Modeling the transmission of livestock associated methicillin-resistant *Staphylococcus aureus* along the pig slaughter line☆

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ABSTRACT

The study introduces a new approach for a qualitative transmission assessment of MRSA throughout the pig slaughter process. Based on prevalence data found in literature the MRSA contamination and elimination rates of each individual slaughter step were estimated. The rates were used to set up a Monte Carlo simulation for modeling the propagation of MRSA along the process chain and to quantify the impact of a variable initial prevalence on the outcome prevalence of the carcasses. Sensitivity analyses for the model as well as three different scenarios were performed to estimate the impact of cross contamination during slaughter and to determine the process stages where hygiene interventions are most effective.

Regardless of the initial extent of MRSA contamination low outcome prevalences ranging between 0.15 and 1.15% were achieved among pig carcasses indicating that the pig slaughter chain generally includes process steps with the capacity to limit carcass contamination. Especially scalding and singeing can lead to a significant reduction of superficial MRSA contamination during the first half of the slaughter process. Nevertheless, scenario analyses showed that the low MRSA outcome prevalence can only be guaranteed if recontamination during the ongoing slaughter process is obviated. In order to ensure a low MRSA load on pig carcasses at the end of slaughter the abattoir should primarily concentrate on controlling the process parameters of scalding and singeing and avoiding recontamination at subsequent process steps.

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1. Introduction

Staphylococcus (S.) aureus has been relevant for the food producing industry particularly as a major cause of food born intoxications due to the production of various enterotoxins (Argudin, Mendoza, & Rodicio, 2010). As a frequent colonizer of the skin and mucous membranes, *S. aureus* can primarily enter the food chain via colonized personnel and food-producing animals (Hennekinne, De Buyser, & Dragacci, 2012). Standards for personal hygiene as well as cleaning and disinfection included in common recommendations for good manufacturing practice have been considered

sufficient to control both the introduction and transmission of *S. aureus* during meat processing (Borch, Nesbakken, & Christensen, 1996).

The emergence and spread of methicillin-resistant *S. aureus* (MRSA) causing severe healthcare- and community-associated infections is a major global public health concern (Deurenberg et al., 2007; Köck et al., 2010). The fact that *S. aureus* can rapidly adapt to the selective pressure of antimicrobials may have contributed to the wide spread observed. Beyond the well characterized burden of MRSA in healthcare and community settings, livestock has recently gained increasing significance as a zoonotic reservoir of MRSA. In Europe, these livestock associated MRSA strains (LA-MRSA) can predominantly be assigned to multilocus sequence types of clonal complex 398 (CC398)(EFSA, 2009).

Since MRSA was first detected at a Dutch pig farm in 2004 (Voss, Loeffen, Bakker, Klaassen, & Wulf, 2005), several investigations could confirm the presence of MRSA at farm level in herds of pigs (Cui et al., 2009; EFSA, 2009; Smith et al., 2009) and veal calves (Bundesamt für Verbraucherschutz und Lebensmittelsicherheit, 2012; Graveland et al., 2010), as well as in broiler (Bundesamt für Verbraucherschutz

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und Lebensmittelsicherheit, 2010; Mulders et al., 2010; Persoons et al., 2009) and turkey flocks (Bundesamt für Verbraucherschutz und Lebensmittelsicherheit, 2012; Richter et al., 2012).

In Germany, the prevalence of LA-MRSA was assessed at different stages of the pig production chain. Pigs at primary production were shown to be an important reservoir for LA-MRSA with prevalences ranging between 41.3 and 70% on herd level (Alt et al., 2011; EFSA, 2009; Frick, 2010; Köck et al., 2009). Pig prevalences between 58.5 and 80% were found among batches of slaughter pigs at the beginning of the slaughter process (Tenhagen et al., 2009). 16% MRSA positive samples from pork and pig meat products were identified at retail level in the course of a representative monitoring program throughout Germany (Bundesamt für Verbraucherschutz und Lebensmittelsicherheit, 2010) indicating transmission along the process chain. However, the relative contribution of the slaughter process to the MRSA transmission from farm to fork has not been quantified so far. Investigations could demonstrate that MRSA is present on carcasses and different slaughter equipment at various stages of the pig slaughter process (Beneke et al., 2011; Kastrup, 2011). However, MRSA prevalence data from longitudinal sampling of a sufficient number of pigs along the slaughter line are not available so far. Longitudinal investigations are cost intensive and would bring perceptible interruption of the process routine of the abattoirs under study.

In case of incomplete data, epidemiological modeling is a supplementary and cost effective method to study MRSA transmission routes in complex food production processes to estimate MRSA transmission rates and to evaluate possible control measures or intervention strategies. In this context, two substantially different methods may be distinguished: (i) Quantitative assessment methods (McKellar & Lu, 2003; Nauta, 2002) which analyze the change in the concentration of a particular microorganism along the production process and (ii) qualitative assessment methods (Nauta, van de Giessen, & Henken, 2000) which focus on the chance of detecting a germ regardless of its concentration. Both approaches model the food production process as a modular chain of several production steps (Clough, Clancy, & French, 2006; Nauta, 2001).

The objective of this study was to describe the transmission of MRSA throughout the pig slaughter process using a qualitative model which is based on published prevalence data. The model was used to quantify the impact of the initial MRSA herd prevalence among slaughter pigs on the outcome prevalence of the carcasses, to estimate the impact of cross contamination during slaughter and to determine the process stages where interventions are most effective.

2. Materials and methods

2.1. Data used

Assumptions concerning the transmission of MRSA from pigs to carcasses during slaughter are based on data about the presence of coagulase positive *Staphylococcus aureus* (CPS) on pig carcasses throughout the slaughter chain described by Spescha, Stephan, and Zweifel (2006). These data were generated in 2005 by investigations at two EU-approved abattoirs in Switzerland. Samples were obtained from the neck, belly, back and ham of 100 pig carcasses after bleeding, scalding, dehairing, singeing, polishing, trimming, washing and chilling in abattoir A and 100 pig carcasses after bleeding, scalding, a combined dehairing and singeing step, polishing, trimming, washing and chilling in abattoir B, respectively. Both abattoirs were visited weekly within 10 month and at each sampling occasion, 5 carcasses at each stage were sampled by means of the wet-dry double swab technique. All swabs were analyzed for the presence of CPS. The detection rate expressed as the percentage of CPS positive swabs out of the total number of

samples was included in the model. The prevalence rates available from the two abattoirs A and B showed two different situations. In abattoir A the prevalence of CPS was reduced early in the process chain during scalding and the prevalence level was kept low throughout the remaining process steps. In abattoir B scalding also reduced the CPS prevalence to a very low level but recontamination occurred during further processing.

2.2. Modeling prevalence changes throughout the pig slaughter line

A qualitative model has been developed to describe the transmission of MRSA through the pig slaughter process. Due to the process flow of abattoir B, dehairing and singeing had to be combined to a single process step in the modeled average abattoir. Therefore, the slaughter process consisted of 6 modular steps each denoted with the index i ($i = 1...6$). The state of an individual carcass at a particular production step i was denoted as s_i. An individual can have two states: positive and negative. Hence, s_i can be viewed as a random variable with two realizations: (s_i^+) and (s_i^-). The prevalence at a production step i, $P(s_i^+)$ can in turn be viewed as the probability of observing a positive individual at step i. If the prevalence $P(s_i^+)$ is known, the complementary prevalence $P(s_i^-)$ can be calculated as follows:

$$P\left(s_i^-\right) = 1 - P\left(s_i^+\right) \tag{1}$$

The consecutive prevalences were assumed to exhibit a first order Markov property: The individual's state at a given processing step i only depends on its state in the preceding production step $i - 1$ (Markov, 1954, pp. 3−375). Therefore, the proposed model is completely described when all probabilities for an individual's state conditional to its state in the preceding production step $P(s_i|s_{i-1})$ are known. The quantity $P(s_i|s_{i-1})$ depends on two terms: (i) The probability of a negative individual to become positive $P(s_i^+|.s_{i-1}^-)$, which is referred to as the contamination rate and (ii) the probability of a positive individual to become negative $P(s_i^-|.s_{i-1}^+)$, which is called the elimination rate. The respective complementary quantities can be calculated applying equation (1). Each individual can change its state at every processing step.

The value range of both, the contamination and elimination rate, were narrowed down by calculating their upper and lower limits from the prevalence data given by Spescha et al. (2006).

Based on the definition of the conditional probability of an event X given Y:

$$P(X) = P(X|Y)*P(Y) + P(X|\overline{Y})*P(\overline{Y}) \tag{2}$$

and the definition of the respective total probability

$$P(X) = \sum_i P(X, y_i) \tag{3}$$

The following marginal distributions

$$P\left(s_i^+\Big|s_{i-1}^+\right) = 1 \tag{4a}$$

$$P\left(s_i^-\Big|s_{i-1}^+\right) = 1 \tag{4b}$$

$$P\left(s_i^-\Big|s_{i-1}^-\right) = 1 \tag{4c}$$

$$P\left(s_i^+\Big|s_{i-1}^-\right) = 1 \tag{4d}$$

were used to calculate the lower and upper bounds for the contamination rate $c(\underline{c}; \overline{c})$ and elimination rate $e(\underline{e}; \overline{e})$ from the

prevalences $P(s_i{}^+)$ and $P(s_{i-1}{}^+)$ in two successive production steps $i-1$ and i:

$$\underline{c} = \underline{P}\left(s_i{}^+ \middle| s_{i-1}{}^-\right) = \begin{cases} \frac{P(s_i{}^+)-P(s_{i-1}{}^+)}{1-P(s_{i-1}{}^+)} & , P(s_i{}^+) > P(s_{i-1}{}^+) \\ 0 & , \text{else} \end{cases}$$
(5a)

$$\overline{c} = \overline{P}\left(s_i{}^+ \middle| s_{i-1}{}^-\right) = \begin{cases} \frac{P(s_i{}^+)}{1-P(s_{i-1}{}^+)} & , 1-P(s_{i-1}{}^+) \rangle P(s_i{}^+) \\ 1 & , \text{else} \end{cases}$$
(5b)

$$\underline{e} = \underline{P}\left(s_i{}^- \middle| s_{i-1}{}^+\right) = \begin{cases} 1-\frac{P(s_i{}^+)}{P(s_{i-1}{}^+)} & , P(s_{i-1}{}^+) \rangle P(s_i{}^+) \\ 0 & , \text{else} \end{cases}$$
(5c)

$$\overline{e} = \overline{P}\left(s_i{}^- \middle| s_{i-1}{}^+\right) = \begin{cases} \frac{1-P(s_i{}^+)}{P(s_{i-1}{}^+)} & , P(s_{i-1}{}^+) \rangle 1-P(s_i{}^+) \\ 1 & , \text{else} \end{cases}$$
(5d)

For both abattoirs A and B, values for the upper and lower bounds of the contamination and elimination rate were individually calculated for all four carcass sampling sites after each of the six processing steps. Therefore, up to a maximum of eight different values for the lower as well as upper bound of c and e for each of the process steps scalding, dehairing/singeing, polishing, trimming, washing and chilling can be achieved. All contamination rates which are based on sampling points with more than 95% positive pigs and all elimination rates based on sampling points with less than 5% positive pigs were excluded from subsequent calculations. In addition, all rates which simultaneously exhibited a lower bound of 0 and an upper bound of 1 were excluded because this means that no information on the particular rate can be obtained from these data.

For modeling the course of the MRSA prevalence along an average slaughter process, the remaining contamination and elimination rates of abattoir A and B were combined for each of the six process steps. The minimum value of all lower bounds of a process step was taken as the new lower bound ($\underline{c}^*$ and $\underline{e}^*$) for the respective process step of the average abattoir and the maximum value of all upper bounds was taken as the new upper bound ($\overline{c}^*$ and $\overline{e}^*$), respectively. Furthermore, the mean value of all considered rate values between the upper and lower bounds were calculated and the most likely value for the average abattoir is set as the mean of these mean values ($c_\mu{}^*$ and $e_\mu{}^*$). The rates are then expected to follow a PERT distribution

$$c^* \sim PERT\left(\underline{c}^*, c_\mu{}^*, \overline{c}^*\right)$$
(6a)

$$e^* \sim PERT\left(\underline{e}^*, e_\mu{}^*, \overline{e}^*\right)$$
(6b)

After calculating the contamination and elimination rates of each individual process step of the average abattoir, a Monte Carlo simulation was set up for modeling the propagation of MRSA along the slaughter chain. A group of pigs enters the slaughter line with a certain fraction of MRSA positive individuals. In each process step and for each individual the probability of contamination with or elimination of MRSA is determined according to the previously calculated contamination and elimination rates for this process step. As the probability of MRSA contamination during a process step depends directly on the preceding MRSA presence, the contamination rate c^* of each process step i was multiplied with the proportion of MRSA positive individuals in the previous process step $i-1$. The model was set up by simulating 500 slaughter groups with 100 animals each.

This modeling framework allows for estimating the herd prevalence along the slaughter line for each process step and for determining the outcome prevalence dependent on a varying initial MRSA state of the herd. Sensitivity analyses were performed to determine potential process steps where interventions are expected to be most effective to reduce MRSA cross contamination. Finally, the transmission model was used to simulate various changes in the slaughter process within three different scenarios in order to evaluate resulting effects.

3. Results

3.1. Contamination and elimination rates

Table 1 summarizes the combined lower and upper bounds of the contamination and elimination rates c^* and e^* and the expected values $c_\mu{}^*$ and $e_\mu{}^*$ for each process step which were calculated for the average slaughter chain. $\underline{c}^*$ remained 0 throughout the entire process whereas $\overline{c}^*$ varied between 0.01 and 1. The probability for a pig to get contaminated during scalding was calculated to be 0.083. However, only one single sampling occasion could provide applicable data concerning the contamination rate of scalding. $c_\mu{}^*$ was identified to be highest during dehairing/singeing and washing with 0.45 and 0.33, respectively. However, the value range could not be narrowed down due to the high variability of the measured data originating from multiple body sites at both abattoirs. A similarly broad value range was estimated for chilling and $c_\mu{}^*$ was calculated to be low (0.09). A more precise estimation of the contamination rate was possible for polishing and trimming. With an expected value of 0.009 and 0.008, both process steps hardly contributed to contamination.

$\overline{e}^*$ was calculated to range between 0.47 and 1. For scalding, a precise estimation of the elimination rate was possible with a high expected value $e_\mu{}^*$ of 0.94. A similarly high elimination rate (0.82) could be calculated for dehairing/singeing. The value range of polishing and trimming could only be narrowed down slightly due to the variability of the underlying data. Elimination rates of 0.25 and 0.30 were estimated. A more accurate estimation could be gained for washing $e_\mu{}^* = 0.19$. The elimination rate of chilling was estimated to be 0.65.

3.2. Impact of initial MRSA prevalence

The impact of the initial MRSA prevalence among the incoming slaughter pigs on the prevalence of the carcasses at the end of the slaughter process was low. As Fig. 1 summarizes, the variation of

Table 1
Calculated model parameters per slaughter process.

s_i	Process steps	c^*				e^*			
		$\underline{c}^*$	$c_\mu{}^*$	$\overline{c}^*$	n	$\underline{e}^*$	$e_\mu{}^*$	$\overline{e}^*$	n
s_1	Scalding	0	0.0833	0.1667	1	0.9000	0.9434	1	8
s_2	Dehairing/singeing	0	0.4467	1	8	0.7500	0.8160	1	4
s_3	Polishing	0	0.0088	0.0102	4	0.1075	0.2473	0.4699	4
s_4	Trimming	0	0.0076	0.0303	4	0.0658	0.2997	0.7869	4
s_5	Washing	0	0.3264	1	7	0	0.1889	0.5070	4
s_6	Chilling	0	0.0877	0.8056	5	0.2674	0.6534	1	4

c^* = contamination rate.
$\underline{c}^*$ = lower bound of the contamination rate.
$c_\mu{}^*$ = most likely value of the contamination rate.
$\overline{c}^*$ = upper bound of the contamination rate.
n = number of observations.
e^* = elimination rate.
$\underline{e}^*$ = lower bound of elimination rate.
$e_\mu{}^*$ = most likely value of the elimination rate.
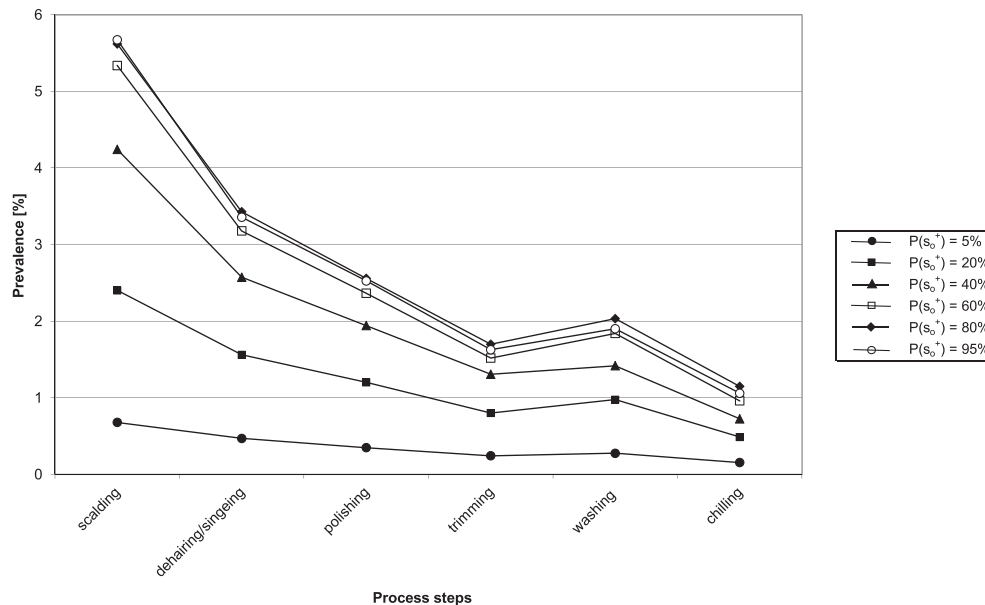$\overline{e}^*$ = upper bound of the elimination rate.

Fig. 1. Change in the MRSA prevalence along the slaughter line depending on the variation of the initial MRSA prevalence $P(s_0^+)$.

the initial MRSA prevalence between 5% and 95% led to a final MRSA prevalence ranging between 0.15 and 1.15% in the basic model. Slaughter groups with a high prevalence at the beginning of the slaughter process tended to have a slightly higher contamination rate at the end of the slaughter process compared to those with a low initial prevalence.

3.3. Sensitivity analysis

A sensitivity analysis was performed by changing the values of the contamination and elimination rates of every process step individually between 0 and 1 and assessing the effect on the outcome prevalence at the end of the slaughter chain. Fig. 2a/b present the final prevalences in comparison to a baseline scenario which was determined as the outcome prevalence of the simulation based on an initial prevalence of 60%, which corresponds to the MRSA prevalence among slaughter pigs in Germany (Lassok & Tenhagen, 2013).

By the increase of the contamination rate in each processing step, the prevalences of the carcasses at the end of the slaughter process range between 0 and 1. The variation of the elimination rate results in final carcass prevalences between 0 and 6.02%. The increase of the contamination rate has a greater impact on the outcome prevalence than the increase of the elimination rate. The impact of changes in the contamination or elimination rate on the final prevalence is most effective if they are performed at final stages of the slaughter chain.

The transmission model was also used to perform three different scenario analyses. In scenario 1, an insufficient scalding process was simulated by fixing the elimination rate to 0.5 and increasing the contamination rate by 50%. Cross contamination during dehairing/singeing and polishing was hypothesized within scenario 2. Therefore, the contamination rate of both process steps was fixed to 0.5, the elimination rates were reduced by 50%. Scenario 3 was based on scenario 2 with the addition of an increased decontamination during washing, e.g. by the use of hot water. Therefore, the elimination rate of washing was increased to 0.5 with a simultaneous decrease of the contamination rate by 50%. All scenarios were also run with an initial prevalence of 60%. All scenarios end with an increased MRSA prevalence ranging between 4.6 and 20.2% positive carcasses compared to the baseline value of

0.96%. Fig. 3 summarizes the propagation of MRSA prevalences throughout the slaughter process in the three different scenarios.

4. Discussion

The current study presents the first qualitative approach for modeling the transmission of MRSA along the pig slaughter process. The applied concept is suitable to quantify the impact of the initial slaughter batch prevalence of MRSA on the outcome prevalence of the carcasses, to identify appropriate stages for relevant hygiene interventions in the chain and to simulate the impact of cross contamination and elimination on the course of MRSA throughout the pig slaughter line. The presented model is purely based on probabilistic considerations based on prevalence data from literature. The inclusion of further assumptions based on expert opinions was avoided to achieve a model which is only based on collected data to represent the course of MRSA throughout the pig slaughter chain.

In order to model the course of MRSA along the pig slaughter process, data generated from continuous sampling of the same batch of animals both before and after each process step are needed. Searching the literature, only an insufficient amount of investigations which have proven the presence of MRSA on pigs at different stages of the slaughter chain were available and all of the results were based on occasional sampling during the process (Beneke et al., 2011; Kastrup, 2011; Molla et al., 2011; Tenhagen et al., 2009). However, one single study could be identified which investigated the prevalence of CPS on a sufficient amount of pigs at several consecutive steps along the slaughter line (Spescha et al., 2006). As there is no scientific evidence of any differences between MRSA and its susceptible variant concerning the transmission and survival during the slaughter processes, the data generated from CPS by Spescha et al. were included in the model and applied to MRSA.

The prevalence data of CPS were used to estimate the contamination and elimination rates of MRSA for every step of the pig slaughter chain by calculating the lower and upper bounds of the rates. The exact values of the rates, however, cannot be calculated from the prevalences alone. This limitation was accepted because the presented method provides a mathematically sound way to link the separated prevalences together. When interpreting the model
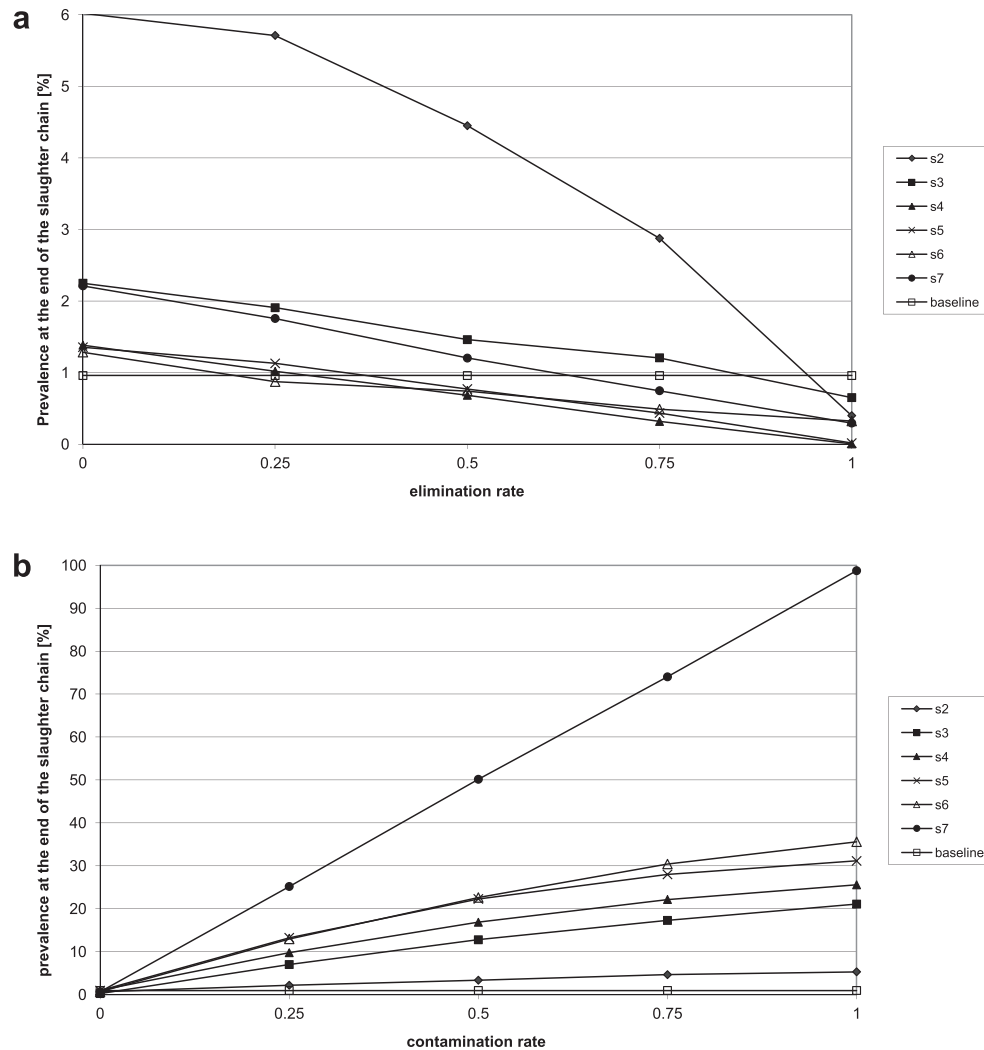
a

b

Fig. 2. a/b: Influence of a gradually increasing elimination and contamination rate at various process steps on the MRSA prevalence at the end of the slaughter chain, with s_2 = scalding, s_3 = dehairing/singeing, s_4 = polishing, s_5 = trimming, s_6 = washing, s_7 = chilling.

results, it has to be considered that the calculation of the contamination and elimination rates is based on prevalence data from only two different abattoirs. As both abattoirs show a different course of positive pigs throughout the process, a wide variability in MRSA prevalence data was observed. The degree of representativeness of the model parameter cannot be improved unless data from a higher number of pig abattoirs are available.

Moreover, the used data were generated in 2005 and therefore, any modernization in slaughter techniques could not be considered in the model. Finally, with respect to estimating the prevalence of MRSA on carcasses, the wet–dry double swab technique probably has some limitations with respect to sensitivity (Tenhagen, Arth, Bandick, & Fetsch, 2011). On the other hand, these limitations will probably only have effects on the level of the MRSA prevalence, but not on the changes in prevalence.

Assuming effective hygiene management the transmission model showed that the burden of MRSA on batches of slaughter pigs can be reduced to a low level throughout the process chain, regardless of the extent of the initial MRSA prevalence. Scalding was shown to be a particularly efficient process step for superficial carcasses decontamination. Due to the low contamination rates of subsequent process steps, the MRSA prevalence stays low until the end of slaughter.

During scalding the carcasses undergo a controlled heating process which is carried out at 60° to 62 °C for 6–8 min (Borch

et al., 1996). Since *S. aureus* is known to have a D_{55} value of approximately 66 s a significant reduction of MRSA during scalding can be expected (Bergdoll, 1989). The elimination rate of scalding could be assessed precisely and the high most likely value of 0.94 confirms the expectations. The observed contamination rate of scalding ranges between 0 and 0.17 with a most likely value of 0.08. The calculation of this value could only be based on results generated from one carcass compartment in one abattoir. The limited diversity of data at scalding is due to the high initial prevalence (93–100%) of positive pigs in the primary data source. The small number of negative animals in the sample hampers the estimation of how scalding may contribute to the contamination of pigs with MRSA. However, applying our method on data from older studies about the superficial prevalence of *Salmonella*, similar contamination rates for scalding could be observed ranging between 0 and 0.33 with a most likely value of 0.09 (data not shown) (Davies, McLaren, & Bedford, 1999; Pearce et al., 2004). However, in comparing results from investigations from various countries, differences in the slaughter technology and hygienic status should be generally considered.

Singeing is known to be another potential process step for the superficial decontamination of pig carcasses during slaughter. Conventional automatic singeing systems with a passage of 10–15 s at 900–1200 °C were shown to result in a reduction of total
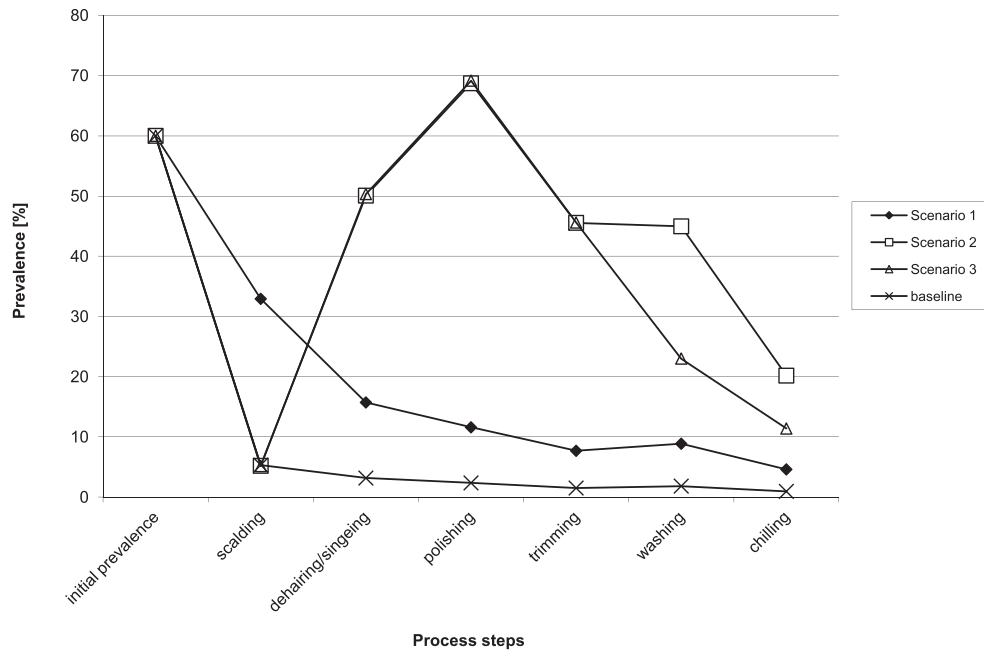
Fig. 3. Course of the MRSA prevalence during three different scenarios with an initial prevalence of 60%; Scenario 1: inefficient scalding process; Scenario 2: cross-contamination during dehairing/singeing and polishing; Scenario 3: cross-contamination during dehairing/singeing and polishing, washing with hot water; Baseline scenario: course of the MRSA prevalence for the average abattoir.

bacterial counts (Bolton et al., 2002; Pearce et al., 2004). However, inefficient singeing can also lead to surviving MRSA that can be distributed over the surface of the carcasses during further processing or contaminate slaughter machines and therefore, contribute to MRSA cross contamination (Davies et al., 1999). As one abattoir in the primary data set used a combined dehairing/singeing process, separated rates for both processes could not be included into the model.

The process of trimming rather contributes to the reduction of MRSA prevalence. This result reflects the data published in Spescha et al. but was unexpected. Older investigations detected an increased number of faecal bacteria on the surface of slaughter pigs after evisceration, the step which directly precedes the trimming procedure in the slaughter process chain (Pearce et al., 2004; Rivas, Vizcaíno, & Herrera, 2000; Yu et al., 1999). As results from actual investigations are lacking, it can only be assumed that modernization of the slaughter technology might have also improved the hygienic status of pig carcasses after evisceration. The intestinal tract was identified to be the main source of faecal contamination on this process stage. As staphylococci including MRSA can be isolated from rectal swabs of pigs (Khanna, Friendship, Dewey, & Weese, 2008), transmission from the intestines to the surface of carcasses was expected. In comparison to other intestinal microorganisms like *Salmonella* or *Escherichia coli* however, staphylococci play a minor role in the gut flora and therefore, recontamination with MRSA during evisceration might be low.

A slight increase in the MRSA prevalence was recorded during washing. This might be, to a large extent, due to a redistribution of present bacteria on the carcass surface potentially increasing the detection rate.

Previous investigations have also shown that post evisceration washing with cold water is indeed effective in removing visible contamination but does not provide any significant reduction in the prevalence and number of bacterial counts (Bolton et al., 2002; Gill, McGinnis, Bryant, & Chabot, 1995).

Sensitivity analyses showed that the variation of the contamination rate has a greater impact on the outcome prevalence than the variation of the elimination rate. This result might indicate that the pig slaughter process includes enough potential to reduce any superficial MRSA contamination in the early state of the chain. The burden of MRSA on pig carcasses can be kept low by avoiding any recontamination by further slaughter steps. The impact of rate changes on the value of the final prevalence is most effective if they are performed at final stages of the slaughter chain. This effect might be partly influenced by the method used for calculating the model as due to the Markov Chain principle, the MRSA state of the individual pig at a given production step only depends on its state at the preceding production step (Markov, 1954, pp. 3–375). Especially cross contamination during the last part of the slaughter process can significantly increase the final prevalence of the carcasses as subsequent process steps which might dilute the contamination are lacking. As the contamination rate of each process step was multiplied with the proportion of MRSA positive individuals in the previous process step, the model concentrates on the cross contamination within the slaughter batch.

The impact of different deviances from optimal slaughter procedures was analyzed using three different scenarios. Scenario 1 simulates an ineffective scalding process which might have been realized by an insufficient water temperature, insufficient duration of scalding or cross contamination via contaminated scalding water. The resulting higher MRSA prevalence after scalding however could be reduced by subsequent process steps. Cross contamination during dehairing and polishing was simulated at scenario 2. Several previous studies concluded that dehairing is a major source of carcass contamination (Davies et al., 1999; Gill & Bryant, 1992; Nerbrink & Borch, 1989; Pearce et al., 2004). Rotating scrapers and rubber flails mechanically scour the surface of the carcasses to remove the bristles. The associated compression of the carcass results in an increased segregation of porcine bacteria from mouth, nose and the intestinal tract. While driving through the dehairer, the scalded carcasses can get contaminated by the detritus which accumulates in the machine (Borch et al., 1996; Gill & Bryant, 1993). Conventional dehairing equipment is difficult to clean and in case of insufficient hygiene performance, a persisting microbiological

flora can get established (Rivas et al., 2000). Various studies indicated that polishing frequently reverses the reduction of microorganisms previously achieved through singeing. Recontamination is mainly explained by the accumulation of microorganisms in the scrapers and nylon brushes of the polishing systems (Pearce et al., 2004; Yu et al., 1999). The amount of recontamination seems to depend on the cleaning status of the polisher as well as on the effectiveness of the singeing process. During singeing, certain sectors of the carcass might be insufficiently exposed to flaming and surviving bacteria might be redistributed over the carcass during polishing (Borch et al., 1996; Gill & Bryant, 1992). Although the high MRSA prevalence of 68.7% after polishing could be reduced during further processing, scenario 2 ends with a significantly increased proportion of positive carcasses of 20.2%.

Decontamination technologies are gaining interest in the pig slaughter process in order to reduce bacterial contamination levels or inhibit microbial growth. However, with the exception of hot water treatments, no decontamination procedures are currently authorized in the European Union (EFSA Panel on Biological Hazards (BIOHAZ), 2010). Scenario 3 which simulates the process of hot water spraying by increasing the elimination rate of the washing process could show that this particular intervention could only induce a slight reduction of previous recontamination.

This result was in line with previous investigations which reported spraying with hot water to yield low bacterial reductions up to 3.3 $\log_{10}$ CFU/cm^2 (Loretz, Stephan, & Zweifel, 2011).

5. Conclusion

The present study demonstrated that the transmission of MRSA throughout the pig slaughter chain can be analyzed by using a probabilistic model based on prevalence data from literature. However, data from a higher number of pig abattoirs are needed to improve the representativeness of the model parameters.

Regardless of the initial extent of MRSA contamination a low MRSA prevalence could be achieved among carcasses at the end of the chain. This finding indicates that pig slaughtering includes process steps with the capacity of superficial carcass decontamination. Especially the heat treatment during scalding and singeing can lead to a significant reduction of MRSA on the surface of pig carcasses during the first half of the slaughter process. However, scenario analyses demonstrated that low MRSA outcome prevalence can only be ensured if additionally any recontamination with MRSA is efficiently controlled throughout the ongoing slaughter process.

It can be concluded that a low burden of MRSA on slaughtered pig carcasses may be realized by a strict monitoring of important process parameters during scalding and singeing, like temperature and duration, combined with efficient hygiene practices reflected in increased elimination and reduced contamination rates of the individual pig slaughter process steps.

Acknowledgment

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