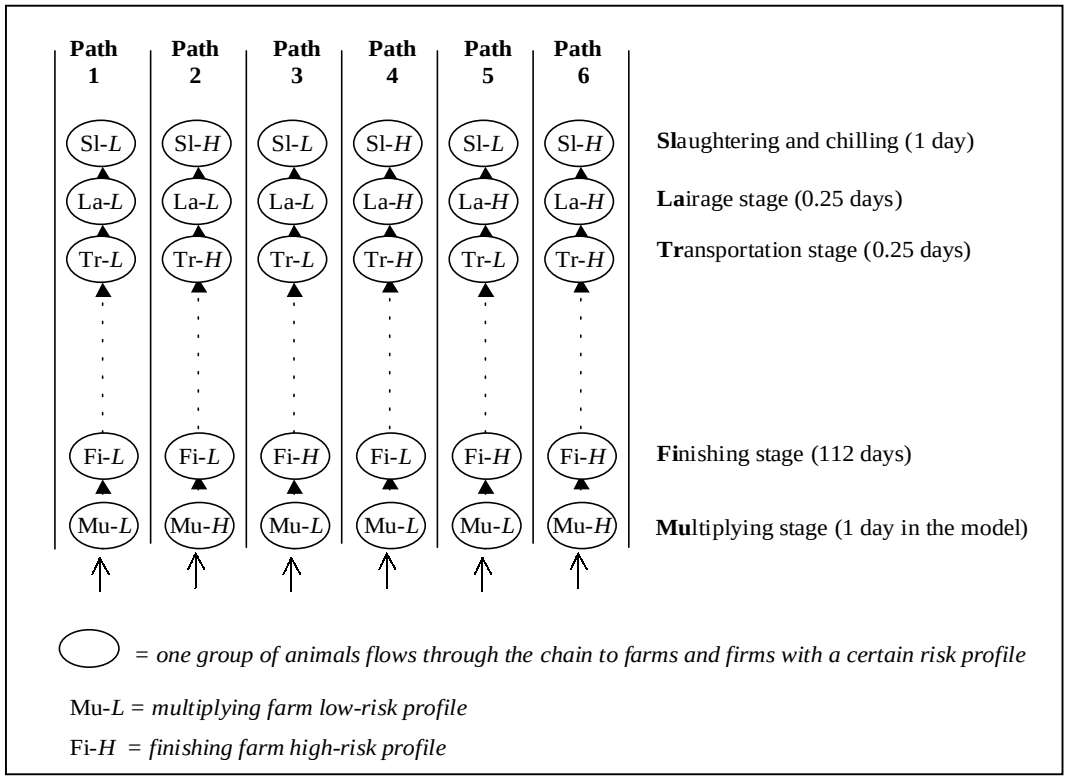


Fig. 1. Design of the contact structure of the pork supply chain in the simulation model

Table 1. Most important measures taken at low- and high-risk farms and firms

	Low risk profile	*High risk profile*
Multiply	- certified S. free feed - fermented feed for piglets - functional hygiene lock - cleansing and disinfecting each round	- pelleted feed with unknown S. status - free entrance for visitors - no structural rodent control
Finishing	- purchase of certified S. free piglets - fermented feed for pigs - functional hygiene lock - no contacts between compartments	- pelleted feed with unknown S. status - free entrance for visitors - no structural rodent control - no all in-all out
Transport	- cleansing and disinfecting each ride - smooth, good cleansable materials - quite driving and short distances	- no fasting of pigs before transport - pigs from several compartments of finishing farm in one truck
Lairage	- good internal hygiene - reduced duration in lairage (< 2 hours)	- mixing of pigs from different origin - open fences between compartments
Slaughter	- cleansing equipment during the day - careful evisceration	- no direct packing of rectum - less time per pig for evisceration

The simulation model

The stochastic state-transition approach is most convenient for modelling the epidemiology of infectious diseases (Buijtels et al., 1997). Such an approach consists of two elements: states represented in a columnar state vector $\mathbf{x}(t)$ and transition probabilities defined in a time-dependent matrix of transition probabilities $\mathbf{P}(t)$ (Winston, 1994). From one time step to the next, transitions between states can occur, depending on the transition probabilities. The probabilities $p_{i,j}(t)$ determine how the process will evolve over time. Every time step the number of individuals in each state is calculated thereby providing a new distribution of the individuals over the states in state vector $\mathbf{x}(t+1)$. The probabilities $p_{i,j}(t)$ in the matrix ($\mathbf{P}(t)$) are used for a Monte Carlo simulation for each individual in $\mathbf{x}(t)$. The values of the probabilities depend on the risk profile of the farm or firm. The time step used in the Mu-, Fi- and Sl-stage is one day and for the stages Tr and La 0,5 days. One run carried out 10.000 timesteps.

Six different states are distinguished and the transitions depend on the risk profile of the farm or firm. The basic unit of the model is a group of 100 pigs. For live animals the course of infection is described by the following transition through the six states (see Figure 2). All animals start being non-infected in state S1 (susceptible). When the animal gets infected it goes to I1 (infected and infectious, negative serology), after the seroconversion period it goes to I2 (infected and infectious, positive serology). After the infectious period has ceased naturally, the animal becomes a carrier (bacteria present in e.g. lymph nodes) for a certain period and then becomes susceptible again (S2, positive serology). A S2 animal can be re-infected (I3) or become serological negative (S1).

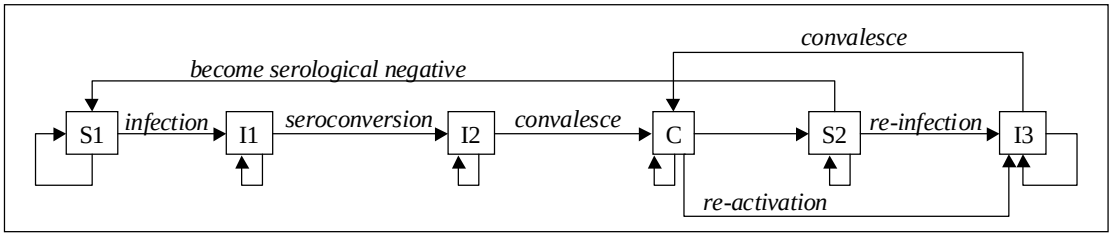


Fig. 2. Course of Salmonella infections over six states in live pigs.

At the slaughterhouse the possible transitions are decreased and after chilling a carcass has four possible states, which determine the bacteriological and serological status: S1, S2, I1, I3.

The input and output of the model

The input parameters used in the model for this paper are exemplary values, because most values are not known (yet) in literature. The major input parameter is $p_{S1,I1,}$ because this transition is the driving force in the model. $P_{S1,I1}$ has three components: Pgroup(t) (probability for an individual to become infected by an infectious group member), Pfarm(t) (probability to become infected by indirect contact with infectious animals in other groups at the same farm) and PE (probability to become infected by external vectors like visitors, feed, rodents etc.). Pfarm(t) as applied in finishing stage and Pgroup(t) for all stages except the slaughter stage depend on the number of infectious individuals in the group and farm (Buijtels et al. 1997) and are calculated by:

$$P(t) = 1 - e^{-\beta*(I/N)} \quad (1)$$

β = infection rate (# animals that can be infected by one infectious animal in Δt)
I/N = fraction infectious animals (# infectious animals/ total # animals)

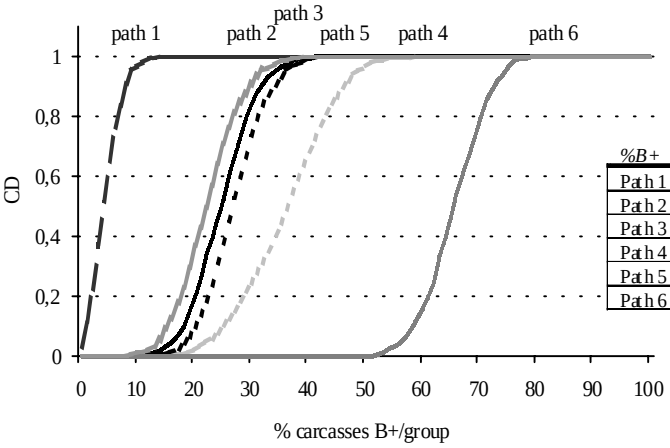
The infection rate within a group (βgroup) for low-risk farms is 0.2 and for high-risk farms βgroup is 2. The infection rate within a low-risk finishing farm is 0.005 and within a high-risk finishing farm 0.05. The PE for low-risk farms is set to 0.001 and for high-risk farms 0.01. In the lairage groups from different finishing farms are gathered together, so the Pfarm(t) is calculated by determining an infection pressure for the lairage using the prevalence of groups entering the lairage. In the slaughter stage the animals from one group are slaughtered in random order. During evisceration bacteriological positive animals may become negative (probability for low-risk slaughterline is 0.5 and for high-risk 0.25). Bacteriological positive animals may contaminate animals that are slaughtered subsequently. This risk depends on the number of subsequent positive animals and on the risk profile of the slaughterline.

The output of the model is the prevalence distribution of infected animals and contaminated carcasses at the end of each stage.

RESULTS AND DISCUSSION

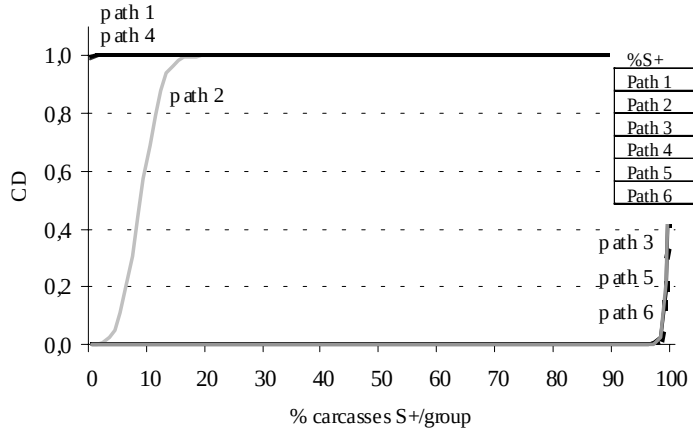
Because the purpose is to improve food safety, the number of contaminated carcasses at the end of the slaughterline is most interesting. Figure 3 presents the cumulative density function (CDF) of the percentage of bacteriological positive carcasses (B+) per group at the end of the slaughterline for each path and the minimum, maximum, average percentage and the variance. As expected, path 1 with all stages low-risk profile, shows the lowest average prevalence of bacteriological carcasses (5% B+) and path 6, with all stages high-risk profile, the highest average prevalence (65% B+). The increase of B+ in path 3 compared to path 1 is totally attributable to the high-risk finishing farm. If besides the finishing farm the lairage also has a high-risk profile (path 5) the percentage of contaminated carcasses after slaughter does not increase. Animals that became infected at the lairage do not become contaminated carcasses, because of the low-risk slaughtering. The impact of a high-risk profile finishing farm is high. In path 2 three stages have a high-risk profile and the percentage B+ is similar to path 3. Path 4 is interesting because prevalence before transport is very low (low-risk MU and Fi), but the contamination during transport, lairage and slaughter causes a higher average prevalence

(36%) and the variance doubles as a consequence of the stochastic elements in the introduction and spread in all stages.



%B+	Min. %	Max. %	Avg %	Var.
Path 1	0	15	5	7
Path 2	7	43	23	31
Path 3	7	44	25	29
Path 4	15	65	36	65
Path 5	10	44	27	28
Path 6	50	82	65	29

Fig. 3. Cumulative density function of the percentage of bacteriological positive carcasses/group and the minimum, maximum, average and variance/path



%S+	Min. %	Max. %	Avg %	Var.
Path 1	0	1	0	0
Path 2	1	19	9	8
Path 3	97	100	99.7	0.2
Path 4	0	1	0	0
Path 5	98	100	99.7	0.2
Path 6	97	100	99.7	0.2

Fig. 4. Cumulative density function of the percentage of serological positive carcasses/group and the minimum, maximum, average and variance/path

Figure 4 shows the CDF of the percentage of serological positive carcasses (S+) per group at the end of the slaughterline. It takes approximately 12 days to become serologically positive after an infection, so infections as from 11 days before slaughter are not detectable with serology testing. A positive serology indicates that the animal has been infected during its live. A negative serology indicates either the animal has never been infected or the level of antibodies is below the detection level. The latter possibility is less likely than the first one. All paths where the finishing farm has a high-risk profile almost all animals are serologically positive. The percentage of S+ carcasses at the slaughterline in path 2 is attributable to the high-risk multiplying farm. When both the multiplying and the finishing farm have a low-risk profile (path 1 and 4) only a few animals are serological positive. At these farms there is also a small probability to get infected (PE), but the measures taken prevent further spread within the group and farm.

Promising measures as logistic transport and logistic slaughter are based on the serology of the animals. The results from the path 1 and 4 show that the risk-profile of the stages transport, lairage and slaughter have to included to reach a better food safety.

CONCLUSIONS

Results using a detailed simulation model for the entire chain clearly indicate that the efforts of one farm or firm are highly associated with the efforts in the other stages of the chain. So specific information exchange on performance at other stages is essential to improve the safety of pork products. The impact of the multiplying stage is limited, because the animals may recover during the finishing stage. Recovery after the finishing stage is not possible, although the transport and lairage can prevent further transmission. At the slaughterhouse the number of contaminated carcasses is highly dependent on the prevalence of the supplied animals and from the own risk profile. Measures in the finishing stage are effective for the reduction of Salmonella in pork, but may be cancelled out if the following stages do not take preventive and reductive measures.

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