9th International Society for Veterinary Epidemiology and Economics (ISVEE) Symposium, 2000 August 6-11, Breckenridge Colorado

SALMONELLA CONTROL IN THE PORK SUPPLY CHAIN

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In industrialised countries, foodborne illness of microbial origin is considered the most serious food safety problem (3) of which *Salmonella* spp. are the most costly ones. The occurrence of human salmonellosis seems to follow the presence of *Salmonella* in farm animals (4). It is estimated that 10-15% of the human salmonellosis cases is caused by pork (1). 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. Simulation modelling is a very suitable tool to get more insight in the epidemiological effects of measures throughout the pork chain. In this paper the design and type of output of a conceptual simulation model is presented.

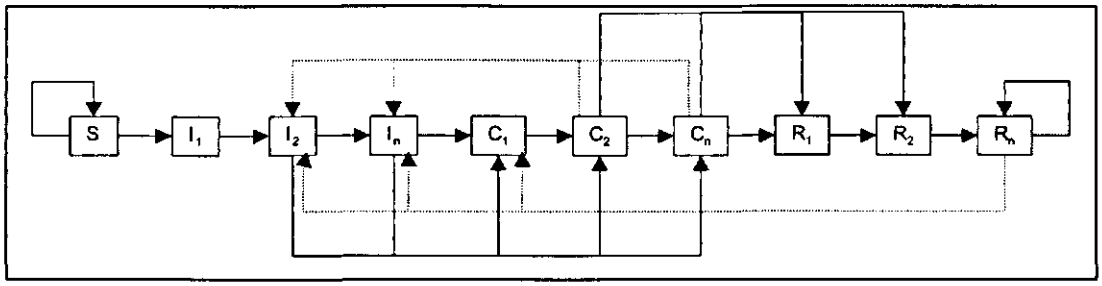
Salmonella in the pork supply chain

One of the complexities of salmonellosis is the existence of over 2400 serotypes. The model focuses on *S.* typhimurium, the most common type in pigs in the EU. The following stages of the pork supply chain are included: multiplying – transportation piglets – fattening – transportation pigs – slaughtering. The estimated percentage of farms with some degree of any *Salmonella* prevalence is rather high (in the Netherlands about two third), although the percentage of infected pigs at the farm can vary strongly between and within farms (1). Many risk factors with respect to *Salmonella* are known qualitative, but the knowledge of the quantitative impact is limited. The control measures included in the model are based on risk factors that are important for the introduction and internal spread of *Salmonella* and for the interactions between the stages, e.g. measures on hygiene protocol, cleansing and disinfecting procedures, number of suppliers and feeding management.

Method: a stochastic simulation model

The model is built in Borland Delphi 5 and based on the Markov chain approach combined with Monte Carlo simulation. The duration of the time steps varies from a week (primary stages) to an hour (slaughterhouse). The basic unit of the model is a group of 100 pigs. The animals of each group are situated in the following distinguishable, time dependent states in state-vector X_t: susceptible to an infection (S), infected and shedding the pathogen (I), carrier of the infection but not shedding (C), recovered from an infection and temporarily immune for re-infection (R), or dead (D) (2). In the primary production the I-, C- and R-state are subdivided in 5 sub-states, resulting in a state matrix of 17 states: S, 5 I, 5 C, 5 R and D. At the end of the

slaughterhouse there are only two states effective (susceptible and infected). In this way distribution of a group to the different states is simulated.
Figure 1 State transition model with Susceptible (S), Infected (I_x), Carrier (C_x),



Recovered (R_x). The arrows represent the transitions, no arrow means that transition is set to zero (not shown: in all states there is a small natural probability to die).

Each time step (t) the state vector X_t is multiplied by the transition matrix (P_t) in order to calculate the distribution of the state vector X_{t+1}. Transition probabilities can be zero, a fixed probability, stochastic or driven by other elements or parameters (e.g. the total number of infected animals in the group). The probabilities in the matrix also depend on the size of the farm or company and the control measures that are taken.

The supply chain is represented as a network, consisting of five stages (or layers). Within a layer, a number of farms or companies (or nodes) are distinguished (figure 2). The groups flow through the network and are traceable over time.

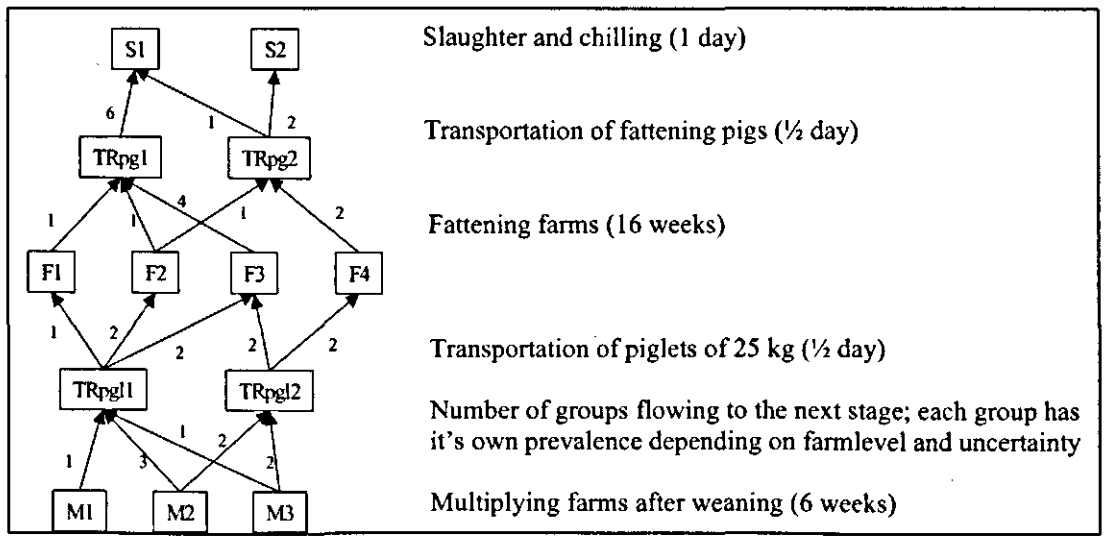


Figure 2 Design of the pork supply chain and the flow of groups of pigs

Preliminary results

Although the model is still in development, in figures 3 and 4 some important characteristics of the results are shown (note: mortality rate is set to zero). In figure 3 an example of the development of an infection in a group of fattening pigs during the

fattening period (16-17 weeks) is shown. The distribution of S, I, C and R in figure 3 is the outcome of one model iteration. In figure 4 the effects of control measures on the prevalence of delivered groups of pigs is illustrated, using 30 iterations per farm. Farm A practices stricter measures than farm B. The possible fluctuation per group in farm A is compared with farm B.

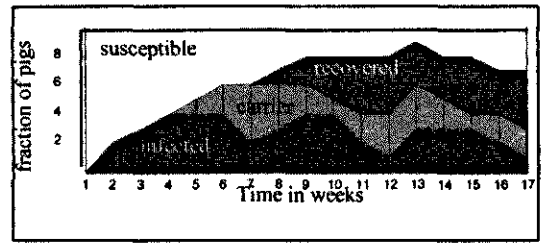


Figure 3 Prevalence of *Salmonella* in one group over time in fattening

In both farms there is a lot of fluctuation in the incidence of *Salmonella*. As expected the mean prevalence on farm A is much lower. The shape of the prevalence distribution of farm A seems to show less variance and a more even distribution than farm B, which also indicate more control.

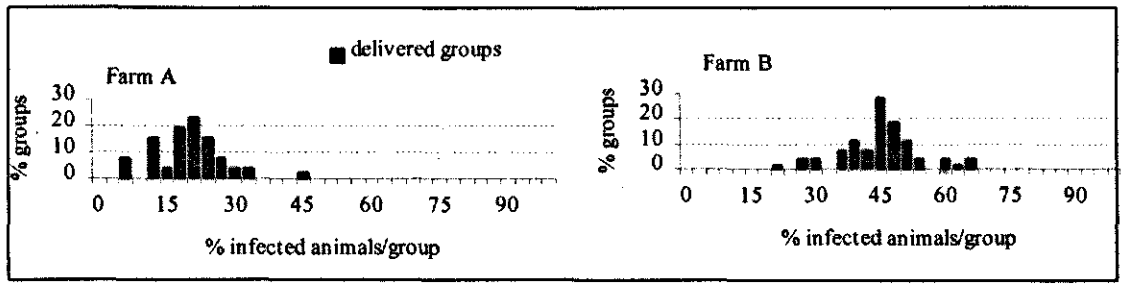


Figure 4 *Salmonella* incidence of groups of pigs in two farms with a different policy (farm A is stricter than farm B)

Discussion

The preliminary results indicate that the model allows exploration of the effects of control measures on the development of the infection in one group over time (figure 3) and the mean *Salmonella* level of groups of pigs with the variance (figure 4). Further development of the model includes improvement of the model input and calculation rules. Next, an extensive sensitivity analysis and validation will be realised and the economic consequences will be included. A major difficulty is to obtain input data from publications for the model, because of the different serotypes, aims, testing methods and experimental designs. Nevertheless, the model is useful to give insight in gaps of knowledge, weight of parameters, effects of investments in stages and effects in case of calamities. For future regulations these aspects are essential.

References

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