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Developing a risk management framework to improve public health outcomes by enumerating *Salmonella* in ground turkey – RETRACTION

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Abstract

Salmonella spp. continue to be a leading cause of foodborne morbidity worldwide. To assess the risk of foodborne disease, current national regulatory schemes focus on prevalence estimates of *Salmonella* and other pathogens. The role of pathogen quantification as a risk management measure and its impact on public health is not well understood. To address this information gap, a quantitative risk assessment model was developed to evaluate the impact of pathogen enumeration strategies on public health after consumption of contaminated ground turkey in the USA. Public health impact was evaluated by using several dose–response models for high- and low-virulent strains to account for potential under- or overestimation of human health impacts. The model predicted 2705–21 099 illnesses that would result in 93–727 reported cases of salmonellosis. Sensitivity analysis predicted cooking an unthawed product at home as the riskiest consumption scenario and microbial concentration the most influential input on the incidence of human illnesses. Model results indicated that removing ground turkey lots exceeding contamination levels of 1 MPN/g and 1 MPN in 25 g would decrease the median number of illnesses by 86–94% and 99%, respectively. For a single production lot, contamination levels higher than 1 MPN/g would be needed to result in a reported case to public health officials. At contamination levels of 10 MPN/g, there would be a 13% chance of detecting an outbreak, and at 100 MPN/g, the likelihood of detecting an outbreak increases to 41%. Based on these model prediction results, risk management strategies should incorporate pathogen enumeration. This would have a direct impact on illness incidence linking public health outcomes with measurable food safety objectives.

Introduction

Non-typhoidal *Salmonella* species are responsible for an estimated 1.2 million illnesses, 23 000 hospitalisations, 450 deaths and approximately $365 million in direct medical costs annually in the USA [1]. Rates of *Salmonella* cases in the USA (15.9 culture-confirmed cases per 100 000 population in 2015) have not appreciably declined over the past 15 years [2].

Poultry and poultry meat products are considered some of the main carriers of the organism and represent a significant share of the attributed sources of salmonellosis in humans. Approximately 33% of all food-related salmonellosis cases were associated with meat products regulated by the US Department of Agriculture's Food Safety and Inspection Service (FSIS) [3]. Out of those, poultry represented about 58% of the cases, with 85% being associated specifically with chicken [4]. Although not specifically estimated, one can assume that most of the other human cases related to poultry could be attributed to turkey consumption.

The characterisation of the occurrence of *Salmonella* spp. along the poultry production chain has been an area of research and policy focus for many years. Joint efforts between policymakers, poultry producers and industry have reduced the overall *Salmonella* prevalence in poultry products and, as a result, reduced the public health burden associated to their consumption. These efforts have reduced the prevalence of *Salmonella* spp. in ground turkey from 36.6% in 1998 to 15.2% in 2013 [5]. FSIS has recently modified the *Salmonella* spp. performance standards for ground turkey allowing contamination rates no greater than 13.5% over a 52-week moving window test period [5]. This new standard is in alignment with the Healthy People 2020 initiative by the US Department of Health and Human Services to achieve a 25% reduction in human illnesses attributed to *Salmonella* spp. in poultry products [6]. Despite these efforts, five *Salmonella* outbreaks attributed to ground poultry products have been reported in the USA since 1998. Recent multistate outbreaks of human salmonellosis have led to hundreds of reported illnesses and the recall of millions of pounds of raw ground meat and poultry products [7].

While most of the regulatory efforts have been focused on reducing the overall prevalence of *Salmonella* spp. (presence or absence), very little has been done to estimate the impact on

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public health by reducing the actual concentration of *Salmonella* in positive lots. As suggested by other authors, there is already evidence from microbiological risk assessment studies that levels of contamination can be even more important to public health than prevalence as they are directly related to the likelihood that the ingested dose exceeds the minimum infectious dose needed for disease development [8, 9]. There is a need to test new performance standards that are based on prevalence and enumeration levels rather than just on absence or presence alone.

Dose–response models have been developed to estimate the relationship between the probability of illness and the ingested *Salmonella* spp. dose in a food product. Models, based on the β-Poisson distribution, have been developed through use of volunteer and mouse feeding trials (a repository of dose–response models has been created by the Center for Advancing Microbial Risk Assessment (CAMRA), http://camra.msu.edu/) and outbreak data [10]. Recently, a two-tiered approach has been proposed to model separately the probability of infection and probability of illness using a hypergeometric β-Poisson model using data from *Salmonella* outbreaks [11]. As pointed out by the authors, dose–response models from feeding trials seem to underestimate the risk of illness by using laboratory-adapted or low-virulence strains not involved in outbreaks. In contrast, dose–response models from outbreak data may overestimate the risk of illness by only accounting for high-virulence serotypes capable of producing outbreaks and ignoring the fact that a high proportion of *Salmonella* serotypes found in food are rarely involved in outbreaks, indicating a low-virulence profile. A combined approach using two different dose–response relationships for high- and low-virulence serotypes could better estimate the true incidence of *Salmonella* human cases due to the consumption of contaminated ground turkey.

The main objective of this study was to develop a risk management framework for *Salmonella* spp. in ground turkey based on the evaluation of public health risk associated with varying concentrations of *Salmonella* contamination.

Methodology

Input data

Prevalence and concentration levels of *Salmonella* spp. in ground turkey (2011–2016) were obtained from FSIS samples collected at processor and retail locations throughout the USA through a FOIA request (FOIA 2017-00288) (Table 1). *Salmonella* serotypes found in ground turkey were classified as low- and high-virulence depending on their involvement in human outbreaks [12] (Table 2). Data available from the scientific literature and provided by industry through personal communication were gathered to characterise the model inputs (Tables 2–4). Figure 1 shows the two main consumption scenarios evaluated separately in the risk assessment model (home and restaurant setting). For each one, consumer handling and cooking practices of ground turkey were used (in some cases, ground turkey data were not available and ground beef data were used instead). Fresh and frozen states were taken into account to estimate the impact of thawing methods (microwave, room temperature and refrigerator) on the final *Salmonella* concentration in the home consumption scenario. Current undercooking practices among US consumers at home and restaurant settings [13, 14] were modelled to estimate the ingested dose of *Salmonella* spp. at the time of consumption [15, 16]. No cross-contamination was modelled in the current

scenarios to account solely for the direct effect of proposed risk mitigations strategies.

Dose–response relationship

Dose–response models have been published using volunteer and mouse feeding trials and outbreak data to characterise the relationship between the dose ingested and probability of illness. The first approach has been to use data from feeding trials to characterise the dose–response relationship. The CAMRA has created a repository of dose–response models by fitting the exponential and β-Poisson models to feeding trials data to find the optimal model. They have estimated dose–response parameters for several *Salmonella* serotypes, namely *Salmonella* Anatum, *Salmonella* Meleagridis, *Salmonella* Newport and generic non-typhoidal *Salmonella*.

The second approach has been to use outbreak data that relate the dose ingested with the attack rate. A recent risk assessment used a β-Poisson model to estimate the number of human cases using *Salmonella* outbreak data in chicken meat and egg products (Table 3) [10]. More recently, outbreak data with all products combined were used to characterise the dose–response relationship by using a Poisson γ mixture distribution [11]. The authors used a two-tiered approach by estimating first the probability of infection (P_{inf}) and then the conditional probability of the illness given infection ($P_{ill/inf}$) and finally the probability of illness (P_{ill}) as the product of both probabilities ($P_{inf} \times P_{(ill/inf)}$) (Table 3).

In this study, a combined approach selected separate dose–response models for high- and low-virulence strains to avoid over- and underestimation. For high-virulence strains, three different dose–response models were used: (i) WHO and FAO β-Poisson single hit model; (ii) two-tiered approach suggested by [11]; and (iii) β-Poisson model for *Salmonella* Typhimurium estimated by the CAMRA using data published by [17] in mice. Low-virulence strains were characterised by a β-Poisson model corresponding to *Salmonella* Anatum estimated by CAMRA using data from volunteer feeding trials [18].

Risk assessment model framework

A risk assessment model was developed to estimate key public health metrics (mean risk of illness, predicted number of cases and reported cases) in the US population after consumption of contaminated ground turkey at home and restaurant settings (Fig. 1 and Tables 2–5). Data on cooking practices for ground turkey were not available, thus data on ground beef were used instead assuming a similar thermal profile. Cooking practices observed at the restaurant level were safer (reaching or surpassing FDA and USDA recommended cooking temperatures more frequently) than those reported at home [13, 14]. Several dose–response approaches were evaluated using different models for high-virulence serotypes (Fig. 1 and Table 3). The stochastic risk assessment model was developed using Excel and @Risk 6.3 (Palisade Corp., NY, USA). Model outputs were obtained by Monte Carlo simulation techniques for 100 000 iterations. During each iteration, a Latin Hypercube sampling technique was used to select one random value of each variable or parameter from its respective distribution. Output simulation curves showed a positive skewness and high kurtosis values indicating a long tail to the right (higher values) due to the inherent variability and uncertainty of some of the input variables. This fact indicated the suitability of expressing the results as the median and 90%

Table 1. Summary of FSIS data on prevalence and concentration of *Salmonella* spp. in ground turkey

Year	Samples	Prevalence (%)[a]	High-virulence (%)	Concentration (log MPN/g)[b]
2010	577	12.48	50.0	
2011	857	23.57	55.4	
2012	1178	11.80	38.1	
2013	151	9.27	14.3	
2015	1489	4.97	No data	
2016	526	12.93	No data	
Total	4778	11.91	35.7	0.16 ± 1.00

[a]Excluding mechanically separated meat.
[b]Mean and standard deviation.

Table 2. Model inputs on *Salmonella* spp. prevalence and concentration levels in ground turkey in the USA

Input variable	Value	Source
National *Salmonella* prevalence	11.9%	Average proportion (2010–2016) FSIS (FOIA request)
Concentration levels	Normal (0.16, 1.00) log MPN/g	FSIS (2010–2016) FOIA request
Proportion of *Salmonella* high- and low-virulent serotypes[a]	37% (High) 63% (low)	Average proportion (2010–2016) FSIS (FOIA request)
Proportion of *Salmonella* cells in ground turkey centre point	Pert (0.1,0.16,0.2)	[9]

[a]High-virulent *Salmonella* serotypes as implicated in 2002–2012 outbreaks: Heidelberg, III_18:z4, z23 (Enterititidis), Saintpaul, I4,[5],12:I:-, Muenchen, Newport, Typhimurium, Montevideo, Infantis, Javiana, Anatum, Agona, Berta. Low-virulent *Salmonella* serotypes as not implicated in outbreaks: Schwarzengrund, Reading, Kentucky, Worthington, Hadar. CDC, 2014.

confidence intervals. A sensitivity analysis was carried out by a tornado graph showing the effects of changing the input variable values over the output (predicted number of illnesses).

Public health impact of different risk management strategies

The baseline scenario was compared with different risk management strategies by assuming the enumeration of *Salmonella* spp. on every positive lot of ground turkey (2000 pounds/907 kg) and removing high-contaminated lots (>1 MPN/g) or following FSIS guidelines of absence of *Salmonella* spp. in 25 g and removing lots with ≥1 MPN per 25 g from the production chain. The baseline model and the different scenarios were run and compared by the impact on the public health metrics (mean risk of illness, number of illnesses and reported cases) (Table 6).

Effect of level of contamination on outbreak detection

Salmonella is a nationally reportable disease, and isolates are routinely submitted to Public Health Laboratories for molecular characterisation by pulsed-field gel electrophoresis (PFGE) or whole genome sequencing (WGS). Individual cases are routinely interviewed to identify risk factors, and when multiple cases are linked by PFGE or WGS, the case cluster is investigated as a possible outbreak. The likelihood of identifying a common source increases with the number of cases in the cluster and the cluster investigation methods. In a FoodNET cluster investigation study, an outbreak source was identified for 8% of clusters involving two cases, 13% of clusters involving 3–5 cases, 19% of clusters involving 6–10 cases and 41% of outbreaks involving more than 10 cases [19].

The public health impact (predicted number of illnesses, reported cases and likelihood of outbreak detection) of a single contaminated lot of ground turkey was estimated assuming different contamination levels (−1 to 2 log MPN/g) to identify the level that would produce at least one reported case by using the feeding trial (Fig. 3a) and outbreak dose–response models (Fig. 3b).

Results and discussion

Overall prevalence, microbial load and serotype distribution in ground turkey

The mean prevalence of *Salmonella* spp. in ground turkey was slightly over 10% during the 2010–2016 period (Table 1). The mean *Salmonella* concentration was 1.8 (95% CI 0.016–137) MPN/g. Half of the samples had a concentration lower than 1 MPN/g, whereas 37% were between 1–10 MPN/g, 16% >10 MPN/g and 2% of the samples >100 MPN/g. This is consistent with other observations that higher concentrations of contamination may be associated with a relatively few farm production sources [20].

The median ingested dose at home and restaurant settings was 5.4 (95% CI 0–333) and 0.5 (95% CI 0–253) MPN, respectively. The median dose from both consumption scenarios was lower than that reported from outbreak data as [10] estimated an ID_{50} of 39.6–55.5 CFU from all *Salmonella* outbreaks combined and the ingested dose estimated by [20] from *Salmonella* Typhimurium 4,5,12:i:− in beef burgers was 315 MPN (142–685, 95% CI).

Serotype distribution in the FSIS 2010–2016 database included Heidelberg (12.6%), Saintpaul (9.9%), III_18 (5.2%), Muenchen (2.5%), Berta (1.4%), Newport (1.3%), Agona (1.3%), Typhimurium (0.7%), Anatum (0.7%), Montevideo (0.5%) and Enteritidis (0.4%). Sixty-three per cent of the positive samples contained serotypes rarely involved in human outbreaks as outlined in the CDC National *Salmonella* Surveillance Annual Report [12]. FSIS data showed highly contaminated samples corresponding to serotypes of Agona, Berta, Hadar, Heidelberg and Saintpaul. The high prevalence and concentration observed in S. Heidelberg may explain the previous outbreaks occurred in ground turkey in the USA involving that serotype [7].
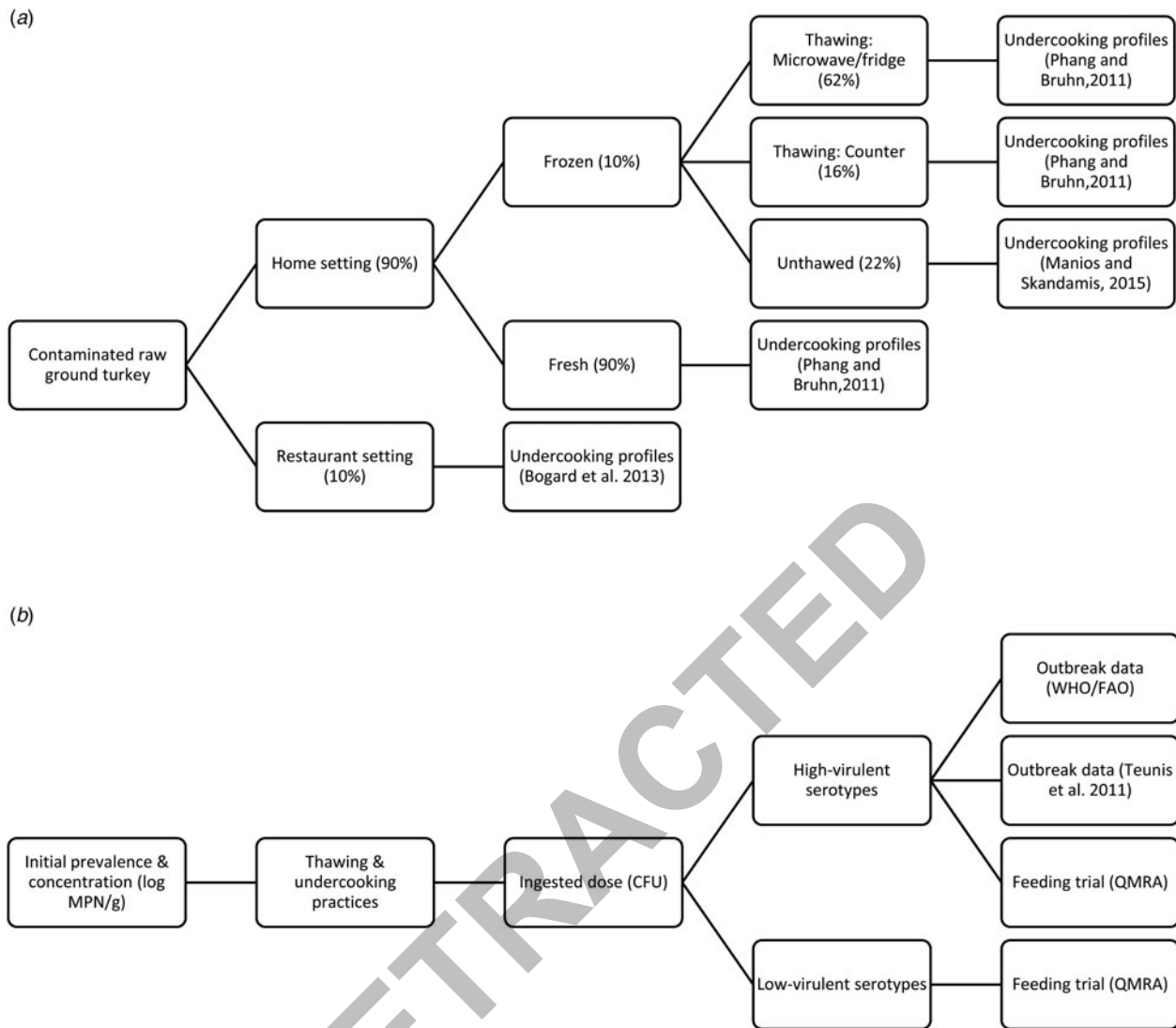
(a)

(b)

Fig. 1. Risk assessment model framework. (a) Thawing and cooking scenarios. (b) Dose–response approach.

Predicted illnesses and reported cases under different dose–response approaches

The median number of *Salmonella* illnesses ranged from 2705 to 21 099 by using different dose–response models (Table 6). The estimated median number of *Salmonella* cases reported to public health officials was 93–727. There were no observed differences in the number of predicted illnesses between the two models based on outbreak data (chicken and egg products *vs.* all products combined) for the high-virulence strains (Table 6). This can be explained by the fact that most of the outbreaks are caused by *S.* Enteritidis and *S.* Typhimurium which are also the most predominant serotypes found in egg and chicken meat products [10, 11]. This dose–response relationship may change in the future as more serotypes are involved in outbreaks that have different attack rates. Median number of cases using the model based on mouse feeding trial data for high-virulence strains was 10× lower indicating a potential lower range prediction in the incidence of *Salmonella*-related cases.

Assuming that 15% of all poultry-attributed non-typhoidal *Salmonella* cases in the USA could be attributable to turkey corresponds to 34 500 estimated illnesses [3, 4]. Our estimates for ground turkey-related illnesses range from 8% of these illnesses based on the feeding trial model to 57% based on the outbreak-based models. The dispersion seen in the attributed cases predicted by the three dose–response modelling approaches can be explained by the limitations of each approach in under- or overestimating the risk of illness. A combined approach where outbreak-based and feeding trial-based models are combined for high- and low-virulence serotypes seems to better represent the true incidence of *Salmonella* human cases.

The high dispersion and wide confidence intervals were due to the inherent variability and uncertainty shown in the model inputs. The model proposed by [11] showed narrower confidence intervals and lower dispersion and thus was selected among the two outbreak-based models to further compare the effect of different risk mitigation strategies.

Public health impact of risk management strategies

The sensitivity analysis highlighted distribution of cooking temperatures and microbial concentration as the most influential input variables on the number of illnesses predicted, which may

Table 3. Model inputs on population and *Salmonella* dose–response data

Input variable	Value	Source
Total number of servings	1.8×10^9	Industry personal communication
Serving size (turkey burger)	Pert (85 113 170) g	Industry personal communication
Salmonella D values in ground turkey	$D = 10^{(-0.1676 \times T + 10.837)}$ min	[15]
Dose–response model outbreak data in chicken meat and egg products	β-Poisson model $P\,(\text{response}) = 1 - \left[1 - \dfrac{D}{\beta}\right]^{\alpha}$ where D is the ingested dose (CFU), $\beta = 51.45$ and $\alpha = 1.3 \times 10^{-1}$	[10]
Dose–response model outbreak data all food products	Poisson γ mixture distribution $P_{\text{inf}} = 1 - \dfrac{\Gamma(\alpha + \beta)\,\Gamma(\beta + D)}{\Gamma(\beta)\Gamma(\alpha + \beta + D)}$ $P_{\text{ill/inf}} = 1 - (1 - \eta\,D^{-\rho})$ $P_{\text{ill}} = P_{\text{inf}} \times P_{\text{ill/inf}}$ where D is the ingested dose (CFU), α: 0.00853, β: 3.14, ρ: 8.23 and η: 69	[11]
Dose–response model mice and volunteer feeding trials	β-Poisson $\beta = 1301$, $\alpha = 2.1 \times 10^{-1}$ (*S.* Typhimurium) $\beta = 291\,002$, $\alpha = 3.18 \times 10^{-1}$ (*S. anatum*)	Estimated by the Center for Advancing Microbial Risk Assessment. Original references: [17, 18]
Under-reporting rate	One out of 29 cases	[1]

Table 4. Model input data on consumption patterns at home

| Input variable	Value	Source
A. Consumption of fresh products		
Proportion of ground turkey consumed at home	90%	Industry personal communication
Proportion of fresh turkey	90%	Industry personal communication
Temperature achieved in centre point (fresh beef burgers cooked at home)	Histogram ({48.3, 93.3}, {4, 0,1,0,1,11,10,15,18,24,24,20,17,13,13,8,9,11})	[13]
Equivalent cooking time at T_{ref}[a]	$\text{Etime}_{T_{\text{ref}}} = \dfrac{10^{(T - T_{\text{ref}}/z)}}{t}$ where $T_{\text{ref}} = 60\ °C$, $D_{60\,°C} = 6.73$ min and z value = 5.96 for *Salmonella* in ground turkey	[10, 15]
Reduction after cooking[a]	$\text{Log reduction} = \dfrac{\text{Etime}_{T_{\text{ref}}}}{D_{T_{\text{ref}}}}$	[10]
B. Consumption of frozen products		
Proportion of frozen ground turkey	10%	Industry personal communication
Reduction after freezing (log CFU/g)	Uniform (0.3, 0.7)	[16]
Thawing scenarios	62% (fridge or microwave) 16% (counter) 22% (unthawed)	[13]
Cooking time (frozen beef burgers)	Normal (9.40, 0.33) min	[18]
Temperature achieved in centre point (frozen beef burgers)	$T = 0.8304 \times t^2 - 0.3023 \times t - 11.826$	Dr Stavros Manios, personal communication

[a]Same equations were used to estimate the log reduction (log CFU/g) after cooking for the rest of scenarios.

Table 5. Model input data on consumption patterns at the restaurant

Input variable	Value	Source
Proportion of ground turkey consumed	10%	Industry personal communication
Level of doneness in beef burger (proportion)	Medium rare (0.06), medium (0.15), medium well (0.29), well (0.22), preference not considered (0.28)	[14]
Temperature achieved in the centre point of beef burger (different doneness level)	Pert (45, 70, 84.4) (medium-rare), pert (53.3, 74.4, 85.6) (medium), pert (62.8, 78.9, 96.1) (medium-well), pert (57.2, 81.7, 98.9), (well), pert (58.3, 80.6, 98.9) (random)	[14]

Table 6. Model outputs by using different dose–response models

Output variable	Outbreak data chicken meat and egg products[a]	Outbreak data all food products combined[a]	Mice feeding trials[a]
Mean risk of illness per serving home consumption	0.0078 (0–0.160)	0.0082 (0–0.035)	0.00084 (0–0.045)
Mean risk of illness per serving restaurant consumption	0.00035 (0–0.105)	0.00082 (0–0.031)	7.29×10^{-5} (0–0.032)
Total number of illnesses	21 099 (241–1 087 137)	19 253 (374–917 326)	2705 (23–289 136)
Total number of reported illnesses	727 (8–37 487)	664 (13–31 632)	93 (1–9970)

[a]Median and 90% CI.
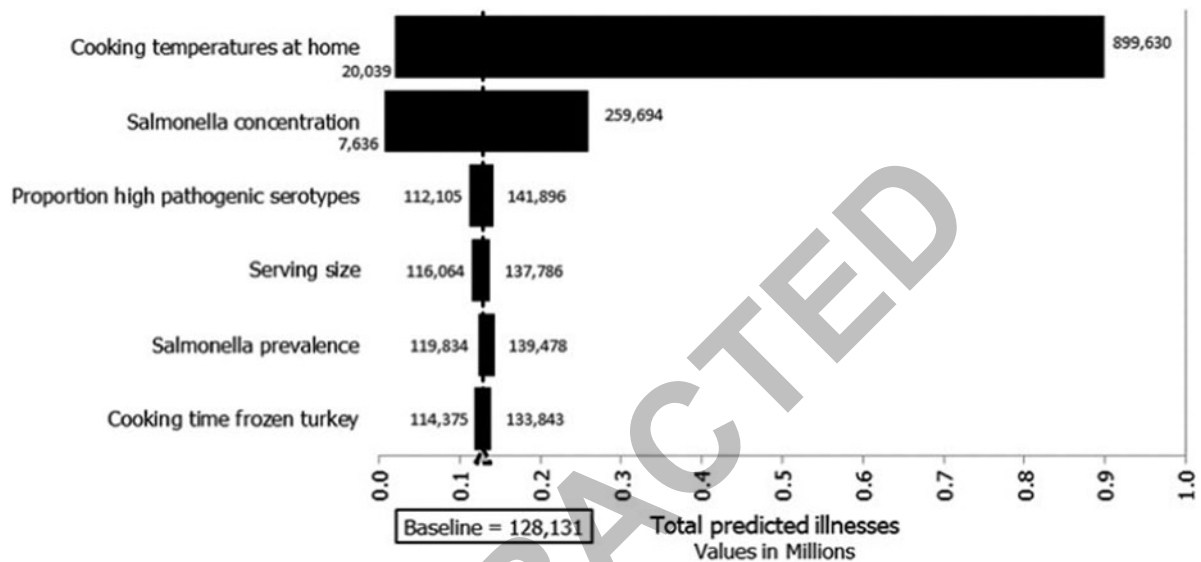
Fig. 2. Sensitivity analysis of the influence of the model inputs on the predicted number of illnesses.

be expected as concentration and cooking are intimately related to the ingested dose (Fig. 2). A reduction in the mean concentration of the pathogen in the food portions consumed would have a direct impact on public health. This is in agreement with previous risk assessment studies of *Salmonella* in poultry and pork products [10, 21, 22], indicating that concentration of contamination and consumer education on adequate handling and cooking practices have the greatest impact on public health, and efforts at any stage of production or processing that reduces the level of *Salmonella* on the end product will reduce risk to a greater extent. A better understanding of cooking practices for ground turkey (or chicken) will improve the estimate of the influence of this variable on public health.

The proportion of high-virulence serotypes and *Salmonella* spp. prevalence in ground turkey had a negligible effect on the predicted number of cases. The distribution of cooking temperatures at home and cooking time in the frozen scenario were negatively correlated (an increase in the cooking temperatures or time will decrease the number of illnesses) (Fig. 2). The mean risk of illness (probability of illness after a single exposure) after eating in a restaurant was 10× lower than the one predicted at home due to these differences in cooking. A very small fraction of consumers (2.2%) reported cooking an unthawed food portion [13], yet, this scenario represented the highest mean risk of illness accounting for 38–52% of the total number of illnesses at home (Table 6). Better consumer education on thawing practices and

the use of digital thermometers would decrease the overall risk of illness.

FSIS data showed 53% of positive samples enumerated contained a concentration higher than 1 MPN/g. Removing lots with a microbial load >1 MPN/g reduced the overall prevalence to 5.6% and mean concentration to 0.2 (95% CI 0.018–0.50) MPN/g (Table 7). Through removal of these samples above the 1 MPN/g threshold, the model predicted 159–2572 illnesses that would lead to 6–89 reported cases, which is a reduction of 86–94% and 84–96.5% in the median and upper limit of the confidence interval number of illnesses, respectively. This far exceeds the proportionate share of the Healthy People 2020 goal for a 25% reduction in *Salmonella* associated with poultry products. Absence of *Salmonella* spp. in 25 g criteria would remove 90% of the FSIS-positive samples enumerated in the 2011–2016 period. Through removal of samples above the 1 MPN/25 g threshold, the model predicts that the prevalence of contamination would be reduced to 1.19% and the mean concentration to 0.035 (95% CI 0.032–0.038) MPN/g, resulting in a net reduction of 99% of illnesses (6–110) and reported cases (0–4). Although the absence of *Salmonella* in 25 g guideline would reduce the number of illnesses, it would also reduce the availability of fresh ground turkey. An estimated 10.7% of production lots would need to be diverted to a thermal process, or potentially wasted, whereas only 6.3% would be removed or diverted if 1 MPN/g guidelines were used (Table 7).
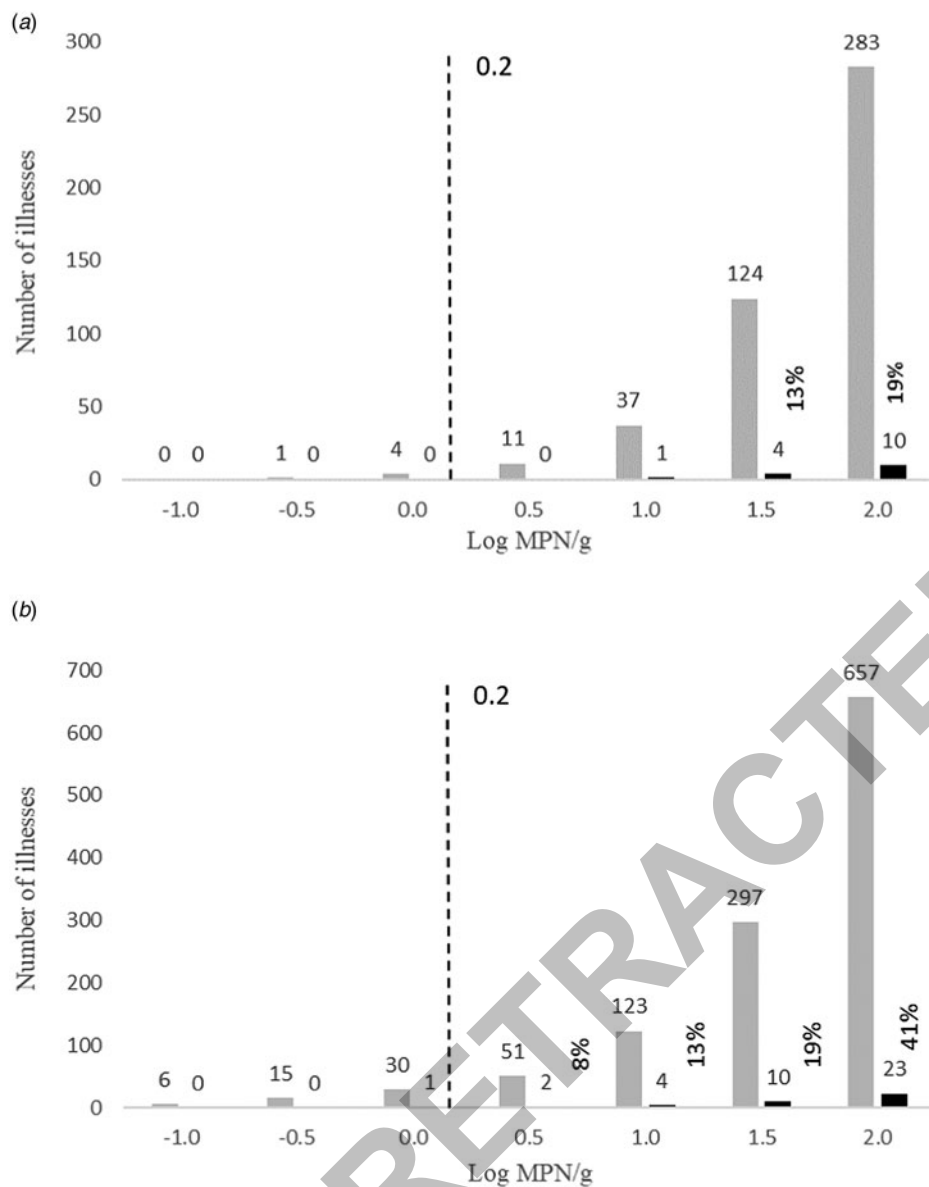
Fig. 3. Number of illnesses and reported cases predicted by the feeding trial dose–response model (a) and the outbreak data dose–response model (b) at various contamination levels of a single 2000 lb lot of contaminated ground turkey. Shaded bars correspond to predicted illnesses. Black bars correspond to reported cases. Dotted lines correspond to the mean *Salmonella* spp. concentration in a positive lot (log MPN/g). Percentages correspond to the probability of a later investigation identifying an outbreak source.

Table 7. Public health impact by using different risk management enumeration strategies

	Removing lots with microbial load	
Output variable	>1 MPN/g[a]	⩾1 MPN/25 g[a]
Total number of illnesses	159 (7–10 190) (feeding trial), 2572 (132–144 241) (outbreak data)	6 (1–356) (feeding trial), 110 (11–6483) (outbreak data)
Total number of reported illnesses	6 (0–480) (feeding trial), 89 (5–4974) (outbreak data)	0 (0–12) (feeding trial), 4 (0–224) (outbreak data)
Per cent of change with the baseline (number of illnesses)	86–94% decrease (median), 84–96.5% decrease (upper bound)	99.4–99.8% decrease (median), 99.3–99.9% decrease (upper bound)
Per cent of production lots diverted	6.3%	10.7%

[a]Median values and 90% confidence intervals.

Effect of level of contamination on outbreak detection

Industry usually uses 2000 lb (907 kg) lots of ground turkey in their daily production schemes in the USA (Industry personal communication). Figure 3 shows the number of illnesses, reported cases and likelihood of outbreak detection at various contamination levels of a single contaminated lot using the two

dose–response approaches (feeding trial 2A and outbreak data 2B). The mean *Salmonella* concentration in a lot needs to be higher than 1 MPN/g to produce at least one reported *Salmonella* case to public officials (Fig. 3b). This single case would not stimulate a cluster or outbreak investigation. At contamination levels of 10 MPN/g, there would be 13% chance of detecting an outbreak, and at 100 MPN/g, the likelihood of detecting an outbreak increases to 41%, based on the outbreak dose–response model (Fig. 3b). These data suggest that a high proportion of outbreaks and poultry-associated sporadic infections are attributable to products with relatively high levels of *Salmonella* spp. contamination.

Conclusions

Different dose–response approaches based on feeding trial and outbreak data models for high- and low-virulent serotypes were used to estimate the *Salmonella* annual number of illnesses and reported cases from consumption of contaminated ground turkey. This combined approach allowed balancing under- and over-reporting. Removing highly contaminated lots reduced the occurrence of illnesses and the notifiable number of outbreaks. Risk management strategies focused on interventions that can reduce *Salmonella* spp. load to low levels of contamination will have great public health benefits while avoiding costs associated with the destruction of products with detectable but low levels. Currently, proposed regulatory practices do not consider dose–response, and are instead focused on the presence compared with the absence of pathogen. Ideally, regulatory efforts in food safety should link public health metrics with quantifiable food safety metrics based on the results of a risk assessment [23].

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