Predicting the Risk for Human Salmonellosis from Stochastic Modelling of *Salmonella* carcass Contamination and Decontamination in Slaughter Pigs

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ABSTRACT

A model was developed, that could supply estimates of the *Salmonella* concentration on carcass surfaces before and after decontamination and estimate the relative risk of human salmonellosis as a consequence of differences in Salmonella concentration between hygiene levels and decontamination effects.
From 5 Danish abattoirs app. 2000 paired samples of quantitative measurements of *E. coli* in faeces and *E. coli* in carcass swabs were obtained. From the same carcasses semiquantitative *Salmonella* concentrations were determined in faeces and carcass swabs. A stochastic simulation model was constructed to simulate the amount of faecal contamination per carcass and the distribution of *Salmonella* concentration associated herewith. Using a beta-poisson dose-response model the number of probable human cases was estimated.
A number of decontamination procedures were tested and the resulting reduction in *Salmonella* was used as input for modelling the number of human cases after decontamination
A difference in hygiene between abattoirs was observed and relative risk (RR) estimates for human salmonellosis were calculated for the various hygiene levels. Abattoir C served as reference as having the lowest risk. RR for the other abattoirs ranged from 1.24 to 3.57.
The effect of decontamination procedures gave a log reduction in the range 0.97 to 3.34 resulting in RR after decontamination in the range 0.28 to 0.004.
The output of the model allows calculating the value of improving slaughter hygiene by different means (HACCP, decontamination at the slaughter line, on-farm management procedures lowering the *Salmonella* count on the surface and in the gut contents of slaughter pigs).

KEYWORDS

Salmonella, slaughter hygiene, decontamination, risk, dose-response, stochastic modelling

INTRODUCTION

Hygienic slaughter procedures are essential in order to prevent faecal contamination of carcass surfaces with the associated risk of contamination of zoonotic pathogens as *Salmonella* and *Yersinia* (Borch et al, 1996). In connection with transport and lairage before slaughter the external surfaces of slaughter pigs are contaminated with faeces from pigs from the farm of origin and from pigs from other farms and a consequence there is a risk of external contamination with e.g. S*almonella* (Berends et al, 1996, 1997). Application of good hygiene practices in association with Hazard Analysis Critical Control Point (HACCP) is important for the microbiological quality of carcasses after slaughter and dressing (Hugas et al 2008). Recently, different decontamination technologies (physical, chemical and biological) have been investigated in order further to improve the hygienic standard of the end products (Huffman 2002)
In order to be able to evaluate the effect of hygienic measures in connection with slaughter and the effect of different decontamination procedures for pig carcasses, quantitative *Salmonella* data on carcasses after slaughter is needed. In addition the specific reduction effect of the decontamination has to be quantified. The model aims to supply estimates of the *Salmonella* concentration before and after decontamination and to estimate the relative risk of human salmonellosis as a consequence of differences in *Salmonella* concentration between hygiene levels and decontamination effects.

MAIN TEXT

From 5 Danish abattoirs app. 2000 paired quantitative samples of Escherichia coli in faeces and E. coli in carcass swabs were obtained. From the same carcasses semiquantitative Salmonella concentrations were determined in faeces and carcass swabs as described elsewhere (Sørensen et al., in prep). In short, presence of salmonella was studied by the MSRV method (ISO 6579, Annex D, Anonymous, 2007). The amount of faecal contamination per carcass (Amountfaeces) was calculated based on the concentration of E. coli in faeces (CFU_{gram_faeces}), the number of E. coli on the swabbed carcass area (CFU_{swab}) and the swabbed area in relation to the whole skin area of the carcass (app. one fifth of total skin area).

$CFU_{carcass} = CFU_{swab}*5.$ (1)

$Amount_{faeces} = CFU_{carcass}/ CFU_{gram\_faeces}$ (2)

For all abattoirs combined and for each individual abattoir the mean ($\bar{x}$) and standard deviation (sd) for $\log(CFU_{swab})$ and $\log(CFU_{gram\_faeces})$ was calculated.

The semiquantitative analysis of the concentration of Salmonella in faeces for all abattoirs yielded the number of Salmonella - positive observations in each of the intervals in Table 1 and the probability for a positive sample to fall into a specific interval was calculated.

Table 1

Semiquantitative intervals: 81 Salmonella-positive samples (out of 1716, prevalence 0.0472)

Interval CFU/g	Pos Obs	Probability
< 0.07	17	0.210
0.07-0.7	25	0.309
0.7-7.5	22	0.272
7.5-75	11	0.136
75-670	3	0.037
> 670	3	0.037
Total	81	1.000

A stochastic simulation model was constructed in @Risk (Palisade Corporation).

The model calculated the amount of faecal contamination per carcass by sampling from the normal distributions (Normal($\bar{x}$,sd)) for $\log(CFU_{swab})$ and $\log(CFU_{gram\_faeces})$ and inserting into equations (1) and (2). From the calculated amount of faeces per carcass the number of Salmonella organisms was estimated by sampling the Salmonella intervals in table 1 with the probabilities associated with each interval and utilizing a uniform distribution within the intervals. The resulting number of Salmonella (CFU/g) was then multiplied with the calculated amount of faeces yielding the number of Salmonella per carcass.

The distribution of Salmonella per carcass for each abattoir is summarized in a histogram distribution with classes below 1 CFUcarcass and 1 – 9 log CFUcarcass. This distribution is the output from the first part of the model.

The number of positive carcasses (out of 5000 carcasses, corresponding to a day's production in a medium sized Danish abattoir) is modelled in each iteration of the model as

Npos = Binomial(5000, Ppos)

For each positive carcass $CFU_{carcass}$ was estimated by sampling the Salmonella intervals in the output distribution from the first part of the model with the probabilities associated with each interval and utilizing a uniform distribution within the intervals. The number of servings is modelled as the weight of a carcass (75 kilogrammes) divided by the weight of a serving (200 grammes).

The number of Salmonella per serving (the dose) is then calculated as the number of Salmonella per carcass divided by the number of servings. The probability of human infection (P_{inf}) per serving is obtained by inserting the dose (D) into a beta-poisson dose-reponse model with the α and β parameters (0.1324; 51.45) (FAO/WHO 2002).

$$P_{inf}(D;\alpha,\beta) = 1-(1+D/\beta)^{-\alpha}$$

Finally the number of human cases of infection (C) is estimated from the number of servings (N_{serv}) and the dose-dependant P_{inf} by sampling from the binomial distribution:

$$C = Binomial(N_{serv}, P_{inf})$$

The model allows for calculating 2 simultaneous scenarios and prevalences in each scenario (Prev1 and Prev2) is calculated as the estimated number of cases out of 5000. The relative risk (RR) is calculated as

$$RR = Prev1/Prev2$$

CONCLUSION

Relative risk (RR) estimates for human salmonellosis for the 5 abattoirs are shown in Figure 1. Abattoir C served as reference as having the lowest risk. The effect of decontamination procedures gave a log reduction in the range 0.97 to 3.34 resulting in RR after decontamination in the range 0.28 to 0.004. Table 2 shows the influence of different log reductions on RR for human salmonellosis modelled on data from abattoir D as an example.
Our method offers the possibility to compare alternative strategies for hygienic improvement and to express the possible benefit in terms of relative risk for human disease.

Figure 1

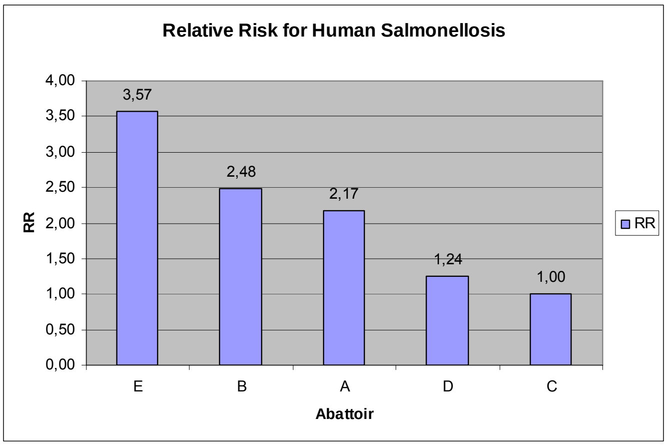

Table 2

Log reduction	Relative Risk
0.25	0,57976
0.5	0,33674
1.0	0,10561
1.5	0,03477
2.0	0,01115
2.5	0,00344
3.0	0,00072
3.5	0,00045

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