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Within-herd biosecurity and *Salmonella* seroprevalence in slaughter pigs: A simulation study

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ABSTRACT: In Europe, on-farm biosecurity measures, involving a strict all-in/all-out batch-management system and decontamination of the rearing rooms between consecutive batches, are recommended to control *Salmonella* infection in growing pigs. However, implementation of these measures is often relaxed under common farming conditions. Therefore, this study was conducted to assess the relative contributions of batch-management system and room decontamination efficacy on *Salmonella* seroprevalence for different growing rates and subsequent slaughter ages of pigs. Because the impact of these factors cannot be easily evaluated by an observational approach in commercial farms, a stochastic simulation model representing the population dynamics, herd management, and *Salmonella* infection within a farrow-to-finish pig herd was used. Realistic levels were set for each factor under study (3 for batch-management system and slaughter age; 4 for room decontamination) to generate 54 simulation scenarios. *Salmonella* shedding prevalence in groups of slaughter pigs was then compared. A sensitivity analysis was performed to rank the impacts of the 3 factors on output. Batch-management system had little effect. In contrast, room decontamination efficacy had the greatest impact on *Salmonella* prevalence in pigs at slaughter. A drop in decontamination efficacy from 100 to 50%, with a strict all-in/all-out batch-management system and for all slaughter ages tested, noticeably increased ($P < 0.001$) the prevalence and almost doubled it for the reference slaughter age. Our results suggest that the control of *Salmonella* in pig herds should primarily focus on room decontamination efficacy. Provided that a good level of room decontamination is ensured, some flexibility in batch management, in terms of pig mixing, would be acceptable to limit the number of underweight pigs delivered to the slaughterhouse.

Key words: batch-management system, farrow-to-finish herd, hygiene, modeling, *Salmonella*, swine

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INTRODUCTION

Pork, after eggs and poultry meat, is a major source of human foodborne salmonellosis in the European Union (EFSA, 2006). *Salmonella* are ubiquitous bacteria that can enter and hence need to be controlled at each stage of the pork supply chain. When infected by *Salmonella* ingestion, pigs are asymptomatic carriers and shedders. Although they do not exhibit clinical signs of infection, they can intermittently shed bacteria in their environment. At the preslaughter level, reducing the number of shedding pigs at departure for slaughter limits the possible cross-contamination during transport and lairage. It can then also imply a reduction in the probability of further contamination during the slaughter process (Berends et al., 1996; Lo Fo Wong et al., 2004). Particular on-farm biosecurity measures have been recommended by the European Food Safety Authority (EFSA, 2006). The EFSA combines a strict all-in/all-out batch-management system and a room decontamination process between 2 consecutive batches. However, these measures are difficult to fully implement under common farming conditions. As a consequence, the efficacy of decontamination process may vary in the field and depending on batch-management adaptations. Actually, mixing pigs from different batches creates direct contacts between animals from these batches, which can increase the risk of *Salmonella* transmission.

In terms of feasibility and costs, the effect of biosecurity-measure implementation on *Salmonella* spread within the pig herd can be tested advantageously by a modeling approach (van der Gaag et al., 2004). A

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model describing the *Salmonella* spread within a farrow-to-finish pig herd (Lurette et al., 2008b) was previously developed. This model was used here to assess the impact on *Salmonella* prevalence in groups of slaughter pigs, of discrepancies between 1) a reference scenario for biosecurity-measure [i.e., close to the EFSA recommendations (EFSA, 2006)] and 2) common practices of producers.

MATERIALS AND METHODS

Animal Care and Use Committee approval was not obtained for this study because only published data were used.

A model was developed to describe the dynamics and management of a farrow-to-finish pig herd (Lurette et al., 2008a). This model was then coupled to a *Salmonella* epidemiological model (Lurette et al., 2008b). The management system and assumptions that were implemented in the coupled model correspond to the reference scenario defined as the best one in terms of on-farm biosecurity measures. We first described the main features of the basic model, then how it was modified to implement the deteriorated scenarios and to test the impact of infection at weaning. Finally, we presented model outputs and the sensitivity analysis method used to compare the scenarios.

Basic Model Features Corresponding to the Reference Scenario

The basic model consists of 2 components: the population dynamics within a farrow-to-finish pig herd (reproductive sows and growing pigs) detailed in Lurette et al. (2008a), and the *Salmonella* transmission dynamics detailed in Lurette et al. (2008b). The components were easily coupled because the simulated infection is subclinical and therefore does not affect pig demography and growth rate. The main features are given below. The time step was a week and the modeling unit a batch.

Sow and Pig Population Model. To represent the population of sows and pigs, animals were grouped in batches according to age (pigs) or reproductive status (sows). At each time step, a batch was associated to a room. The population dynamics component described the reproductive cycle of sows, including gilt recruitment, birth and the growth of pigs until slaughterhouse delivery, batch movements between rearing rooms, and animal outflows from the batch (mortality, culling, and slaughterhouse delivery). Sows in a batch were mated simultaneously. A 3-wk, between-mating interval was modeled. A batch of sows gave birth to a batch of piglets. A strict all-in/all-out batch-management system was implemented for pigs (with no pig mixing), so they remained in their batch until their slaughterhouse delivery. Each batch of sows occupied 3 successive rooms during each reproduction cycle: a mating room (4 wk), a gestating room (12 wk), and a farrowing room (5 wk). In turn, each batch of pigs occupied 3 rooms: a farrowing room (4-wk suckling period), a postweaning room (8 wk), and a finishing room (around 14 wk). To account for pig growth variations, the time pigs remained in the finishing room varied within a batch and among batches. On average, pigs spent 25.5 wk (SD = 1.5 wk) in the herd to reach slaughter weight. This duration corresponded to the mean age at slaughter. For more details on the herd dynamics, see Lurette et al. (2008a).

Salmonella Transmission Model. To represent *Salmonella* transmission, animals in each batch were distributed into 4 exclusive and successive health states: susceptible, seronegative shedder, seropositive shedder, and seropositive carrier (no longer shedding). Shedding was intermittent and could be reactivated, so carriers could go back to the seropositive shedder state. For more details, see Figure 1 in Lurette et al. (2008b). The model implemented indirect transmission of *Salmonella* via the environment. Shedding pigs contaminated their rearing room, thereby exposing susceptible pigs of their own batch to the bacteria. A drop of 20% in the shedding quantity was assumed to occur after seroconversion, so seropositive shedders contribute less than seronegative shedders to the room contamination. The probability of infection within a batch depended on the quantity of bacteria per pig in the room. This quantity was updated at each time step by taking into account shedding, natural bacterial degradation, and room decontamination.

The decontamination process was performed after a batch left the room. The farrowing, postweaning, and finishing rooms were emptied between 2 consecutive batches, so the decontamination process was very efficient and reduced the quantity of bacteria by 99%. In contrast, the mating and gestating rooms were each occupied by several batches of sows at any time. As a

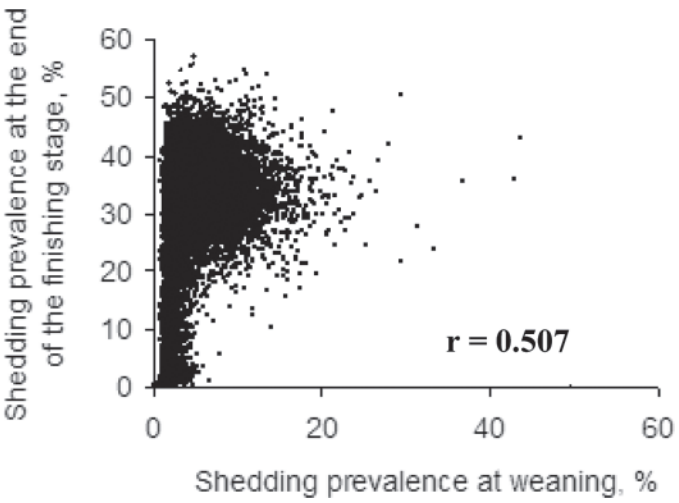

Figure 1. Correlations ($P < 0.0001$) between the prevalence of shedding in batches at weaning and at the end of the finishing period under the reference scenario Mix0-Growth1-Decont99.9, which is described by no mixing of pigs, a mean age at slaughter of 25 wk, and a decontamination efficacy of 99.9%. Three hundred replications over a 400-wk simulation period were considered, corresponding to 60,000 groups of slaughter pigs.

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Table 1. Definition and values of the parameters used in the *Salmonella* epidemiological model (based on Table I in Lurette et al., 2008b, issue 5; http://www.veterinaryresearch.org/)

Description	Value[1]	Source
Infection probability to represent dose effect relation	Increasing function of the logarithm of the number of infectious units (Q) with 2 plateaus	Fravalo et al., 2003
Inferior threshold of infection (number of Q) below which the probability is the lowest saturation threshold above which the probability reaches a maximum value	$Log(10^4)$ $Log(10^6)$	
Minimum infection probability	$p_{I_min} = 10^{-6}$	
Maximum infection probability	$p_{I_max} = 0.08$	
Seroconversion delay	2 wk	
Shedding period duration	Lognormal distribution Mean: $\alpha_{\lambda 2} = 4$ wk SD $\sigma_{\lambda 2} = 1.8$ wk	
Weekly probability of shedding reactivation	0.2	Lurette et al., 2009[2]
Weekly probability of shedding reactivation due to stress	0.4	Lurette et al., 2009[2]
Protective factor–passive immunity	0.75	Lurette et al., 2009[2]
Weekly survival probability of *Salmonella*	0.4	
Salmonella infectious units (SIU)[3] shedded by a seronegative shedding finishing pig or sow	Normal distribution Mean = 5.10^4 SIU SD = 10^2 SIU	Lurette et al., 2009[2]
Ratio of shedding for piglets and postweaner compared with a shedder finisher pig	1/10 (piglets/finisher) 1/2 (postweaner/finisher)	Lurette et al., 2009[2]

[1]The values chosen for variables used in the epidemiological model are estimated based on experimental data reported in the literature.

[2]The values of parameters were calibrated from a sensitivity analysis performed in Lurette et al., 2009.

[3]*Salmonella* infectious unit is defined as the smallest quantity of *Salmonella* that can infect a susceptible pig.

consequence, these rooms could not be emptied and the decontamination efficacy was reduced there to 80%. For more details on the epidemiological model, see Lurette et al. (2008b).

Calibration and Initial Condition

Epidemiological variables used in the model are detailed in Table 1. Values of variables were chosen based on *Salmonella* Typhimurium because this serovar is the most frequently detected in European pig herds (EFSA, 2006). See Lurette et al. (2008a) for zootechnical variables.

The initial herd consisted of 7 batches of 20 sows and 10 batches of pigs. The size of a batch of pigs decreases from 180 pigs at birth to 30 pigs at the end of the finishing period (some pigs having already been delivered to the slaughterhouse). An annual replacement rate of 40% was obtained in the model, which took into account the recruitment of 4 gilts at each new reproductive cycle. At each gilt recruitment, 7% of the gilts were seropositive (shedding or not). The model was initialized with prevalences similar to the results obtained in Lurette et al. (2008b): a mean shedding prevalence of 21% in batches of sows and of 13% in groups of slaughter pigs.

Modifications of the Model and Biosecurity Scenarios Tested

The reference scenario and biosecurity-measures commonly implemented were compared by constructing 54 scenarios combining different levels of the following 3 factors (see Table 2): batch-management system corresponding here only to the possible mixing of pigs from consecutive batches (**Mix**), mean age at slaughter (**Growth**), and decontamination efficacy in the rearing rooms (**Decont**). The reference scenario (Mix0-Growth1-Decont99.9) was the strictest scenario in terms of biosecurity obtained under field conditions.

Introduction of Pig Mixing. The model was modified to include the possibility of mixing pigs from different batches at the end of the postweaning period and at the end of the finishing period. Pig mixing was the only variable component of the batch-management system in the model. From here on, this practice will be called pig mixing in the text. At the end of the finishing period, if some pigs have not reached the market weight when their room needed emptying, producers may mix them with the next batch (3 wk younger) to avoid profit losses. Similarly, underweight piglets may be mixed with the next batch at the end of the postweaning period. However, pig mixing was limited by room capacity: 180 animals in a postweaning room and 150 in a finishing room. Three types of batch-management systems were then modeled: 1) a batch-management system with strict all-in/all-out without mixing (corresponding to the reference scenario and called **Mix0**), 2) a batch–management system with a strict all-in/all-out occupation of farm facilities, except at the end of the finishing period when pig mixing may occur (**Mix1**), and 3) a batch-management system where pigs may be mixed at the end of both the postweaning and the finishing periods (**Mix2**).

Mean Age at Slaughter. As end BW was fixed, increasing this variable allowed us to simulate a decrease

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Table 2. Description and values of 3 factors (pig mixing, mean age at slaughter, decontamination efficacy) according to their implementation modalities (3 modalities for pig mixing and mean age at slaughter; 5 modalities for decontamination efficacy) within biosecurity measures[1]

		Mix0	Mix1		Mix2	
Item	Description	No pig mixing	Mixing of pigs at the end of the finishing period		Mixing of pigs at the end of the postweaning and the finishing periods	
Mean age at slaughter	Name	Growth1	Growth2	Growth3		
	Value, wk	25	27.5	30		
Decontamination efficacy	Name	Decont100	Decont 99.9	Decont99	Decont80	Decont50
	Value, %	100	99.9	99	80	50

[1]The factor modalities are combined to define the 54 simulation scenarios tested in this study. The reference scenario corresponds to Mix0-Growth1-Decont99.9.

in pig growth. Its reference value was 25 wk (**Growth1**). We tested mean ages of 27.5 wk (**Growth2**) and 30 wk (**Growth3**), keeping the same confidence interval as before (i.e., 1.5 wk).

Reduction of the Decontamination Efficacy. The reference value for the decontamination efficacy (**Decont99.9**: 99.99%) corresponded to an optimum under field conditions. Four other values were tested in rooms that can be emptied between consecutives batches (farrowing, postweaning, and finishing rooms), to represent the large range of variation observed under actual herd conditions: 99% (**Decont99**), 90% (**Decont90**), 80% (**Decont80**), and 50% (**Decont50**). Although unrealistic, an extra 100% efficacy value (**Decont100**) was added to simulate extreme scenarios with no contamination between batches through the rearing rooms. The decontamination efficacy in mating and gestating rooms remained equal to 80%, except for scenario Decont50 in which it was reduced to 50%, as in the other rooms.

Modifications of Herd Supplying

In Lurette et al. (2008b), the mean shedding prevalence within batches of weaned pigs was 2.9% (5th percentile = 0; 95th percentile = 9.5%) with 68% of *Salmonella*-positive batches in 68% of positive batches. A 0.507 correlation coefficient was observed between the prevalence of shedding at the end of the weaning and of the finishing periods under the reference scenario (Figure 1). Considering this result, to explore the impact of *Salmonella* infection in batches of weaned pigs on the prevalence at slaughterhouse delivery, we introduced in the herd batches of negative weaned piglets 100 wk after the beginning of the simulation for the 5 values of decontamination efficacy.

Simulation Outputs

Every 2 wk, pigs that had reached market weight or pigs with finishing rooms that needed to be emptied were delivered to the slaughterhouse. The pigs usually stemmed from several batches and constituted a group of slaughter pigs. First, the prevalence of shedding (i.e., pigs in the seronegative shedder and seropositive shedder states) in each group of slaughter pigs was calculated. Two outputs were derived from this variable: the mean prevalence and the cumulative frequency distribution (Figure 1A).

Second, pig mixing was studied in more detail by calculating, for scenarios that allowed pig mixing at the end of both the postweaning and the finishing periods (Mix2), 1) the frequency of batch in which pig mixing occurred (i.e., the number of batches receiving pigs from another batch divided by the total number of batches delivered to slaughter during the 520-wk simulation and for all repetitions), 2) the global mean number of pigs mixed per batch when mixing occurred, and 3) the prevalence of shedding pigs in group of mixed pigs (i.e., the number of shedding pigs on the total number of pigs mixed over all delivery time steps and all replications). The mixing frequencies were calculated independently at these 2 periods.

Results were obtained from 300 replications of each scenario tested over 400 wk. This number of replications provided a stable distribution of the simulated results. So, for each scenario, our results were based on 60,000 groups of slaughter pigs. Analysis of variance, followed by a Tukey test, was implemented to compare the results of shedding prevalence obtained from the different scenarios tested with the R software.

Sensitivity Analysis

To compare the contributions of pig mixing, mean age at slaughter, and decontamination efficacy with the frequency distribution of the prevalence of shedding, a sensitivity analysis method suitable for multivariate outputs was used (Lamboni et al., 2009). This method is based on principal components analysis (**PCA**) and ANOVA. The cumulative distribution of prevalence of shedding in groups of slaughter pigs over time can be represented in a "No. × p" table, where No. was the number of scenarios, which was 54, and p was the number of 5% intervals from 0 to 100% of prevalence, which was 20. A PCA was performed on this table. The first component obtained was the linear combination of the 5% intervals that explained the maximum variabil-

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ity between the scenarios. The second component was the second-best combination to explain the variability. Each scenario was given a score for each component, corresponding to its projection on the component. An ANOVA was then performed on the scores for each of the first 2 principal components to compare the influence of the 3 factors on the prevalence output. The regression model included all main effects and interactions. The sensitivity index associated with each factorial term (main effect or interaction) was defined as the ratio between the sum of squares associated with that term and the total sum of squares. It represented the impact of that term on the output variability. This analysis was performed with the R software (The R Project for Statistical Computing: http://www.r-project.org/).

RESULTS

Qualitative Comparison of the Biosecurity Scenarios

For the reference scenario (Mix0-Growth1-Decont99.9), the mean prevalence of shedding in groups of slaughter pigs was 15.2%, the values ranging from 0 to 52% among groups (Figure 2A). Fifty percent of the groups of slaughter pigs exhibited a prevalence of shedding less than or equal to 9%.

The distribution of prevalence of shedding in groups of slaughter pigs for the 54 scenarios tested was highly variable. However, scenarios differing only by pig mixing exhibited similar patterns (results not shown), so we only illustrated the results obtained without pig mixing (Mix0) in Figure 2.

The greater the curve corresponding to a scenario, the less the mean prevalence of shedding in the groups of slaughter pigs. Clearly, the greatest curve was the one obtained for the scenario Mix0-Growth1-Decont100, but this curve was very close to the one obtained for the reference scenario Mix0-Growth1-Decont99.9. Results of cumulative frequency exhibited very similar patterns for decontamination efficacies equal to 100, 99.9, and 99%.

The lowest curve corresponded to the worst-case scenario Mix0-Growth3-Decont50, in which the prevalence was greater than 32% in 50% of the groups of slaughter pigs. Scenarios with Growth2 and Growth3 exhibited large numbers of slaughter groups with low prevalence and high prevalence, whereas all scenarios with Growth1 but the Decont50 exhibited a regular increase of the curve from 0% prevalence to 40% prevalence.

Contribution of Pig Mixing, Mean Age at Slaughter, and Decontamination Efficacy to the Distribution of the Prevalence of Shedding

The first component of the PCA explained 81.5% of the prevalence distribution variability. All scenarios contributed equally to this component (results not shown). The decontamination efficacy contributed 69.8% of the output variability for this component (Figure 3A). The mean age at slaughter contributed 15.1%, and the pig mixing contributed 0.9%. Interactions explained very little of the output variability.

The second component of the PCA explained 17.2% of the output variability. The scenarios that contributed most to this component included many extreme groups of pigs at slaughter, with either low or high prevalences of shedding (results not shown). These scenarios corresponded to the curves in Figure 2 that differed most from the median curve. The mean age at slaughter, decontamination efficacy, and corresponding interaction explained more than 95% of the output variability for this component (Figure 3B).

Effect of Biosecurity Measures on the Mean Prevalence of Shedding

Pig Mixing. The contribution of pig mixing to the mean prevalence of shedding in groups of slaughter pigs was small compared with the other factors. Figure 4 illustrates the effect of changes in pig mixing on the mean prevalence in groups of slaughter pigs. The difference in mean prevalence ($P > 0.05$) for scenarios combining the same values for mean age at slaughter and decontamination efficacy but differing in terms of pig mixing was smaller than 3 points (Figure 4). The difference between the batch-management systems Mix1 and Mix2 was smaller than the difference between Mix0 and Mix1. This suggests that pig mixing has less influence at the end of the postweaning period than at the end of the finishing period. Focusing on pig mixing at the end of the finishing period, the frequency of batches mixed with another batch varied between 63 and 73% for scenarios with batch-management Mix2, whatever the mean age at slaughter (Table 3). The global mean number of pigs mixed per batch concerned varied from 16.9 to 53.2 pigs when the mean age at slaughter increased from 25 to 30 wk. The scenarios tested showed little variation in the mean prevalence of shedding in the groups of mixed pigs (around 20 to 30% for Growth1 to Growth3).

Mean Age at Slaughter. For a strict all-in/all-out batch-management system without pig mixing (Mix0; Figure 4A), an increase in the mean age at slaughter (Growth1 to Growth3) induced an increase in the mean prevalence of shedding. The increase was much greater between 27.5 (Growth2) and 30 wk (Growth3) than between 25 (Growth1) and 27.5 wk (Growth2; 4 to 5 points vs. 1 to 2 points) except for the least decontamination efficacy for which shedding prevalences were very close (see on Figure 4 for significant differences; $P < 0.05$).

Decontamination Efficacy. For a strict all-in/all-out batch-management system (Mix1), a progressive decrease in the decontamination efficacy (levels Decont100 to Decont50) led to a sharp increase in the

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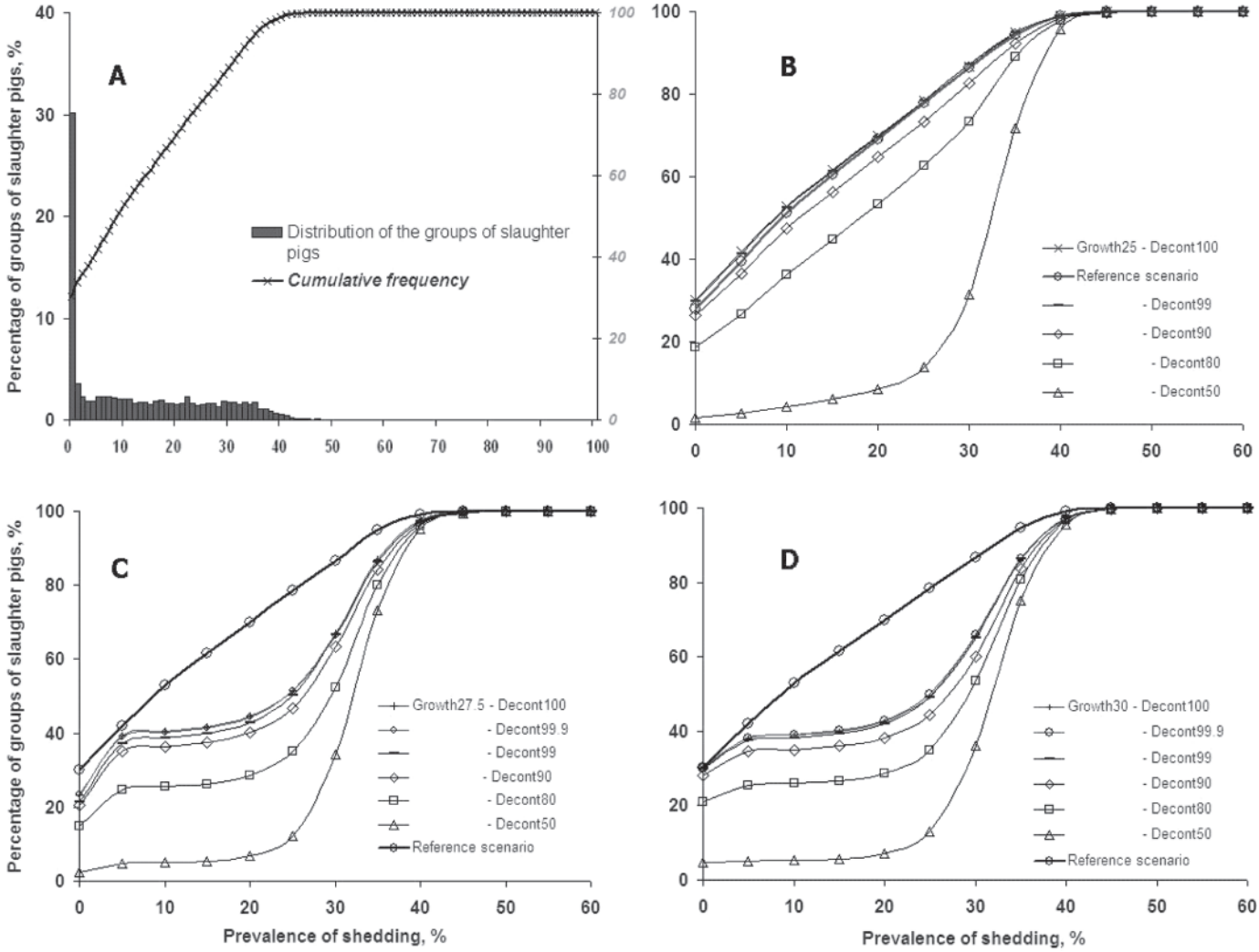

Figure 2. Cumulative frequency distribution of the *Salmonella* prevalence of shedding in groups of slaughter pigs according to several scenarios, with a strict all-in/all-out batch management (Mix0). Panel A: reference scenario (Mix0-Growth1-Decont99.9); panel B: scenarios with a mean age at slaughter of 25 wk (Growth1); panel C: scenarios with a mean age at slaughter of 27.5 wk (Growth2); and panel D: scenarios with a mean age at slaughter of 30 wk (Growth3). Decontamination efficacy (Decont) ranged from 100 to 50%. The distributions were calculated over 60,000 groups of slaughter pigs for each scenario (300 simulations performed over 400 wk).

mean prevalence of shedding in groups of slaughter pigs (Figure 4A). This increase was not linear. Whatever the batch-management system combined with a mean age at slaughter of 25 wk (Growth1), a decrease in the decontamination efficacy from C1 to C4 led to a significant increase ($P < 0.001$) in the mean prevalence of around 15 points (Figure 4).

Effect of Infection at Weaning Age. In the scenarios presented above, which differed in their biosecurity practices, the *Salmonella* prevalence at weaning varied only with different decontamination efficacies. The proportion of positive batches at weaning increased from 68% of positive batches for the greatest values of decontamination to 79% for Decont50. At this stage, the within batch prevalence (in positive batches) increased from 4.6% (5th percentile = 0.6%; 95th percentile = 12.4%) for scenarios with a 100% decontamination efficacy to 10.1% (5th percentile = 2.1%; 95th percentile = 19.4%) for scenarios with 50% decontamination (the only scenario in which decontamination of the rooms of the sows was decreased).

Introducing only negative batches of weaned pigs induced a dramatic decrease in the shedding prevalence in groups of delivered pigs. One hundred percent of the simulations led to a *Salmonella*-negative herd for the Decont100 and Decont90, 45% of the simulations for Decont80, and only 5% of the simulations for Decont50.

DISCUSSION

We showed in this study that a model coupling herd dynamics and infection dynamics as the one we previously proposed (Lurette et al., 2008b) was a suitable tool to assess the impact of biosecurity measures on *Salmonella* spread within a farrow-to-finish pig herd. The model we used took into account the main components of the pig management system and *Salmonella* epidemiology in a fairly detailed and realistic way. It can therefore be adapted to represent different scenarios, combining several batch-management systems, mean ages at slaughter, and rearing room decontamination efficacies.

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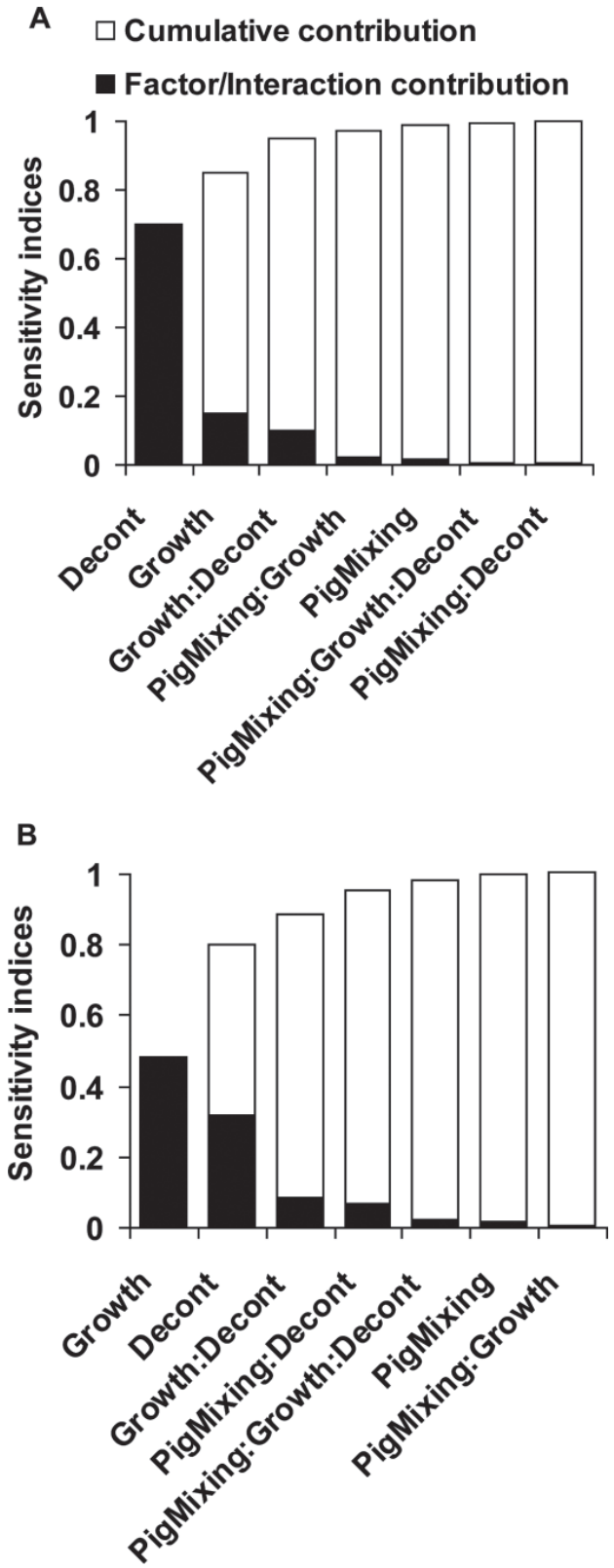

Figure 3. Contribution of 3 factors: pig mixing, mean age at slaughter, decontamination efficacy (Decont), and their interactions to the variability of the frequency distribution of the *Salmonella* prevalence of shedding in groups of slaughter pigs. Factors and their interactions are ranked in descending order of contribution. Sensitivity indices were computed according to a method based on principal components analysis (PCA) and ANOVA (in black: factor or interaction index; in white: cumulative contribution). Panel A: indices corresponding to the first component of PCA, which explained 81.5% of the prevalence distribution variability; panel B: indices corresponding to the second component of the PCA, which explained 17.2% of the variability.

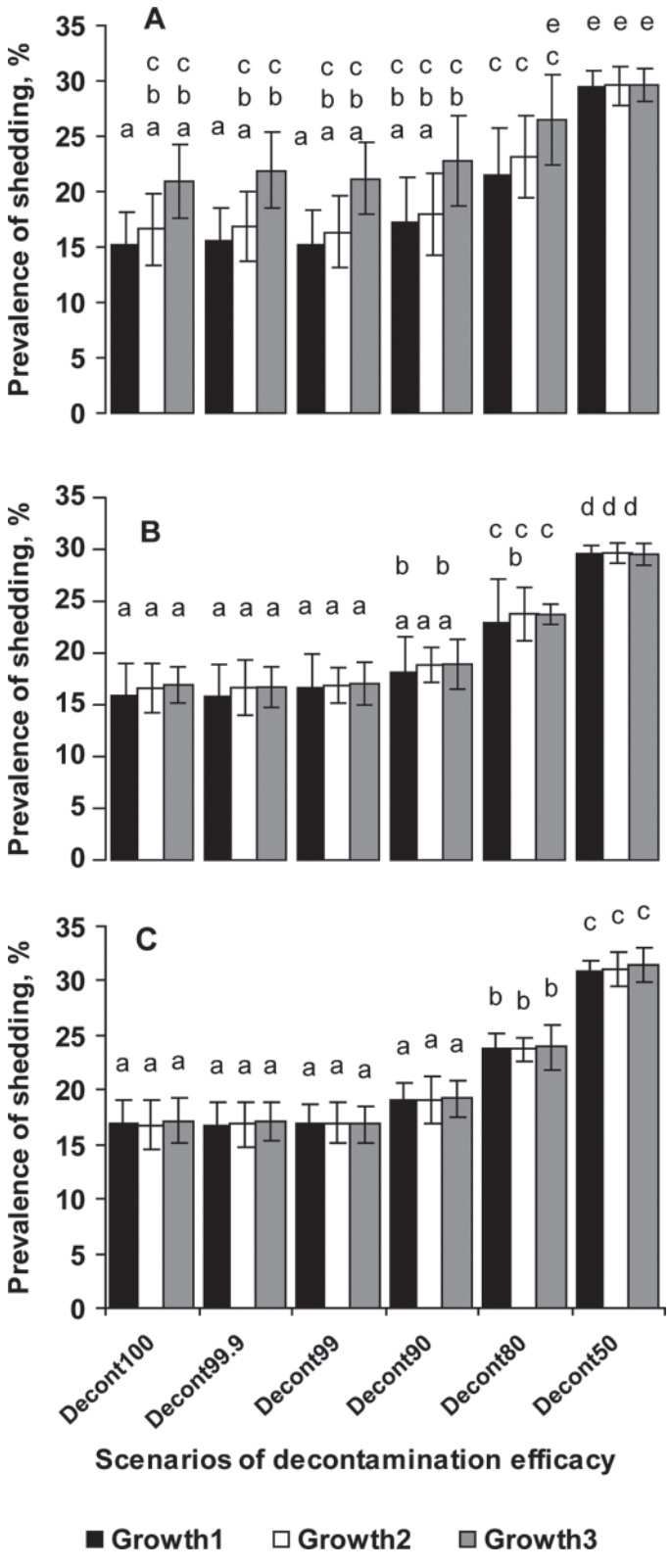

Figure 4. Mean and SD for the *Salmonella* prevalence of shedding in groups of slaughter pigs according to 54 scenarios. Panel A: scenarios with an all-in/all-out batch-management system (Mix0); Panel B: scenarios with pig mixing at the end of the finishing period (Mix1); Panel C: scenarios with pig mixing at the end of the postweaning and finishing periods (Mix2). The means and SD were calculated over 60,000 groups of slaughter pigs for each scenario (300 simulations performed over 400 wk). Definition of scenarios was based on the factor levels pig mixing (Mix), mean age at slaughter (Growth) ranging from 25 to 30 wk, and decontamination efficacy (Decont) ranging from 100 to 50%. $^{a-e}$Within a panel, prevalences with the same letter are not significantly different ($P > 0.05$).

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A thorough model validation would require prevalence data from herds with constant characteristics (e.g., batch management, hygiene, herd size), which were not available. Given that the seroprevalence distributions reported in the literature were built from several herds, only qualitative validation can be performed. However, consistent with observed data under field conditions, our model captured both the greater variations in prevalence between consecutive groups of pigs at slaughter and the existence of seronegative groups in infected herds.

In this study, *Salmonella* infection was estimated by the prevalence of shedding in groups of slaughter pigs, which included all shedding epidemiological states (seronegative and seropositive shedders). Indeed, this output seemed well suited to assess the potential risk to food safety because pigs shedding the bacteria are responsible for contamination during transport and lairage (Swanenburg et al., 2001). These stages are stressful and can increase shedding in infected animals and then promote new infections. Because the delay between infection and shedding can be very short (i.e., 2 to 6 h; Wood et al., 1989), these newly infected animals can participate to cross-contamination.

Salmonella in pig herds can be controlled by preventing the introduction of bacteria into the herds or by reducing within-herd transmission or both. However, the effect of control measures on *Salmonella* prevalence is difficult to evaluate in herds. Several modeling approaches have identified key factors, which should be targeted by potential control measures. van der Gaag et al. (2004) and Hill et al. (2007) highlighted the major role of transmission variables in the control of *Salmonella* prevalence in positive herds. These variables were tested at the animal level. Our study concentrated on 3 factors at the herd level: 1) herd management with or without the possibility pig mixing among batches, 2) mean age at slaughter, and 3) decontamination efficacy.

The levels of these factors used here were based on observations in actual pig herds. The 3 batch-management systems tested derived from the results of a survey of 36 farms in France (Hébert et al., 2007), which indicated that pig mixing was frequent during postweaning and finishing periods. We used performance results to choose mean age at slaughter (IFIP, 2008) for the mean and the upper bound of the confidence interval and situations in which drastic increases might occur, for example, due to a disease affecting growth rate. Lastly, the decontamination efficacy levels tested were based on the literature. The in vitro efficacy of a disinfectant can produce a 5-log decrease in the quantity of bacteria present in a test sample. However, under farm conditions, the efficacy of disinfectants is likely to be less because of OM remaining after cleaning and low temperatures in the animal houses. Previous studies revealed highly variable and quite poor decontamination efficacy in real-life situations [less than 80% efficacy in poultry transport containers (Ramesh et al., 2002) and poultry houses (Gradel et al., 2004; Wales et al., 2006)].

By comparing the relative contributions of pig mixing, room decontamination efficacy, and increased mean age at slaughter with the *Salmonella* prevalence in groups of slaughter pigs, our study showed that decontamination efficacy was the most influential factor. The decontamination and the implementation of a drying period in rearing rooms between 2 consecutive batches have been identified as protective factors in controlling *Salmonella* shedding by finishing pigs (Lo Fo Wong et al., 2004; Schmidt et al., 2004). However, bacteriological methods are time-consuming and rarely used to monitor *Salmonella* in pig herds. Most published data focused on the number of samples that become negative after a decontamination process, but the quantity of bacteria eliminated is poorly documented. Additional data are needed to better understand and quantify the influence of the decontamination efficacy on *Salmonella* spread within pig herds.

With or without pig mixing, an increase in the mean age at slaughter induced a greater prevalence in pigs at slaughter. Indeed, such an increase led to a greater pig density in the finishing rooms, a longer exposure time for the susceptible pigs, and more *Salmonella* shed by infected pigs.

The minor effect of pig mixing on *Salmonella* prevalence was unexpected, especially when combined with greater values of mean age at slaughter, which exacerbated pig mixing occurrence (Lurette et al., 2008a). Batch-management system, as opposed to continuous flow, has been identified as a protective factor against *Salmonella* spread (Stege et al., 2001; Lo Fo Wong et al., 2004). *Salmonella* prevalence is highly variable between batches within a herd (e.g., in France; Corrégé and Guyomart, 2007), so mixing is expected to help spreading the bacteria. Several hypotheses can be formulated to explain the minimal impact of animal mixing in our study. The first hypothesis is that the number of infected pigs mixed was not great enough to induce a significant modification in the mean prevalence of shedding in groups of slaughter pigs. The rearing room capacity limited the number of pigs mixed. At the end of the postweaning period, even if almost 50% of the batches contained pigs from other batches, the number of mixed pigs remained small. At the end of the finishing period, the number of mixed pigs was relatively large, but these pigs stayed at most 2 wk in their new finishing room. The second hypothesis is linked to our representation of the infection probability, which depended on the quantity of bacteria per pig in a room. The inflow of infected pigs from another batch increased the global quantity of bacteria shed in the room, but also the number of pigs in the room. The prevalence increase was therefore limited. The third and last hypothesis is that the greater impact of batch management observed in previous studies was mainly due to the decontamination of rearing rooms between 2 consecutive batches, which cannot be implemented in continuous flow. This again emphasized the importance of the cleaning/disinfecting process.

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Table 3. Proportion of batches from which pigs are mixed with another batch, mean number of mixed pigs per batch mixed, and prevalence of shedding in mixed pigs; these 3 outputs were computed at the end of the postweaning and finishing periods for the scenarios with pig mixing at the end of the 2 periods (Mix2)[1]

			At the end of the postweaning period			At the end of the finishing period		
Scenario			Pig mixing frequency, % of batches	Mean number of mixed pigs	Prevalence of shedding in mixed pigs, %	Pig mixing frequency, % of batches	Mean number of mixed pigs	Prevalence of shedding in mixed pigs, %
Mix2	Growth1	Decont100	56	12.5	12.8	63	16.9	17.4
		Decont99.9			10.6			19.8
		Decont99			11.7			18.0
		Decont90			17.0			23.8
		Decont80			17.0			23.0
		Decont50			27.4			30.6
	Growth2	Decont100			11.4			22.4
		Decont99.9	50	11.6	8.8	70	44.5	20.4
		Decont99			14.0			20.7
		Decont90			8.3			21.3
		Decont80			22.0			27.8
		Decont50			27.2			33.1
	Growth3	Decont100			15.3			22.7
		Decont99.9	54	13.1	16.0	37	53.2	26.1
		Decont99			12.3			22.9
		Decont90			18.6			28.3
		Decont80			17.7			25.6
		Decont50			31.5			33.0

[1]Definition of scenarios was based on the factor levels pig mixing (Mix), mean age at slaughter (Growth) ranging from 25 to 30 wk, and decontamination efficacy (Decont) ranging from 100 to 50%.

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This importance of the decontamination process was also highlighted by the fact that the introduction of negative batches of piglets in a contaminated herd can lead to *Salmonella*-free groups of slaughter pigs only for high decontamination efficacies. However, between 99 and 100%, the decontamination efficacy had the same impact on the prevalence of pigs at slaughter. Further studies should focus on the combinations of several actions to explore the probability of the infection extinction.

Up to now, there are no direct incentives for French pork producers to reduce the *Salmonella* prevalence in their herds: neither control systems nor financial penalties for the delivery of contaminated slaughter pigs. Indirect incentives, such as the increased interest for food safety and the large competition in the pork (international) market, are gaining importance. At present, to maximize their income, producers prefer to avoid delivering underweight pigs to the slaughterhouse rather than to observe the recommended strict all-in/all-out management. In the context of *Salmonella* control, our simulation results showed that some flexibility in batch management is acceptable, provided that a good level of decontamination is ensured in the rearing rooms. An increase in the age at slaughter is usually due to growth problems that cannot be compensated because they are usually discovered quite late. However, producers should pay a particular attention to batches in which such problems occur, as they give rise to greater *Salmonella* prevalence.

A 3-wk-interval batch-management system is adopted in the majority of French pig farms and is increasingly applied in European countries (Brown, 2006). A system with a 1-wk interval between 2 batches is developing in large pig herds. It is very similar to the 3-wk-interval system (e.g., room occupancy, decontamination process, drying period duration, succession of batches in the rearing rooms), but pig mixing can be more easily implemented due to the small age difference between consecutive batches. It would be interesting to explore the impact of such a management system on *Salmonella* spread.

In conclusion, our simulation results emphasized the need to place priority efforts on the cleaning-disinfecting process of rooms to limit the spread of *Salmonella* within farrow-to-finish pig herds. As a further perspective, the flexibility of our approach makes it a suitable tool to assess the impact of control measures implemented at the animal level (modification of the individual susceptibility by genetic selection or vaccination, for instance) in combination with herd management.

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