RESEARCHREPORT
PORK SAFETY

Title: Risk informed management of Salmonella in deep tissue lymph nodes – **NPB #10-130**

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Industry summary

The objectives of this project were to build and parameterize a quantitative risk model of the *Salmonella* prevalence along the pork production chain, and therefore to apply the model in evaluating the relative impact of potential *Salmonella* source, especially lymph nodes, to human food-borne risk.

Attention has turned to the potential negative role of deep tissue lymph nodes in *Salmonella* contamination in pork products, such as ground pork. Previous research has shown a low likelihood of recovery from non-visceral lymph nodes (deep tissue). The occasional recovery of *Salmonella* from these tissues does not necessarily represent a significant human illness risk. However, needed is a method that could assist decision makers in quantitatively evaluating the relative impact deep tissue lymph nodes on *Salmonella* contamination in pork products, thereafter the impact on public health. Without a firm understanding on the impact, regulators may enforce further control measures to remove deep tissue lymph nodes during swine carcass harvest, which might actually a waste of time and money.

Quantitative risk assessment is an approach that is able to quantify and compare the impact of potential risk factors on outcomes of interest. We developed a risk assessment model quantitatively describing the *Salmonella* distribution and dissemination from chilled swine carcasses to fresh ground pork serving. Deep tissue lymph nodes were simulated in the model as a potential source of *Salmonella* contamination in ground pork. The other targeted source is contaminated carcass surface. A scenario analysis was used to estimate the reduction in *Salmonella* contamination of ground pork if deep tissue lymph nodes were removed and if carcass surface was decontaminated. In the scenario analysis, the amount of deep tissue lymph nodes and the proportion of contaminated carcass surface included in ground pork were tentatively modified. The difference in risk of *Salmonella* contamination in ground pork were then estimated between the baseline and modified levels.

When the amount of deep tissue lymph nodes were changed from baseline value to zero, the probability of *Salmonella* contaminated ground pork servings only reduced from 8.3% to 7.9%. This reflects a situation if the deep tissue lymph nodes would be completely removed in processing plant. If the intervention of deep tissue lymph nodes is the one to consider for the future to provide a high level of ground pork safety, the questions is, how likely is the intervention to occur, and at what cost. In practice, the complete removal of deep tissue lymph nodes could be very time and labor consuming. However, when the probability of *Salmonella* contamination on carcass surface at processing plant reduced from baseline value to its half, the probability of *Salmonella* contaminated ground pork servings would reduce from 8.3% to 6.6%, end even below 2.8% if carcass surfaces were completed decontaminated.

The findings reveal that deep tissue lymph nodes have non-significant impact, and *Salmonella* contamination from carcass surface has a more important influence on *Salmonella* contamination in ground pork. Therefore, compared to intervention strategies, such as mitigation of *Salmonella* on carcass surface, the intervention of DTLNs at processing plants might not be able to effectively reduce the *Salmonella* contamination in ground pork.

Keywords (at least five keywords)

Deep tissue lymph nodes, *Salmonella*, ground pork, relative impact, quantitative risk assessment

Scientific abstract

The objective of this project was to assess the contribution of deep tissue lymph nodes (DTLNs) to the *Salmonella* contamination of ground pork in the United States. A quantitative risk assessment model was developed that described ground pork production starting from chilled swine carcasses. A scenario analysis was conducted to compare the probability of *Salmonella* contaminated ground pork between baseline and alternative scenarios where three main input parameters related to *Salmonella* contamination in DTLNs were intentionally modified. The scenario analysis showed when the *Salmonella* contamination originated from DTLNs was changed from baseline value to zero, the probability of *Salmonella* contaminated ground pork changed from 8.3% to 7.8%, without the evidence of significance based on t-test. In contrast, the probability of *Salmonella* contaminated ground pork significantly increased when *Salmonella* contamination from carcass surface was increased. Our findings indicate that the deep tissue lymph nodes do not have an influential impact on *Salmonella* contamination in ground pork, compared to other sources such as *Salmonella* on carcass surface. Therefore, the intervention of DTLNs' removal at processing plants might not be able to effectively reduce the *Salmonella* contamination in ground pork.

Introduction

The consumption of pork products is considered as a risk factor for human salmonellosis all over the world. It has been estimated that 15% of *Salmonella* infections in humans are caused by the consumption of contaminated pork or processed foods derived from pork in Europe (Hald *et al.*, 2004; Pires *et al.*, 2010). In the United States the attribution of pork to *Salmonella* infection cases it is estimated at about 1% (Guo *et al.*, 2011).

Not all retail pork products are of equal food safety risk. Significantly higher prevalence of

Salmonella contamination in ground pork than whole carcasses has been observed in the United States. Much higher contamination has been observed in ground pork (16%) (White *et al.*, 2001) than pork chops (0.6-1.6%) (FDA, 2005). The discrepancy between these products could be due to 1) comingling of tissue from multiple animals into the ground products; and 2) the inclusion of deep tissue or non-visceral lymph nodes (DTLNs) contaminated with *Salmonella* in ground pork. The rationale for the second hypothesis is that *Salmonella* is able to survive and proliferate in phagocytes and leucocytes of the live animal (Reed *et al.*, 1986; Wells, 1990). The DTLNs, such as sub-iliac, prescapular and popliteal lymph nodes, are likely to be involved in whole or non-intact pork products because they are usually embedded in the fat tissue, and there is no specific process for their removal. Therefore, *Salmonella* in phagocytes and leucocytes within deep tissue lymph nodes may contribute to *Salmonella* in ground pork posing a risk to public health (Anonymous, 2011).

There are few studies evaluating the magnitude of DTLNs' contribution to ground pork contamination. The current knowledge about *Salmonella* contamination in DTLNs is restricted to the reported low prevalence of DTLNs (Bahnson *et al.*, 2006; Hurd *et al.*, 2001; Wang *et al.*, 2010). However, a chain connecting the complex multiple stages of food preparation needs to be considered to assess the relative contribution of DTLNs on the *Salmonella* contamination in ground pork.

One approach to evaluating DTLNs contribute to ground pork contamination is an empirical study that quantifies the contribution. However, such a study is not a trivial exercise as it would require tracing carcasses directly to batches of ground pork and testing many samples due to the low prevalence of DTLNs contamination with *Salmonella* (Wang *et al.*, 2010). An alternative approach is to create a theoretical quantitative risk assessment model of ground pork production based on our best understanding of the system. Quantitative risk assessment modeling is an increasingly popular approach in the ongoing efforts to manage food safety risk. For example, Alban and Stärk (2005) employed a risk assessment model to indicate the potential effective intervention strategies from live pigs on farm to the final carcass by determining the variables with maximum effect on the *Salmonella* prevalence on the final carcass. Hurd *et al.* (2008) developed a model based on computer simulation, covering the modules representing the farm-to-pork continuum. Hurd's study showed the most effective means of reducing the risk of pork-attributable human cases was carcasses decontamination. The advantage of the model approach is that the outcome of interest can be quantitatively measured. The model can provide comparative information about ground pork contamination and therefore inform where it is most likely that contamination arises. Directed by the model results, resources can then be devoted more discriminately.

In general, although previous research has shown an extremely low likelihood of recovery from non-visceral lymph nodes (deep tissue), attention has now turned to *Salmonella* in these tissues. However, the occasional recovery of *Salmonella* from non-visceral lymph nodes does not necessarily represent a significant human illness risk. Needed is a method or tool that will assist decision makers in quantitatively evaluating the relative impact of multiple *Salmonella* sources on the final outcome of concern, human illness. In the absence of this "risk-informed" decision tool regulators may enforce further control measures to remove this "potential risk". Without a firm understanding on the impact these measures will have on risk, time and money will be wasted.

Objectives

The objectives of this project were 1) to build and parameterize a quantitative risk model of the *Salmonella* prevalence from the farm to the whole pork distribution, and 2) to apply the model in evaluating the relative contribution of each Salmonella source, especially lymph nodes, to human food-borne risk.

Materials & Methods

1. Modeling approach

The model represented the production process from the chilled swine carcasses to fresh ground pork servings, including fabricating carcasses into primal and sub-primal cuts which were then trimmed, mixing trim into grinding load which was then portioned into servings. The model was divided into two segments referred to hereafter as modules 1) "fabricating and trimming" and 2) "grinding and partitioning". The outcome of interest was the probability of ground pork servings contaminated with *Salmonella* spp. in the United States.

Input parameters were either deterministic or stochastic depending on data availability. The distribution of stochastic parameters were either predefined or fitted by SAS software (Version 9.2, SAS Institute Inc., Cary NC). Distributions fitted by SAS were applied to the parameters for which systematic literature search was conducted. The selection criteria of input parameters for systematic literature search is explained in a later section 2.10. The risk assessment model was developed using Microsoft Excel® spreadsheet (Microsoft Corp., Redmond, WA) and the Monte Carlo simulation for 10,000 iterations was used to obtain stochastic estimates of the output variables using @Risk® 5.7 (Palisade Corp., Ithaca, NY). To obtain the 95% probability intervals (PI) for output means, a 2-loop simulation was used (10,000 iterations per simulation for 100 simulations). Therefore, 100 means following a normal distribution were obtained for the PI calculation.

2. Process of ground pork production and schematic overview of the model

The model simulated the passage of chilled carcasses through the post-processing procedures. The product of interest was fresh ground pork, defined as finely chopped pork trim by a meat grinder without seasonings and fermentation. Therefore, sausage products were not considered. In pork production, after carcasses have been cooled for at least 12 hours, they enter the fabricating and trimming line, where they are cut into five primal cuts, including head, shoulder, ham, loin, and belly, followed by breaking down the primals into smaller portions called sub-primals. Trim is then obtained as the by-product at multiple lines in the fabrication process by cutting the excess fat and lean off the primals and sub-primals. At each line, trim is loaded into boxes, which is defined as containers that hold a certain amount of trim. The trim production process is shown in Figure 1. Multiple carcasses (c) might contribute trim to a single box till the box is fully loaded. Subsequently, either in the processing plants or grocery stores, multiple boxes (b) of trim is mixed together for grinding. Ground meat is then partitioned into servings (g), each of which is assumed to be consumed by one person. This is the production system that the model aimed to simulate. The contamination level of each carcass was simulated separately. This allowed modeling of the number of *Salmonella* in a box by summing the number of *Salmonella* in the contributing carcasses (c) and the number of *Salmonella* in a grinding load by simply taking the sum of *Salmonella* in the contributing boxes (b). The schematic map of the model is shown in Figure 2.

3. Summary of assumptions

1) All carcasses contributing trim to the same box originated from the same herd. This assumption was made because the carcasses contributing trim to the same box are usually consecutive along the processing line. The consecutive carcasses usually originate from live pigs shipped from the same herd. Therefore, by assuming this, *Salmonella* contamination of DTLNs or carcass surface followed the same probability distribution for the carcasses contributing to the same box. This assumption was likely to reduce output variation.
2) The carcasses contributing trim to different boxes originated from independent herds, which meant *Salmonella* contamination of DTLNs or carcass surface of carcasses distributed to different boxes could follow either the same or different probability distribution by random chance.
3) Trim was split into two parts in the model: DTLNs and trim other than DTLNs. By assuming this, the number of *Salmonella* from trim of a carcass was the sum of *Salmonella* organisms from DTLNs and from trim other than DTLNs of that carcass.
4) All DTLNs in swine carcasses were assumed to be sorted off as trim and completely included in ground pork. This assumption was conservative, meaning higher model simulated *Salmonella* contamination in ground pork then reality.
5) *Salmonella* contamination of trim other than DTLNs occurred from the surface of swine carcass rather than muscle and fat tissue in trim (Humphrey *et al.*, 2000; Swanenburg *et al.*, 2001).
6) DTLNs contamination and surface contamination from the same carcass were assumed to be independent events because no documented evidence showed the correlation between *Salmonella* positive DTLNs and *Salmonella* contaminated surface of swine carcasses.
7) *Salmonella* organisms on DTLNs and carcass surface were homogeneously distributed in trim and ground pork.

4. State parameters of grinding load

Table 1 shows the summary of state parameters that were used to calculate the number of chilled carcasses contributing to one box (*c*) and the number of boxes contributing to one grinding load (*b*). We modeled 13 carcasses contributing trim to a box and 5 boxes combined for a grinding load.

5. Fabricating and trimming module

The output of the “fabricating and trimming” module was the number of *Salmonella* organisms (CFU) in a box (S_{box}), which was the sum of the number of *Salmonella* organisms from DTLNs (S_{DTLN_box}) and from the trim other than DTLNs ($S_{notDTLN\_box}$). Table 2 shows the summary of “fabricating and trimming” module, including the values/distributions, calculation formula and references of the parameters.

6. Grinding and partitioning module

The output of the “grinding and partitioning” module was the probability of the ground pork servings contaminated by *Salmonella* in the United States ($P_{estimated}$). Table 3 summarizes the values/distributions, calculation formula and references of the parameters used in “grinding and partitioning” module.

7. Model validation

The model's ability to produce realistic estimates was appraised by comparing the model-estimated probability of *Salmonella* contaminated ground pork in the United States ($P_{estimated}$) to the observed one. The observed probability was determined by systematically reviewing and synthesizing the reported *Salmonella* prevalence in ground pork produced in the processing plants or at retail stores ($P_{reported}$) in the published literatures. The search strategy and data extraction of this review are explained in Section 2.10. Although those data were reported in different studies, all employed *Salmonella* detection methods with approximately the same detection limit, 1CFU/25g equivalent to 4 CFUs in one ground pork serving. Therefore, the detection limit ($S_{detection}$) used in "grinding and partitioning" module to estimate the final output was also 4 CFU in one ground pork serving, which made it comparable between the model estimated ($P_{estimated}$) and reported ($P_{reported}$) probability of *Salmonella* contaminated ground pork.

8. Scenario analysis

A scenario analysis was conducted to pursue the objective of this study, to quantitatively estimate the impact of *Salmonella* contamination in DTLNs on *Salmonella* contamination in ground pork. The probability of *Salmonella* contaminated ground pork was simulated in seven scenarios. The baseline scenario was run using the baseline data (as shown in Table 1, 2, and 3) and population assumptions at the time of the analysis. Six alternative scenarios were run by modifying the following three input parameters:

Parameter 1) probability of a carcass with *Salmonella* positive DTLNs (P_{DTLN}),

Parameter 2) *Salmonella* concentration in DTLNs (C_{DTLN}), and

Parameter 3) weight of DTLNs from a single carcass contributing to ground pork (W_{DTLN_carc}).

The six alternative scenarios were:

Scenario 1) P_{DTLN} was set to half of its baseline value;

Scenario 2) P_{DTLN} was set to zero;

Scenario 3) C_{DTLN} was set to half of its baseline value;

Scenario 4) C_{DTLN} was set to zero;

Scenario 5) W_{DTLN_carc} was set to half of its baseline value; and

Scenario 6) W_{DTLN_carc} was set to zero.

The alternative scenarios were run using baseline values for all other parameters in the model. All seven scenarios were run using the 2-loop simulation. The set of mean values for each alternative scenario was then compared with the baseline scenario using t-test based on a significance level of 0.05. Additionally, these seven scenarios were evaluated at multiple levels of carcass surface contamination by tuning the parameter of the percentage of carcass surface contributing to ground pork (P_{surf_carc}).

9. Evidence for parameters

The approach to develop evidence for parameters in the model varied. For the following parameters, a comprehensive search of the literature in PubMed database (1956-March 2011) was conducted: 1) probability of a swine carcass with *Salmonella* contaminated surfaces ($P_{cntm\ surf}$); 2) probability of a swine carcass with *Salmonella* positive DTLNs (P_{DTLN}); 3) probability of *Salmonella* contaminated ground pork ($P_{reported}$). The rationale for choosing these parameters was: 1) they were the primary outcomes of interest and of high degree variability among the published literatures, such as $P_{cntm\ surf}$; 2) they had direct impact on the questions that the model was designed to address, such as P_{DTLN}; or 3) they are essential to the model validation, such as $P_{reported}$.

For the probability of a swine carcass with *Salmonella* contaminated surfaces ($P_{cntm\ surf}$), multiple systematic reviews have been published. Therefore, the evidence for this parameter was obtained using primary literature identified in the published systematic reviews. An unpublished systematic review of *Salmonella* contamination at different slaughter steps was also included (O'Connor *et al.*, 2009). For the probability of a swine carcass with *Salmonella* positive DTLNs (P_{DTLN}) and the probability of *Salmonella* contaminated ground pork ($P_{reported}$), the evidence was obtained by searching primary literature directly. The search algorithm is shown in Table 4.

Retrieved articles from initial search were screened for the eligibility for data extraction. Articles were included if they 1) were in English, otherwise excluded due to unavailable translation; 2) were within the United States or Canada; 3) described naturally occurring contamination, otherwise excluded if related to intervention or experimental studies; 4) were about *Salmonella* spp., rather than a specific subtype, such as *Salmonella* Typhimurium; 5); were about *Salmonella* contamination of chilled carcasses and DTLNs of finishing market weight pigs; 6) reported the *Salmonella* percentage with numbers of positive samples and the numbers of total tested samples. Only studies that reported those numbers were included because parameter distributions were fitted by adjusting for sample sizes. Relevant references were restricted to North America, because great difference might be shown in parameter estimates based on evidence from different locations (such as Europe vs North America) due to different nature of swine production and processing systems employed. For example, the final wash before chilling was approved by USDA as a critical control point to reduce bacterial load from previous slaughter steps (USDA FSIS, 1995), but in Europe was not (Bolton *et al.*, 2002).

Extracted data from eligible studies included apparent *Salmonella* prevalence for different parameters with numbers of positive samples and the total tested samples (where available) and number of *Salmonella* organisms in positive samples (where available). To create the distributions used as input parameters for the model, the distribution of prevalence was fitted using a mixed effect logistic regression model for binomial responses. The analysis was performed using the GLIMMIX procedure in SAS software, Version 9.2. Data points were synthesized with adjustment of sample sizes. The fitted distributions are reported in Table 5.

Results

1. Objective 1 To build and parameterize a quantitative risk model of the Salmonella prevalence from the farm to the whole pork distribution

When the baseline parameter estimates were used in the model, the model-estimated mean probability of *Salmonella* contaminated ground pork servings in the United States was 8.3% (Figure 3). The probability distribution was very skewed to the right. Most of the estimated probabilities were located near 0%. Of 10,000 iterations, 88.4% of the estimated probabilities were below the mean value (8.3%) and 90% of estimates less than 17.3%.

Published literatures on the probability of *Salmonella* contaminated ground pork ($P_{reported}$)

were searched and data were extracted and synthesized for model validation. Finally, two studies were eligible for data extraction (Duffy *et al.*, 2001; White *et al.*, 2001) regarding the inclusion criteria. The characteristics of the two studies are shown in Table 6. These two studies were published in 2001 with the time period of sampling and laboratory procedure from 1998 to 2001. In Duffy's study (2001), multiple data points were extracted due to multiple visits to processing plants or retail stores. Totally, six data points were used for the estimation of $P_{reported}$. Three data points were obtained based on the fresh ground pork samples from processing plants, and the remaining were from retail stores.

The reported probability of *Salmonella* contaminated ground pork ranged from 0 to 16.3%, with a weighted average of 11.3%, median of 8.2% and 90% quantile of 25.6% (Table 5). Similar to the model-estimated probability, the reported *Salmonella* contamination probability in ground pork was skewed to the right with a high probability density near the lower end. The model estimated mean value (8.3%) was slightly lower than the reported (11.3%) which were obtained using the data of processing plants and retail stores. When calculated separately, reported probability of *Salmonella* contaminated ground pork in processing plant was 5.8% and 11.2% at retail. The higher contamination at retail stores could be explained because it is likely that higher bacterial amplification occur due to temperature abuse during the transportation and storage at retail. The model estimate was in between the line of the reported contamination probability of processing plants and retail stores (Figure 3). When also considering the variability in results between different empirical data sets and the statistical uncertainty, the model seems to produce realistic results.

2. Objective 2 To apply the model in evaluating the relative contribution of each *Salmonella* source, especially lymph nodes, to human food-borne risk

The main objective of this model was to quantitatively estimate the impact of *Salmonella* contamination in DTLNs on *Salmonella* contamination in ground pork, by comparing the difference in model outputs in alternative scenarios to baseline. Table 7 lists the estimated probability of *Salmonella* contaminated ground pork from baseline and six alternative scenarios. When the probability of carcasses with *Salmonella* positive DTLNs (P_{DTLN}) changed from baseline data to its half and then zero, the mean probability of *Salmonella* contaminated ground pork changed from 8.3% (baseline scenario) to 8.1% (Scenario 1) and 7.8% (Scenario 2) and the 90% quartile value changed from 17.3% (baseline scenario) to 16.5% (Scenario 1) and 10.4% (Scenario 2). Similar minor changes were observed when input values of *Salmonella* concentration in DTLNs (C_{DTLN}) and the weight of DTLNs from a single carcass contributing to ground pork (W_{DTLN_carc}) were modified (Table 7). For all alternative scenarios, there was no evidence to show the significant difference in the probability of *Salmonella* contaminated ground pork between alternative scenarios and baseline scenario based on the t-tests (P-values > 0.05). Figure 4 shows the overlapping probability histogram distributions of baseline and alternative scenarios.

Additionally, the impact of DTLNs on *Salmonella* contamination in ground pork was examined at different levels of the percentage of a carcass surface area contributing to ground pork (P_{surf_carc}). P_{surf_carc} is a parameter that represents *Salmonella* contamination originated from carcass surface. As shown Table 8, for each scenario, the estimated probability of *Salmonella* contaminated ground pork varied significantly depending on the P_{surf_carc}. As expected, the higher the P_{surf_carc}, the higher the probability of *Salmonella* contaminated ground pork. Take the baseline scenario for example, when P_{surf_carc} increased from 10% to 90%, the probability of *Salmonella* contaminated ground pork increased from 2.8% to 8.9%. However, within a specific level of P_{surf_carc}, most of the changes were not significant between scenarios. Between levels of P_{surf_carc}, the difference in the model outputs between alternative and baseline scenarios was similar. For example, for P_{surf_carc} of 75% used as the baseline value in the model, the differences in model outputs between each scenario (from Scenario 1 to 6) and the baseline were 0.2, 0.5, 0, 0.1, 0.2, and 0.4. For P_{surf_carc} of 20% which is a very different level from the baseline value, the differences were 0.2, 0.5, 0.4, 0.7, 0.2, and 0.3. Considering the simulation uncertainty, the differences in the model outputs between alternative and baseline scenarios were very stable through different levels of P_{surf_carc}.

Discussion

The scenario analysis was performed to estimate the effect of all the input parameters in the model that are related to the *Salmonella* contamination in DTLNs on final model output, which was vital to pursue the objective of this study, to assess the contribution of DTLNs to the *Salmonella* contamination in ground pork. The scenario analysis shows that when setting the probability of swine carcasses with *Salmonella* positive DTLNs to zero, the estimated mean probability of *Salmonella* contaminated ground pork decreases from 8.3% to 7.8%. Similar minor differences are observed when comparing other alternative scenarios with the baseline scenario. However, when applied to the ground pork production in the United States, the conclusion may be different. It was estimated that the pork production in the United States is 22,436.5 million pounds for commercial purpose in 2010 (USDA ERS, 2011). If 11.1% of dressed swine carcass weight contributed to ground pork and a single serving is 85 g as simulated in this model, there were approximately 13,282.4 million servings and on average 43 servings per person consumed in the United States in 2010. Therefore, the reduction of probability of *Salmonella* contaminated ground pork from 8.3% to 7.8% could lead to a reduction of 66.4 million contaminated ground pork servings and an average reduction of two *Salmonella* contaminated servings for every ten persons in 2010 (the US population in 2010: 308.75 million, US Census Bureau, 2011).

The real impact of DTLNs on *Salmonella* contamination in ground pork is likely less than the findings in this study, because several input parameters were simulated using conservative values or distributions. The application of these conservative parameters resulted in an overestimated impact of DTLNs on *Salmonella* contamination in ground pork. For example, it was assumed that all DTLNs on swine carcasses contributed to ground pork as baseline, which is an unrealistic upper-bound. Therefore, when halving or turning off the weight of DTLNs contributing to ground pork (W_{DTLN_carc}), the changes in the probability of *Salmonella* contaminated ground pork is greater than it might be in reality. Another parameter is the concentration of *Salmonella* in DTLNs (C_{DTLN}). This parameter was estimated from the concentration of *Salmonella* in gut-associated lymph nodes, which should have higher concentration of *Salmonella* than DTLNs. It is almost impossible to compare the concentration values of *Salmonella* in deep tissue and gut-associated lymph nodes, because of the limited *Salmonella* enumeration data in the tissues of swine sources. However, a much higher prevalence of *Salmonella* in gut-associated lymph nodes than DTLNs was reported in primary studies (Bahnson *et al.*, 2006; Hurd *et al.*, 2001; Wang *et al.*, 2008). In addition, the gut-associated lymph nodes are the primary defense against orally consumed bacteria (Macpherson and Smith, 2006). Therefore, it is reasonable to assume the use of *Salmonella* concentration in gut-associated lymph nodes is an overestimated substitution of that in DTLNs, which might increase the model-simulated contribution of DTLNs to *Salmonella* contamination in ground pork.

The model shows that a higher level of the percentage of swine carcass surface area contributing to ground pork (P_{surf_carc}) could significantly increase the *Salmonella* contamination in ground pork. The positive association indicates that procedures implemented to reduce *Salmonella* contamination on carcass surface might be able to effectively mitigate the *Salmonella* contamination in ground pork. This is probably because a major contamination route of swine carcasses is the contamination on the surface via fecal content and environment (Humphrey *et al.*, 2000, Swanenburg *et al.*, 2001). The model also shows the impact of DTLNs is very stable regardless of different levels of carcass surface contamination. This result strongly suggests DTLNs have less influence on *Salmonella* contamination in ground pork than the contaminated carcass surface. These findings supported the use of USDA recommended swab samples of carcass surface to annually monitor the swine contamination level of swine carcasses (USDA FSIS, 2011).

Although many quantitative microbiological risk assessment models represent pork production from live animal production to consumption (Barron *et al.*, 2009; Bollaerts *et al.*, 2009; Delhalle *et al.*, 2009; Hill *et al.*, 2003; Ranta *et al.*, 2004), this study developed a risk assessment model focusing on the process starting from chilled carcasses at processing plants, not the live pigs on swine farms. One rationale for this approach is that the inclusion of production module is not germane to the question whether DTLNs are an influential source for *Salmonella* contamination in ground pork. If the model was developed starting from live pigs, there would be two more modules before the "fabricating and trimming" module and "grinding and partitioning" module added in the model. One would be the "production" module whose output would be the percentage of live pigs shedding *Salmonella*; and the other would be the "processing" module whose output would be the percentage of carcasses with *Salmonella* contaminated surface. Neither of these two modules would involve the parameters related to the contamination of DTLNs, because DTLNs are usually detected based on the samples collected from carcasses at the processing plants, not from live pigs (Bahnson *et al.*, 2006; Vieira-Pinto *et al.*, 2005; Wang *et al.*, 2010). Further, our prior work provides little evidence of an association between *Salmonella* contamination in DTLNs and *Salmonella* shedding on farm due to the very low prevalence of *Salmonella* positive DTLNs (Wang *et al.*, 2010).

Another reason is that there would be a great gap between the production and processing module due to the lack of clear evidence to support the correlation between on-farm *Salmonella* shedding and *Salmonella* contamination on carcass surface. The *Salmonella* status on swine farms could be measured by serological tests for the *Salmonella* exposure status or by fecal culture methods for the *Salmonella* shedding status. There is evidence of strong correlation between herd seroprevalence and prevalence of *Salmonella* contaminated carcass surface (Sorensen *et al.*, 2004). However, in the United States, the *Salmonella* status on swine farms is usually measured by the *Salmonella* prevalence in farm feces (Bahnson *et al.*, 2005; Davies *et al.*, 1997; Funk *et al.*, 2000; Gebreyes *et al.*, 2006; Hurd *et al.*, 2004; Wang *et al.*, 2010). Unfortunately, some evidence about the disconnection between *Salmonella* fecal shedding and carcass contamination was reported. For example, the disparity in both prevalence and serotypes of *Salmonella* cultured from farm fecal samples and carcasses at slaughter has been reported in studies of swine in earlier investigations (Gebreyes *et al.*, 2004; Hurd *et al.*, 2001; 2002; Morgan *et al.*, 1987; Williams and Newell, 1968). Mechanisms that may explain these disparities include 1) cross-infection from other animals or contaminated vehicles or facilities during transport or lairage holding (De Busser *et al.*, 2011; Hurd *et al.*, 2001; 2002; Swanenburg *et al.*, 2001); and 2) increased populations of *Salmonella* resulting from stress of transport, including feed and water deprivation (Berends *et al.*, 1996; Teunis *et al.*, 1999). Therefore, the disparities are likely to lead to an invalid estimation of the probability of carcass with *Salmonella* contaminated surface, which as the starting point of "fabricating and trimming" module.

However, there is actually a relatively large collection of empirical data about *Salmonella* contamination of swine carcasses in the real world (Algino *et al.*, 2009; Rose *et al.*, 2002; Saide-Albornoz *et al.*, 1995; USDA FSIS, 1996; USDA FSIS, 2011). By starting from chilled carcasses in the current model, we used the empirical data rather than the simulated data from the "production" and "processing" modules, therefore increasing the ability to produce accurate and precise model output.

The model in this study is able to produce realistic results based on a comparison of model output and reports in published literature, but there still is slight difference between model estimated and literature reported *Salmonella* contamination in ground pork. The disparity could be due to the following reasons. First, the literature reported *Salmonella* contamination in ground pork might not be representative of the national level, while the model aimed to estimate the national *Salmonella* contamination in ground pork as we parameterized input variables using the United States data. Limited data of *Salmonella* contamination in published literature was used for model validation. Although a relatively comprehensive literature search was conducted, only two studies were qualified to extract data for the purpose of understanding the prevalence of *Salmonella* contaminated fresh ground pork in the United States (Duffy *et al.*, 2001; White *et al.*, 2001). Ground pork samples were collected from only two cities in Duffy's study (2001) and one city in White's study (2001). Fresh ground pork is not consumed as commonly as other pork products such as pork sausage and pork chops in the United States, which might be the reason why *Salmonella* contamination in fresh ground pork is not a commonly reported outcome. In addition, the sample sizes of the two studies were relatively small (Table 6), 316 in Duffy's study and 49 in White's study, but the national routine *Salmonella* monitoring program usually collected thousands of samples (USDA FSIS, 2011). Second, publication bias might occur. The model indicates high probability at which the *Salmonella* prevalence of fresh ground pork is 0% (Table 7, 75% quantile: 0.02%). However, only one 0% observation of six were reported; and the remaining 5 data points ranged from 7.3%-16.3% in Duffy *et al.* and White *et al.* studies. The difference in the probability of 0% *Salmonella* contamination in ground pork between model estimation and reported observations might be due to the publication bias. Studies reporting a zero contamination prevalence are not likely to be published, especially when sample sizes are small.

One advantage of this risk assessment model is the use of a systematic and transparent method to synthesize findings from qualified studies, which are used to produce input parameters. Since different primary studies were performed using different populations, different designs and a whole-range of other specific factors, it has been suggested that incorporating this diversity into the model could produce estimates that have boarder generalizability than is possible using only a single study (Sutton *et al.*, 2001). For example, the collection of reported probability of swine carcasses with contaminated surface was with a mean of 4.0% ranging from 0 to 18.8%. In the current model, we fit the probability distributions adjusted for samples size to represent variance and uncertainty of *Salmonella* contamination on carcasses and estimate the *Salmonella* prevalence in ground pork of 8.3%. If the model simulation was only based on a single study for this input parameter, the output of *Salmonella* contamination probability in ground pork would be 19.2% when using the maximum value of 18.8% as input and 0.3% when using the minimum value of 0%, which might lead to very different result inference. Furthermore, a systematic method for literature review could highlight areas where there is insufficient scientific evidence or where there are common methodological imperfections in the available research and thereby provide direction for future basic and applied research in a specific food safety area (Sargeant *et al.*, 2005; 2006). For example, we were forced to use the concentration value of *Salmonella* in gut-associated lymph nodes to implement the one in DTLNs. This highlighted the need for studies that quantify *Salmonella* in porcine samples.

As with all models, one limitation of this model is that it is a reduced explanation of the real world. For example, we assume *Salmonella* organisms are homogeneously distributed in trim and ground pork, which ignores the occurrence of pathogen organisms in clusters. However, another quantitative risk assessment of human salmonellosis through household consumption of fresh ground pork conducted in Belgium indicates that the annual salmonellosis in humans due to consumption of ground pork is sensitive to the amount of clustering of *Salmonella* organisms in the grinding load (Bollaerts *et al.*, 2009). Another example is that we use apparent prevalence to implement true prevalence of input parameters because the sensitivity values for the *Salmonella* detection protocols performed in the individual studies are not found. There might be two effects of this assumption on the final model output. First, greater variance of the estimated probability of *Salmonella* contaminated ground pork was obtained. The corrections for test sensitivities do not aim to give absolute approximations of *Salmonella* prevalence for each study but instead to minimize the level of between-study heterogeneity originated from the wide range of *Salmonella* detection protocols used. Second, decreased estimation of the probability of *Salmonella* contaminated ground pork was generated. True prevalence is greater than the apparent prevalence because it is calculated as apparent prevalence divided by test sensitivity that is less than one. Therefore, with the adjustment for test sensitivity, higher values of the probability of carcasses with positive DTLNs (P_{DTLN}) and the probability of carcasses with contaminated surface ($P_{cntm\ surf}$) could be used in the model to generate a greater mean probability of *Salmonella* contaminated ground pork. This might be one of the reasons why the estimated probability of *Salmonella* contaminated ground pork (8.3%) is smaller than the reported (11.3%).

Another limitation of this model is its limited ability of extrapolation. All the input parameters in this model are quantified based on data in the United States. Due to the difference between countries, adjustments are needed before the model can be used for another country. Therefore, the present study can be seen as a part in the process of gradually better understanding and gaining more insight about the application of quantitative risk assessment modeling approach to address pre- and post- harvest *Salmonella* interventions.

We focused on the intervention for DTLNs to investigate its effect of reducing *Salmonella* contamination in ground pork by scenario analysis. The model suggests that intervention related to DTLNs will have a limited effect on the probability of ground pork contaminated with *Salmonella*. If the intervention of DTLNs is the one to consider for the future to provide a high level of ground pork safety, the questions is, how likely is the intervention to occur, and at what cost. For example, we intentionally turned off the weight of DTLNs from a carcass that might be involved in ground pork from the maximum value of all DTLNs in pig to zero. In practice, the complete removal of DTLNs could be very time and labor consuming. In addition, this model indicates DTLNs have less important influence on *Salmonella* contamination in ground pork compared to the contaminated carcass surface. Therefore, the results of this model indicate the intervention of DTLNs at processing plants might not be able to effectively reduce the *Salmonella* contaminated ground pork.

Overall, we developed a quantitative risk assessment model to estimate the impact of DTLNs on *Salmonella* contamination of ground pork. The scenario analysis suggests that change in parameters related to DTLNs has non-significant impact on *Salmonella* contamination in ground pork, and that *Salmonella* contamination from carcass surface has a more important influence on *Salmonella* contamination in ground pork compared to DTLNs. Therefore, compared to intervention strategies, such as mitigation of *Salmonella* on carcass surface, the intervention of DTLNs at processing plants might not be able to effectively reduce the *Salmonella* contamination in ground pork.

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Table 1. Summary of state variables of grinding load, the distribution/calculation of the input parameters and references

	Description (unit)	Distribution/calculation (D/S[1])	Reference
Input			
ACW	Average weight of dressed swine carcasses(Kg)	92.8 (D)	USDA NASS, 2010
P_{trim_carc}	Percentage of carcass weight sorted off as trim (%)	11.1 (D)	Lorenzen *et al.*, 1996
N	Number of boxes to which an individual carcass contributed	5 (D)	Reddish and Leak, 2003
$W_{trim\_carc\_box}$	Weight of trim a carcass contributed to a single box (Kg)	$(ACW \times P_{trim\_carc}) / N$ (D)	
W_{box}	Total weight of trim per box (Kg)	27.2 (D)	Personal communication with Dickson
$W_{grinding}$	Weight of a grinding load (Kg)	136.1 (D)	Personal communication with Dickson
Output			
c	Numbers of chilled carcasses contributing to one box	Int[2]$(W_{box} / W_{trim\_carc\_box})$ =13 (D)	
b	Numbers of boxes contributing to one grinding load	Int[2] $(W_{grinding} / W_{box})$=5 (D)	

[1] D = deterministic parameters; S = stochastic parameters

[2] Int () returned to the integer of the calculation

Table 2. Summary of "fabricating and trimming" module, the distribution/calculation of the input parameters and references

	Description (unit)	Distribution/calculation (D/S[1])	Reference
Input			
P_{DTLN}	Probability of a carcass with *Salmonella* positive DTLNs (%)	Logit (P_{DTLN})= -4.9863 + ε ε ~ Normal (0, σ^2=2.222) (S)	Bahnson *et al.*, 2006; Hurd *et al.*, 2001; Wang *et al.*, 2010
$N_{cntmDTLN\_box}$	Number of carcasses with *Salmonella* positive DTLNs in a box	$\sum_{1}^{c} \text{Binomial}\ [1,\ P_{DTLN}]$ (S)	
C_{DTLN}	*Salmonella* concentration in DTLNs (CFU/g)	Cumulative(1.6487, 181.27, {2.7183,4.4817,7.3891,12.182,20.086,33.115,54.598,148.41}, {0.3478,0.4348,0.5217,0.6522,0.7391,0.8261,0.8261,0.913}) (S)	Gailey, 2004 Substituted by data of *Salmonella* concentration in gut-associated lymph nodes
W_{DTLN_carc}	Weight of DTLNs from a carcass involved in ground pork (g)	239.2 (D)	Gailey, 2004; Sack, 1982
$S_{DTLN\_carc\_box}$	Number of *Salmonella* organisms in DTLNs from a carcass to a box (CFU)	($W_{DTLN\_carc} \times C_{DTLN}$) / N (S)	

[1] D = deterministic parameters; S = stochastic parameters

Table 2. (continued)

	Description (unit)	Distribution/calculation (D/S[1])	Reference
S_{DTLN_box}	Number of *Salmonella* organisms from DTLNs in a box (CFU)	$\sum_{1}^{N_{cntmDTLN\_box}} S_{DTLN\_carc\_box}$ (S)	
$P_{cntm\ surf}$	Probability of a carcass with contaminated surface (%)	Logit ($P_{cntm\ surf}$)= -3.5666 + ε ε ~ Normal (0, σ^2=0.8128) (S)	Algino *et al.*, 2009; Keenliside *et al.*, 2005; Rose *et al.*, 2002; Saide-Albornoz *et al.*, 1995; Tamplin *et al.*, 2001; USDA FSIS, 2011
$N_{cntm\ surf\_box}$	Number of carcasses with contaminated surface in a box	$\sum_{1}^{c} \text{Binomial}\ [1, P_{cntm\ surf}]$ (S)	
$S_{cntm\ surf\_bf}$	Number of *Salmonella* organisms on carcass surface from a carcass before fabrication (CFU)	$C_{cntm\ surf\_bf} \times A_{cntm\ surf\_bf}$ (S)	
$C_{cntm\ surf\_bf}$	Before-fabrication concentration of *Salmonella* on carcass surface (CFU/cm²)	Cumulative(0, 23, {0.03,0.3,3}, {0.544,0.858,0.953}) (S)	USDA FSIS, 1996

Table 2. (continued)

	Description (unit)	distribution/calculation (D/S[1])	Reference
$A_{cntm\ surf\_bf}$	Before-fabrication contaminated surface area (cm^2)	Uniform(300, TA) (S)	USDA FSIS, 1996
TA	Total body surface area of a dressed hog carcass including both inside and outside the carcass (cm^2)	$734 \times ACW^{0.656} * 1.75$ (D)	Kelly *et al.*, 1973; Personal communication with Hurd and O'Connor
F	Fabrication multiplication factor	2 (D)	Personal communication with Dickson
$S_{cntm\ surf\_af}$	Number of *Salmonella* organisms on carcass surface from a carcass after fabrication (CFU)	$S_{cntm\ surf\_bf} \times F$ (S)	
$A_{cntm\ surf\_af}$	After-fabrication contaminated surface area (cm^2)	IF($A_{cntm\ surf\_bf} < TA/2$, $A_{cntm\ surf\_bf} \times F$, TA) (S)	
$C_{cntm\ surf\_af}$	After-fabrication concentration of *Salmonella* on carcass surface (CFU/cm^2)	$S_{cntm\ surf\_af} / A_{cntm\ surf\_af}$ (S)	

Table 2. (continued)

	Description (unit)	Distribution/calculation (D/S[1])	Reference
P_{surf_carc}	Percentage of carcass surface area ending up in trim (%)	75 (D)	USDA FSIS, 2001 Substituted by ground beef data
Y	Contaminated carcass trim surface area from a carcass (cm²)	$A_{cntm\ surf\_af} \times P_{surf\_carc}$ (S)	
$S_{notDTLN\_carc\_box}$	Number of *Salmonella* organisms from trim other than DTLNs from a carcass contributing to a box (CFU)	$Y \times C_{cntm\ surf\_af} / N$ (S)	
$S_{notDTLN\_box}$	Number of *Salmonella* organisms from trim other than DTLNs in a box (CFU)	$\sum_{1}^{N_{cntm\ surf\_box}} S_{notDTLN\_carc\_box}$ (S)	
Output			
S_{box}	Number of *Salmonella* organisms in a box (CFU)	$S_{DTLN\_box} + S_{notDTLN\_box}$ (S)	Results forwarded to grinding and partitioning module

Table 3. Summary of “grinding and partitioning” module, the distribution/calculation of the input parameters and main sources

	Description (unit)	Distribution/calculation (D/S[1])	Reference
Input			
S	Number of *Salmonella* organisms in a grinding load (CFU)	$\sum_{1}^{b} S_{box}$ (S)	
$W_{serving}$	Serving size (g)	85 (D)	USDA, 2010
$S_{serving}$	Number of *Salmonella* in a serving (CFU)	$S \times W_{serving} / (1000 \times W_{grinding})$ (S)	
$S_{detection}$	Detection limit of *Salmonella* in a serving (CFU)	4 (D)	Duffy *et al.*, 2001; White *et al.*, 2001
Output			
$P_{estimated}$	Probability of the ground pork servings contaminated by *Salmonella* in the United States (%)	1-Poisson ($S_{detection}$, $S_{serving}$, Cumulative Poisson probability) (S)	

[1] D = deterministic parameters; S = stochastic parameters

Table 4. The search algorithm and references for developing evidence for three parameters by a comprehensive search of literature in PubMed (1956-March 2011)

Model parameter	Search algorithm	References[1]
Probability of a swine carcass with *Salmonella* contaminated surface ($P_{cntm\ surf}$)	(Salmonel*) AND (hog OR hogs OR swine OR pig OR pigs OR gilts OR sows OR market-weight OR finishers OR boars OR porcine OR piglet) AND (review OR systematic review OR meta analysis)	Review studies: Barron *et al.*, 2008; Barron *et al.*, 2009; Borch *et al.*, 1996; Foley *et al.*, 2008; O'Connor *et al.*, 2009; USDA FSIS, 2011 Primary studies: Algino *et al.*, 2009; Keenliside *et al.*, 2005; Rose *et al.*, 2002; Saide-Albornoz *et al.*, 1995; Tamplin *et al.*, 2001; USDA FSIS, 2011
Probability of a swine carcass with *Salmonella* positive DTLNs (P_{DTLN})	(Salmonel*) AND (hog OR hogs OR swine OR pig OR pigs OR gilts OR sows OR market-weight OR finishers OR boars OR porcine OR piglet) AND (lymph node OR lymph nodes OR tonsil OR tonsils)	Bahnson *et al.*, 2006; Hurd *et al.*, 2001; Wang *et al.*, 2010
Probability of *Salmonella* contaminated ground pork servings ($P_{reported}$)	(Salmonel*) AND (ground pork OR minced pork OR chopped meat OR chopped pork OR sausage OR sausages OR pork product)	Duffy *et al.*, 2001; White *et al.*, 2001

[1] For the parameter $P_{cntm\ surf}$, the evidence base was obtained by using the primary literature identified in the published systematic reviews. For the other two parameters (P_{DTLN} and $P_{reported}$), the evidence was obtained by searching primary literature directly.

Table 5. Fitted distributions of three *Salmonella* probability parameters using the United States data extracted from a comprehensive literature review

Model parameter	Probability of a carcass with contaminated surface ($P_{cntm\ surf}$)	Probability of a carcass with *Salmonella* positive DTLNs (P_{DTLN})	Probability of *Salmonella* contaminated ground pork ($P_{reported}$)
Distribution	Logit($P_{cntm\ surf}$)= -3.5666 + $\alpha_{cntm\ surf}$[a] $\alpha_{cntm\ surf} \sim$ Normal(0, $\sigma_{cntm\ surf}^2$[b]= 0.8128)	Logit(P_{DTLN})= -7.0834 + α_{DTLN}[a] $\alpha_{DTLN} \sim$ Normal(0, σ_{DTLN}^2[b] = 7.18E-18)	Logit($P_{reported}$) = -2.4333 + $\alpha_{reported}$[a] $\alpha_{reported} \sim$ Normal(0, $\sigma_{reported}^2$[b] = 1.1332)
Range of observations (%)	0-7.9	0-0.4	0-16.3
Mean (%)	4.0	1.9	11.3
Standard deviation (%)	3.9	3.7	10.8
Mode (%)	1.3	0.09	1.9
10% quartile (%)	0.9	0.1	2.2
25% quartile (%)	1.5	0.2	4.1
Median (%)	2.7	0.7	8.2
75% quartile (%)	5.0	1.8	15.3
90% quartile (%)	8.4	4.5	25.6

[a] $\alpha_{cntm\ surf}$, α_{DTLN}, and $\alpha_{reported}$ refers to random effects in each generalized linear regression model.

[b] $\sigma_{cntm\ surf}$, σ_{DTLN}, and $\sigma_{reported}$ refers to the standard deviation of normal distribution that the random effect in each generalized linear regression model followed.

Table 6. Summary of the studies used to extract the probability of *Salmonella* contaminated ground pork ($P_{reported}$) for the model validation

Study[1]	Country	Sample source	Number of positive samples	Number of total samples tested	Percentage (%)	Overall percentage (%)[2]
Duffy *et al.*, 2001	USA	Processing plant	4	40	10.0 (4/40)	5.8% (7/120) For samples from processing plants
			3	40	7.5 (3/40)	
			0	40	0 (0/40)	
		Retail store	7	96	7.3 (7/96)	11.2% (27/241) For samples from retail stores
			12	96	12.5 (12/96)	
White *et al.*, 2001	USA	Retail store	8	49	16.3 (8/49)	

[1] The detection methods conducted in all studies were reported to have the same detection limit, 1 CFU/25g.

[2] The overall percentages were calculated by the sum of all positive samples divided by the sum of all samples tested in the group of processing plant data and retail store data regardless of study difference, respectively.

Table 7. Model estimated probability of *Salmonella* contaminated ground pork for baseline scenario and six alternative scenarios[1]

	Baseline scenario	Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5	Scenario 6
Mean	8.3%	8.1%	7.8%	8.3%	8.2%	8.1%	7.9%
10% quartile	0%	0%	0%	0%	0%	0%	0%
25% quartile	1.5E-10%	1.1E-10%	8.3E-11%	1.5E-10%	8.3E-11%	1.9E-10%	8.3E-11%
Median	2.8E-6%	1.4E-8%	1.3E-6%	1.6E-6%	1.4E-6%	2.8E-6%	1.4E-6%
75% quartile	0.02%	0.015%	0.01%	0.01%	0.01%	0.02%	9.5E-3%
90% quartile	17.3%	16.5%	10.4%	16.1%	13.7%	13.3%	10.8%

[1] Baseline scenario was run based on the baseline data and population assumptions at the time of the analysis. In Scenario 1, the probability of a carcass with *Salmonella* positive DTLNs (P_{DTLN}) was set to half of its baseline value. In Scenario 2, P_{DTLN} was set to zero. In Scenario 3, *Salmonella* concentration in DTLNs (C_{DTLN}) was set to half of its baseline value. In Scenario 4, C_{DTLN} was set to zero. In Scenario 5, the weight of DTLNs from a single carcass contributing to ground pork (W_{DTLN_carc}) was set to half of its baseline value. In Scenario 6, W_{DTLN_carc} was set to zero. The alternative scenarios were run using baseline values for all other parameters.

Table 8. Model estimated probability of *Salmonella* contaminated ground pork for baseline scenario and six alternative scenarios[1] at different levels of the percentage of a carcass surface area ending up in trim (P_{surf_carc})

P_{surf_carc} (%)	Baseline scenario	Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5	Scenario 6
	Mean (95% probability interval)						
10	2.8 (2.5-3.1)	2.4 (2.1-2.6)	2.1 (1.9-2.3)*	2.4 (2.2-2.7)	2.3 (2.0-2.6)	2.6 (2.3-2.9)	2.4 (2.1-2.6)
20	4.3 (3.9-4.6)	4.1 (3.8-4.4)	3.8 (3.4-4.1)	3.9 (3.6-4.3)	3.6 (3.3-4.0)	4.1 (3.8-4.5)	4.0 (3.6-4.3)
30	5.4 (5.0-5.8)	5.1 (4.7-5.5)	4.7 (4.3-5.1)	5.0 (4.6-5.4)	4.9 (4.5-5.3)	5.0 (4.6-5.4)	4.8 (4.4-5.2)
40	6.6 (6.1-7.0)	5.7 (5.3-6.1)	5.8 (5.4-6.2)	5.7 (5.3-6.1)	5.6 (5.2-6.0)*	5.8 (5.4-6.3)	5.6 (5.2-6.0)*
50	7.0 (6.5-7.4)	6.9 (6.5-7.4)	6.3 (5.9-6.8)	6.4 (6.0-6.9)	6.4 (6.0-6.8)	6.7 (6.2-7.1)	6.6 (6.1-7.0)
60	7.8 (7.3-8.3)	7.3 (6.8-7.8)	7.2 (6.8-7.7)	7.1 (6.6-7.6)	7.0 (6.6-7.5)	7.1 (6.6-7.6)	6.7 (6.3-7.1) *
70	8.2 (7.7-8.7)	7.9 (7.4-8.4)	7.6 (7.1 -8.0)	8.1 (7.6-8.5)	7.7 (7.2-8.2)	8.0 (7.6-8.6)	7.7 (7.2-8.2)
75	**8.3 (7.8-8.8)**	**8.1 (7.6-8.6)**	**7.8 (7.3-8.3)**	**8.3 (7.8-8.8)**	**8.2 (7.7-8.7)**	**8.1 (7.5-8.5)**	**7.9 (7.4-8.4)**
80	8.7 (8.2-9.2)	8.2 (7.7-8.7)	8.2 (7.7-8.7)	8.7 (8.2-9.2)	8.2 (7.7-8.7)	8.6 (8.1-9.1)	8.4 (7.9-8.9)
90	8.9 (8.4-9.4)	8.9 (8.4-9.4)	8.8 (8.3-9.4)	8.7 (8.1-9.2)	8.3 (7.8-8.8)	8.6 (8.1-9.1)	8.5 (8.0-9.0)

[1] Baseline scenario was run based on the baseline data and population assumptions at the time of the analysis. In Scenario 1, the probability of a carcass with *Salmonella* positive DTLNs (P_{DTLN}) was set to half of its baseline value. In Scenario 2, P_{DTLN} was set to zero. In Scenario 3, *Salmonella* concentration in DTLNs (C_{DTLN}) was set to half of its baseline value. In Scenario 4, C_{DTLN} was set to zero. In Scenario 5, the weight of DTLNs from a single carcass contributing to ground pork (W_{DTLN_carc}) was set to half of its baseline value. In Scenario 6, W_{DTLN_carc} was set to zero. The alternative scenarios were run using

baseline values for all other parameters in the model.

*The labeled alternative scenarios produced mean probabilities of *Salmonella* contaminated ground pork which is significantly different from the baseline scenario at the same level of P_{surf_carc}.

Numbers in bold represent the baseline value of P_{surf_carc} used in the model.

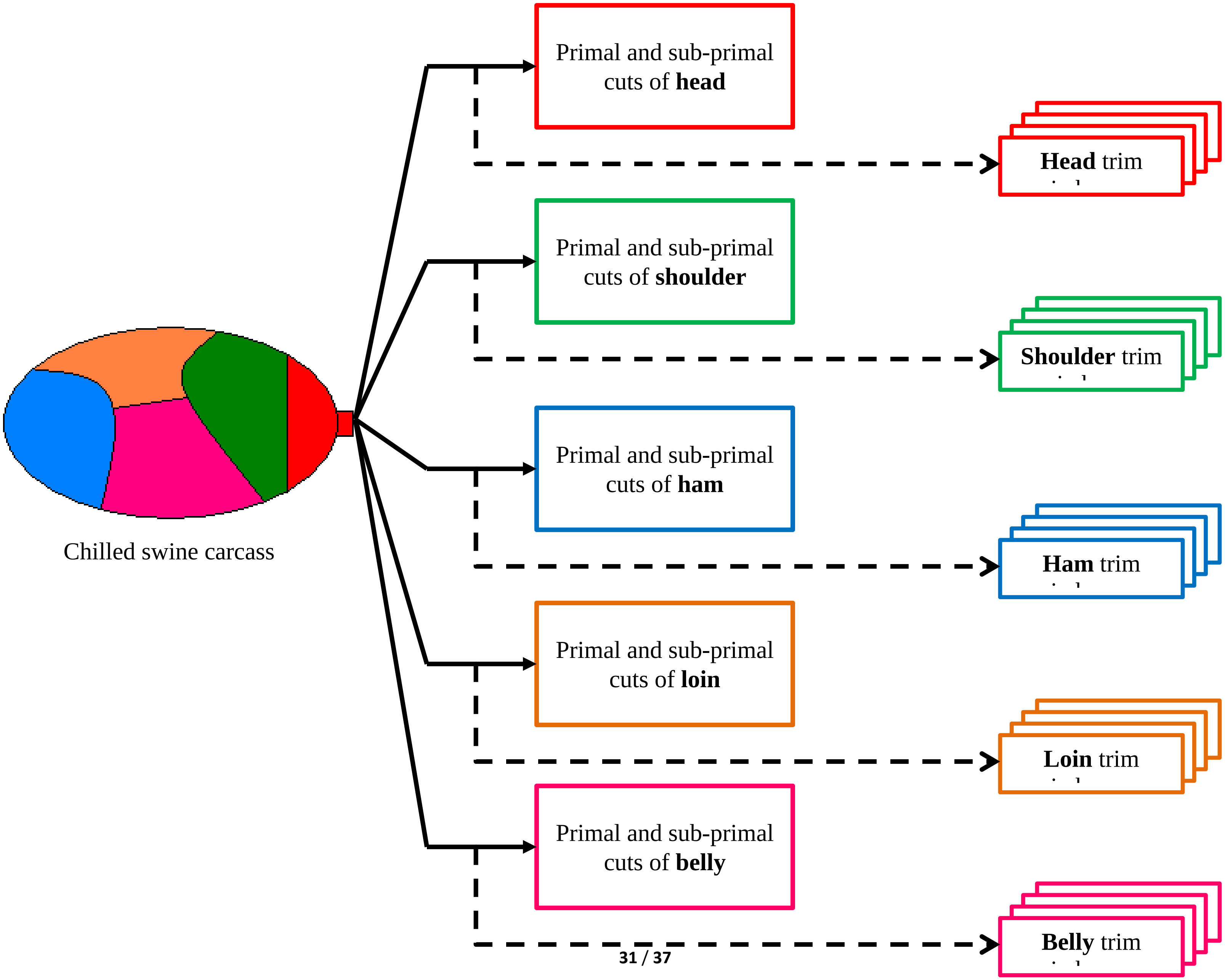
Chilled swine carcass
Primal and sub-primal cuts of **head**
Head trim
Primal and sub-primal cuts of **shoulder**
Shoulder trim
Primal and sub-primal cuts of **ham**
Ham trim
Primal and sub-primal cuts of **loin**
Loin trim
Primal and sub-primal cuts of **belly**
Belly trim

Figure 1. The production process of pork trim

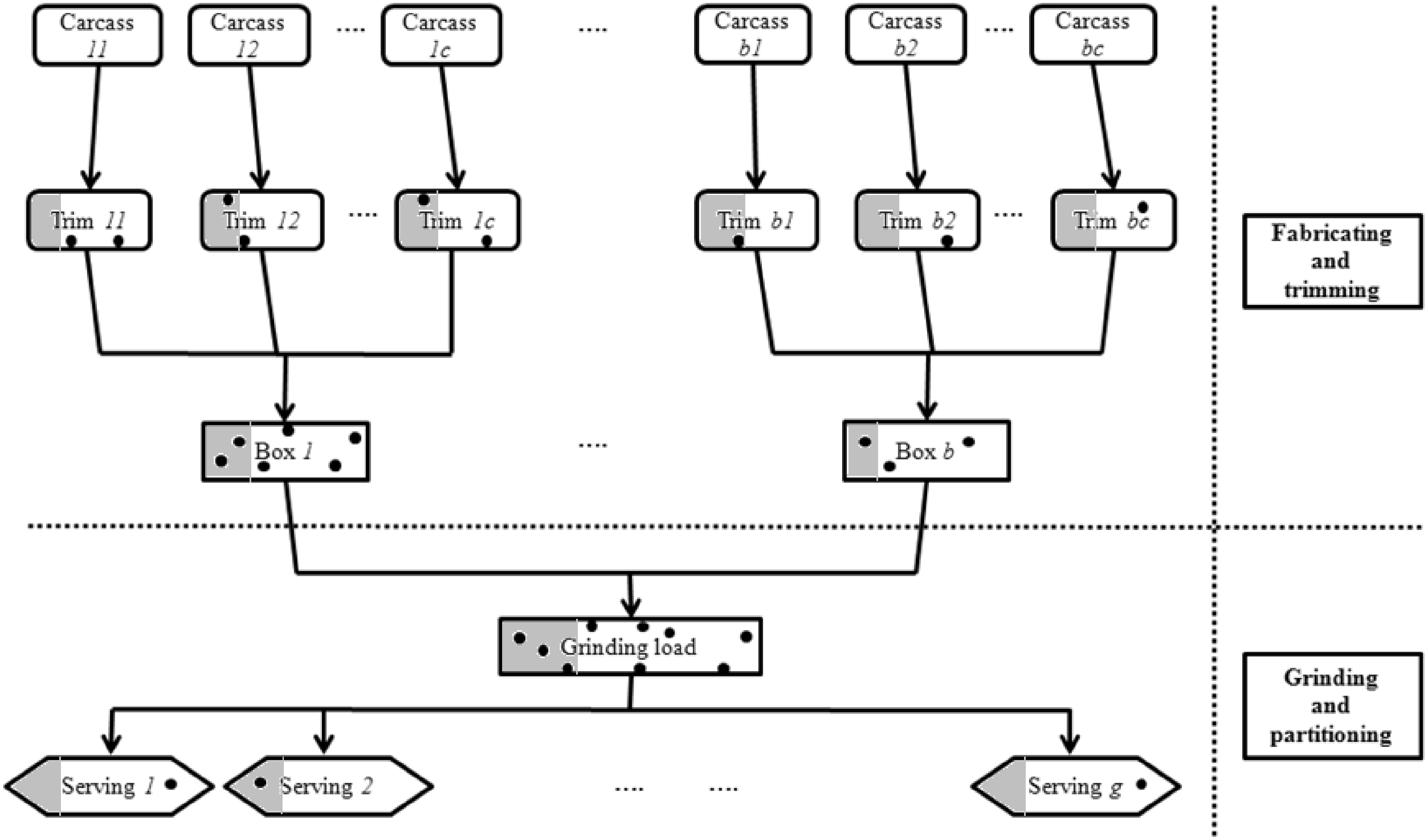

Figure 2. Schematic map of the quantitative risk assessment model. The left side displays a flowchart describing the changes in unit along ground pork production pathway, from carcasses, trim from fabricated carcasses, trim loaded in box, grinding load by mixing and grinding trim, to servings partitioned from grinding load. The right side of the figure is a key that shows where the units are located in the two modules of the model. Trim includes two parts, deep tissue lymph nodes

(DTLNs) represented by gray area and trim other than DTLNs (notDTLNs) represented by white area. The black dot represents *Salmonella* organism. Black dots in gray area refer to *Salmonella* contamination originated from DTLNs, otherwise from notDTLNs. The *Salmonella* contamination sourcing either from DTLNs or notDTLNs passes through units along ground pork production. Trim originated from *c* carcasses is loaded in one box. One grinding load consists of *b* boxes of trim. A single grinding load is then partitioned into *g* servings. Therefore, the number of *Salmonella* in a box is the sum of *Salmonella* number on the contributing carcasses and the number of *Salmonella* in a grinding load is the sum of *Salmonella* number in all the contributing boxes.

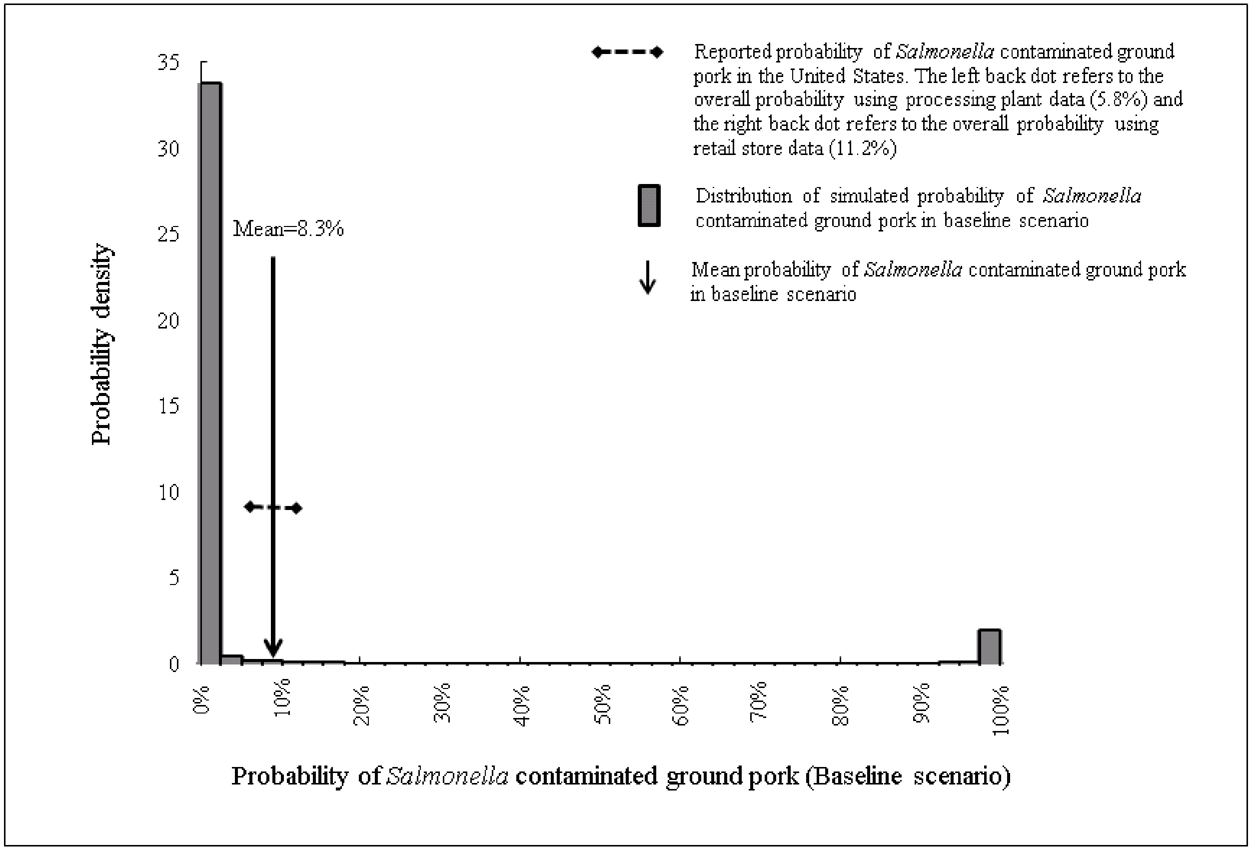

Figure 3. Distribution of model-simulated probability of *Salmonella* contaminated ground pork marked for mean value showing agreement with the available reported data in the United States.

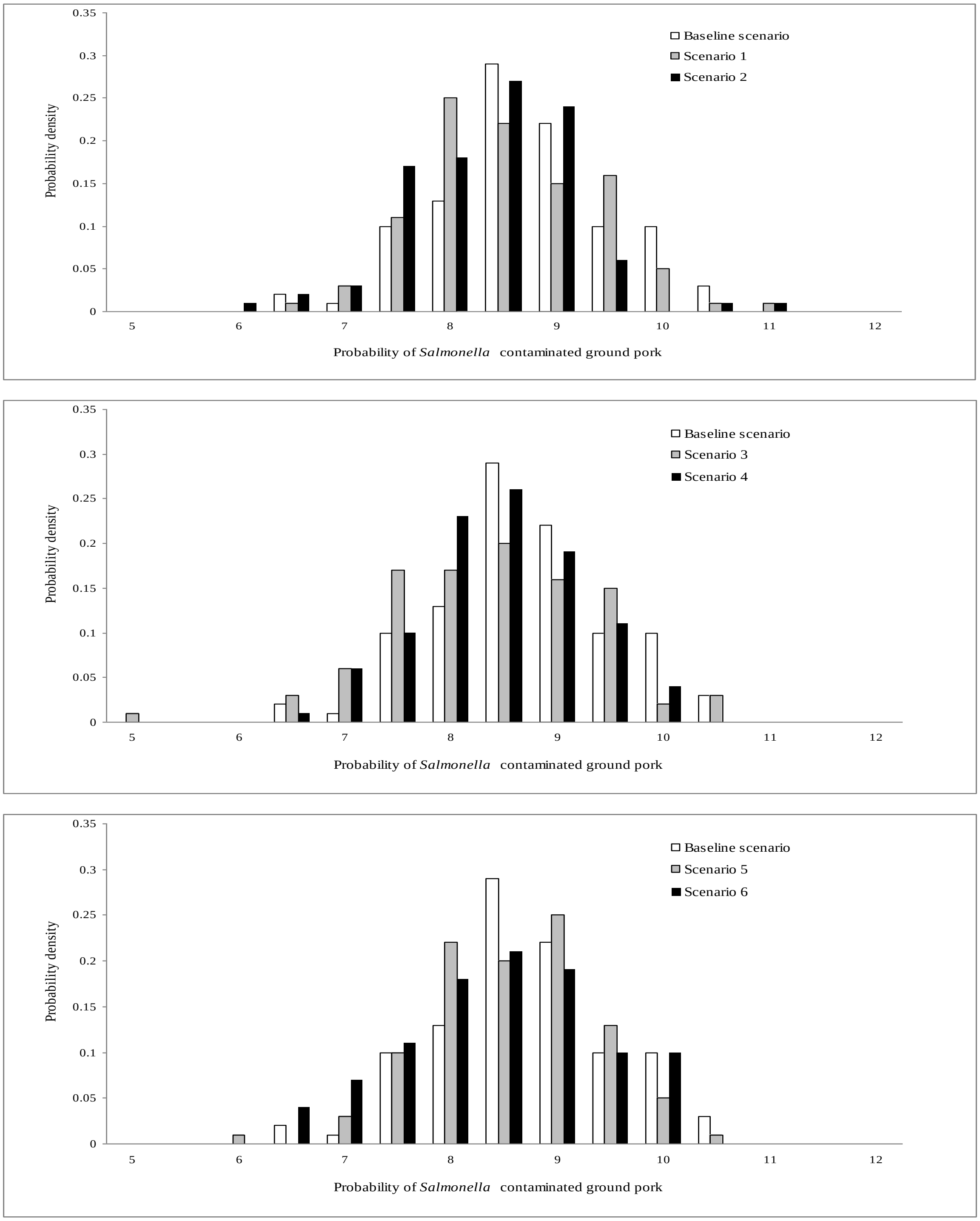

Figure 4. Histogram of mean probabilities of *Salmonella* contaminated ground pork for the comparison between baseline scenario and the six alternative scenarios

Baseline scenario was run based on the baseline data and population assumptions at the time of the analysis. In Scenario 1, the probability of a carcass with *Salmonella* positive DTLNs (P_{DTLN}) was set to half of its baseline value. In Scenario 2, P_{DTLN} was set to zero. In Scenario 3, *Salmonella* concentration in DTLNs (C_{DTLN}) was set to half of its baseline value. In Scenario 4, C_{DTLN} was set to zero. In Scenario 5, the weight of DTLNs from a single carcass contributing to ground pork (W_{DTLN_carc}) was set to half of its baseline value. In Scenario 6, W_{DTLN_carc} was set to zero. The alternative scenarios were run using baseline values for all other parameters in the model. For all alternative scenarios, there was no evidence to show the significant difference in the probability of *Salmonella* contaminated ground pork with the baseline scenario based on the t-tests (P-values > 0.05).