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Research Paper

Quantitative Risk Assessment of *Salmonella* in Ground Beef Products and the Resulting Impact of Risk Mitigation Strategies on Public Health

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ABSTRACT

Salmonellosis incidence rates have not declined over the last 15 years in the US despite a significant *Salmonella* prevalence reduction in meat and poultry products. Ground beef is currently regulated using only qualitative *Salmonella* criteria, and *Salmonella* enumeration values have been proposed as an alternative for implementing risk-based mitigation strategies to prevent illnesses. The purpose of this study was to develop a quantitative microbial risk assessment (QMRA) model to estimate the annual number of salmonellosis cases attributable to the consumption of ground beef contaminated with *Salmonella* and investigate the impact of risk management strategies on public health. Model results estimated 8,980 (6,222–14,215, 90% CI) annual illnesses attributable to ground beef consumption in the US. The removal or diversion of highly contaminated ground beef production lots containing levels above 10 MPN/g (0.4%) and 1 MPN/g (2.4%) would result in a 13.6% (5,369–12,280, 90% CI) and 36.7% (3,939–8,990, 90% CI) reduction of annual salmonellosis illnesses, respectively. Frozen ground beef cooked at home was the consumption scenario of the highest risk for acquiring salmonellosis. Highly virulent serotypes accounted for 96.7% of annual illnesses despite only being present in 13.7% of ground beef samples. The removal of MDR *Salmonella* would result in decreased burden of disease with a 45% reduction in acute DALY annually. Focusing salmonellosis reduction efforts on removing highly contaminated ground beef lots, highly virulent *Salmonella* serotypes, and MDR *Salmonella* from not-ready-to-eat (NRTE) products were predicted to be effective risk prevention strategies.

Nontyphoidal *Salmonella* is the leading cause of foodborne illness hospitalization and mortality in the US causing 1.03 million illnesses, more than 19,000 hospitalizations, and 378 deaths per year (Scallan et al., 2011). Despite being targeted by Healthy People 2020 and 2030 pathogen reduction goals, little progress has been made in reducing salmonellosis cases in the last 15 years (Office of Disease Prevention and Health Promotion, 2010, 2020). Certain commodity products, such as poultry and beef, have shown significant reductions in *Salmonella* prevalence via product sampling in this timeframe, but similar reductions in human illness attributed to these products have not been observed (Food Safety and Inspection Service, 2020a, 2021; IFSAC, 2021). This discrepancy between *Salmonella* reductions in prevalence versus stable human illness rates is not yet well understood.

The most recent salmonellosis attribution data published by the Interagency Food Safety Analytics Collaboration (IFSAC) estimates that 43.3% of annual salmonellosis cases are caused by contaminated meat and poultry products, and 6.2% are directly attributable to beef products (IFSAC, 2021). Ground beef emerged as an important *Salmonella* vehicle in the early 2000s, likely due to increased sensitivity of outbreak detection by the Centers for Disease Control and Prevention (CDC) PulseNet and was implicated in 45% of the 38 beef-related outbreaks identified by the CDC between 2002 and 2011 (Laufer et al., 2015). More recently, antimicrobial-resistant (AMR) *Salmonella* has emerged as a burgeoning threat to public health. AMR surveillance is carried out by the CDC National Antimicrobial Resistance Monitoring System (NARMS) which uses patient samples to track resistance of specific enteric bacteria species to 25 antibiotics. It is estimated that AMR nontyphoidal *Salmonella* causes 100,000 infections annually and is considered one of the leading 18 AMR threats in the US (Costard et al., 2020). AMR *Salmonella* can cause more severe infections and leave healthcare providers with less viable treatment options (Parisi et al., 2018). As such, the CDC now classifies AMR *Salmonella* as a serious threat and places special focus on multidrug-resistant (MDR) *Salmonella* (resistance to one or more agents in three or more antimicrobial categories) which increases

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the burden of disease according to a recent meta-analysis (Centers for Disease Control and Prevention, 2019; Parisi et al., 2018). Disease burden is measured using disability-adjusted life years (DALY) values which is a measurement developed by the World Health Organization to summarize years of healthy life lost due to premature mortality and morbidity from acute disease and sequelae (Scallan et al., 2015).

The USDA Food Safety and Inspection Service (FSIS) is the federal agency tasked with ensuring that meat, poultry, and egg products are safe, wholesome, and properly labeled. Proposed FSIS sampling programs would set performance standards for ground beef processing establishments based on the prevalence of *Salmonella* in a 52-week moving window. Establishments would be classified based upon the volume of production, and allowable *Salmonella* prevalence standards would be set accordingly by establishment volume. Currently, product sampling performance standards are entirely based on qualitative pathogen presence or absence testing of ground beef samples (Food Safety and Inspection Service, 2019).

Pathogen enumeration may be a more effective risk management tool from a public health perspective than the simple presence or absence testing. Enumeration estimates pathogen concentration in a sample and can be used to provide critical insight into the potential ingested dose and adverse outcomes to consumers, including the risk of infection and illness (McEntire et al., 2014). Dose-response functions are parameterized using optimized mathematical models that quantify the risk of a measured response (infection, illness, or death) relative to a pathogen exposure dose (Teunis et al., 2010). By extension of this principle, the removal of highly contaminated products from the food supply is potentially a better risk control strategy than relying on pathogen prevalence alone as it links performance objectives to actual human health outcomes via ingested dose (McEntire et al., 2014; Mead et al., 2010). Dose-response relationships for *Salmonella* are traditionally based on feeding trials (human or mice challenge studies), but more recently, outbreak data where *Salmonella* enumeration from food samples was available have been used to fit dose-response curves (World Health Organization, Food and Agriculture Organization of the United Nations, 2002). Utilizing feeding trial and outbreak-based dose-response relationships in risk assessment offers stratification of serotype virulence since feeding trials typically challenge volunteers with lab-adapted, minimally virulent serotypes, and outbreaks tend to result from more virulent serotypes commonly implicated in human illness. Differences in virulence profiles between the two methods are evident in the number of pathogenic organisms required to cause illness in 50% of the exposed population (ID_{50}). Feeding trials tend to generate high ID_{50} values (exceeding 10^4 CFU) when compared to outbreak ID_{50} values which are captured in each respective dose-response curve (Teunis et al., 2010). This study used a quantitative microbial risk assessment model to estimate the annual reductions in salmonellosis cases when highly contaminated ground beef lots were diverted from consumption. The model also included an estimation of the contribution of high- and low-virulent and MDR serotypes on the total number of illnesses and burden of disease. Results from the QMRA model were used to prioritize risk-based pathogen mitigation strategies.

Materials and methods

Data collection. Data for all ground beef samples that underwent pathogen testing from January 1, 2010 through December 31, 2020 were collected via Freedom of Information Act (FOIA) request (Request ID: 2022-FSIS-00150-F). All beef sampled and reported using the FSIS ground beef project code (MT43) were collected. *Salmonella*-positive samples from FSIS-regulated establishments were pathogen enumerated using the standard most probable number (MPN) serial dilution methodology defined in the FSIS *Microbiological Laboratory Guidebook* (Food Safety and Inspection Service, 2015). Quantitative *Salmonella* enumeration values were used to characterize the *Salmonella* concentration in ground beef. Sample FormID numbers were also collected to merge FOIA data with antimicrobial resistance profiles published in FSIS isolate sequencing data. The level of quantification (LOQ) for the serial dilution enumeration method used by FSIS was 0.03 MPN/g. Any censored data caused by isolates that were above the limit of detection (LOD) for qualitative *Salmonella* testing but below the LOQ were assigned an enumeration value of 0.01 MPN/g.

Data analysis. QMRA models were built out using the FDA-iRISK® 4.2 tool (Food and Drug Administration, 2021a) to estimate annual *Salmonella* illnesses attributable to ground beef consumption in the United States. Models incorporated ground beef consumption setting (home and restaurant), cooking thermal profiles, thawing conditions, product partitioning into individual serving sizes, and initial *Salmonella* prevalence and concentration values to develop a baseline model for annual illness estimates (Table 2). Initial prevalence and concentration values were modified using 'what if' scenarios to evaluate the predicted impact of removal of contaminated lots at levels of >10 MPN/g and >1 MPN/g allowing comparisons to baseline estimates to show relative reductions in annual illnesses (Fig. 1). Individual risk scenarios were summarized to detail the proportion of illnesses directly attributable to low- and high-virulent *Salmonella* serotypes.

Baseline model components. Average *Salmonella* contamination and prevalence values were calculated from FSIS sampling data. Ground beef consumption data and associated processing/preparation methods were collected via literature review and discussion with FSIS staff (Bogard et al., 2013; Davis & Lin, 2005; Phang & Bruhn, 2011). Process stages were developed to capture the contribution of handling, thawing, cooking, and consumption practices in risk estimates. Annual eating occasions were stratified into each relative process stage (Fig. 2) to evaluate the risk posed by each resulting combination of conditions.

Consumption settings were split into restaurant and at-home consumption which were further differentiated by thawing conditions (Davis & Lin, 2005). Ground beef product preparation was split into fresh or frozen to account for the impact of thawing practices on time/temperature cooking profile (Centers for Disease Control and Prevention, 2006). Refrigerator, countertop, and microwave thawing conditions were all considered but did not vary significantly in the resulting temperature profile for fresh products which is consistent with thawing results from previous ground beef studies (Manios & Skandamis, 2015). As such, only fresh and frozen conditions were considered for this risk assessment. Cooking practices in the at-home and restaurant settings provided the probabilities for reaching specific core temperatures for ground beef products depending on consumer done-

Table 1
Dose-response parameters used in risk assessment models

Dose-response Relationship	Distribution and Parameters	Uncertainty around Parameters	Source
FAO/WHO outbreak dose-response (high-virulence serotypes)	β-Poisson (α: 1.32×10^{-1}, β: 51.45)	α: Uniform (2.5th: 0.09, 97.5th: 0.18) β: Uniform (2.5th: 43.75, 97.5th: 56.39)	(World Health Organization, Food and Agriculture Organization of the United Nations, 2002)
Salmonella serotype Anatum dose-response (low-virulence serotypes)	β-Poisson (α: 3.18×10^{-1}, β: 4729.9)	α: Uniform (2.5th: 0.17, 97.5th: 0.67) β: Uniform (2.5th: 97.20, 97.5th: 54603.9)	(McCullough & Eisele, 1951)

Table 2
Consumption and process model inputs

Input Parameter	Value	Source
Ground beef production lot	10,000 lbs (4,536 kg)	(Vial et al., 2020)
Baseline model *Salmonella* prevalence	1.47%	FSIS enumeration data
<10 MPN/g model *Salmonella* prevalence	1.46%	FSIS enumeration data
<1 MPN/g model *Salmonella* prevalence	1.43%	FSIS enumeration data
Baseline model *Salmonella* concentration Mean (95% CI)	−1.78 (−3.00, −0.56) log MPN/g	FSIS enumeration data
<10 MPN/g model *Salmonella* concentration Mean (90% CI)	−1.80 (−2.92, −0.67) log MPN/g	FSIS enumeration data
<1 MPN/g model *Salmonella* concentration Mean (90% CI)	−1.84 (−2.77, −0.91) log MPN/g	FSIS enumeration data
Within- and between-lot *Salmonella* variability	Within: 0.27 log CFU/g Between: *Normal* ($\mu_{\text{all lots}}$, $\sigma_{\text{between lots}}$)	(Flores, 2004)
Maximum population density	3.6 log CFU/g	FSIS enumeration data
Partitioning to serving size	Pert (Minimum: 85, Mode: 113, Maximum: 170) g	Personal communication
Salmonella survival in center point	Pert (Minimum: 0.7, Mode: 0.8, Maximum: 1)	(World Health Organization, Food and Agriculture Organization of the United Nations, 2002)
Inactivation from cooking at home	Chance distribution (Table 8)	(Bogard et al., 2013)
Inactivation from cooking at restaurant	Chance distribution (Table 9)	(Phang & Bruhn, 2011)
Under-reporting rate	1 reported illness per 29.3 cases	(Scallan et al., 2011)
Equivalent cooking time at T_{ref}	$\frac{10^{\left(\frac{T-T_{ref}}{z}\right)}}{t}$ where T_{ref} = 60°C, $D_{60^\circ C}$ = 6.90, and z-value = 5.53	(Murphy et al., 2004; World Health Organization, Food and Agriculture Organization of the United Nations, 2002)
Reduction after cooking	Log reduction = $\frac{ET_{ref}}{D_{ref}}$	(World Health Organization, Food and Agriculture Organization of the United Nations, 2002)

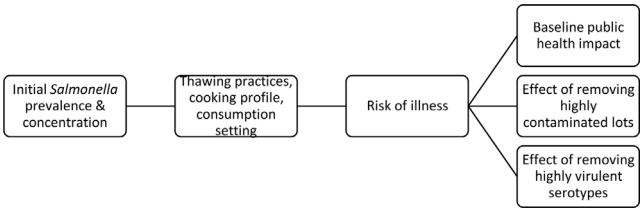


Figure 1. Process used to estimate and compare risk in assessment models.

ness preference (Bogard et al., 2013; Phang & Bruhn, 2011). Cooking time and core product temperature relationships were plotted to simulate cooking scenarios from fresh or frozen ground beef which were defined by a linear and exponential function, respectively (Manios & Skandamis, 2015) (Supplemental figures 1 and 2):

$$Temperature = 9.553(t) + 4.0567 \quad (1)$$

$$Temperature^{\circ}C = 0.8304(t)2 - 0.3023(t) - 11.826 \quad (2)$$

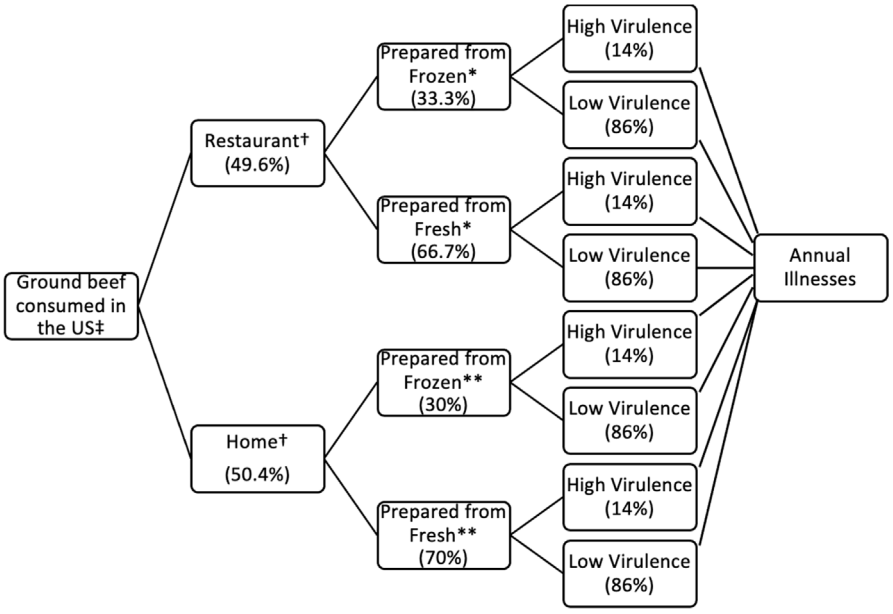
Where: t = cooking time expressed in minutes.

Thermal profile functions were used to estimate the final core temperatures and the time required to achieve specific temperatures depending on the consumption scenario simulated (Tables 8 and 9). Consumer doneness preferences were used to differentiate the at-home from restaurant thermal profiles. Once the product thermal profiles were established for each consumption setting, the North American Meat Institute (NAMI) Process Lethality Determination Spreadsheet (North American Meat Institute, 2008) was used to calculate the *Salmonella* log reduction expected from each cooking scenario by using the D- and z-values from ground beef (Table 2) (Murphy et al., 2004; World Health Organization, Food and Agriculture Organization of the United Nations, 2002). Process lethality calculations for undercooking were only relevant to *Salmonella* cells in the center of ground beef products because *Salmonella* on the outer surface of ground beef products were assumed to be inactivated during cooking (World Health Organization, Food and Agriculture Organization of the United Nations, 2002). This was accounted for by a *Salmonella* cell survival reduction process stage detailed in Table 2. Thermal inactivation was calculated for *Salmonella* spp. (aggregate) as no information was found to estimate serotype-specific log reductions from cooking.

High- and low-virulence *Salmonella* serotype proportions were incorporated into each process model to account for exposure in each consumption scenario. Once the process models were contextualized accordingly, annual illnesses were calculated for each consumption scenario using Monte Carlo simulation with Random Latin Hypercube Sampling. Each risk scenario was simulated by 9,000 initial iterations followed by 3,000 subsequent iterations to test that the difference in risk of illness mean values was less than 1% indicating model convergence. The tool required three convergence tests (12,000 iterations run three times) to end the simulation (Food and Drug Administration, 2021b). The tool used the following equation for the probability of illness:

$$P_{f,h} = E\left[P\left(E_h|AD_{f,h}\right) \times P(\gamma_h|\varepsilon_h) \times P_s\right] \quad (3)$$

(Food and Drug Administration, 2021b)



‡(Mike Williams, Food Safety and Inspection Service, 2022)
†(Davis, Christopher, 2005)
*(Bogard et al., 2013)
**(Centers for Disease Control and Prevention, 2006)
Virulence criteria established high- and low-virulence proportions using serotypes in FSIS dataset

Figure 2. Consumption scenarios and proportion of high- and low-virulence serotypes.

Where: $P(E_h|AD_{f,h})$ is the probability of illness given by the dose-response model for ground beef (hazard h), given the ingested dose $AD_{f,h}$, $P(\gamma_h|\varepsilon_h)$ is the probability of illness due to ground beef consumption resulting from infection after ingesting contaminated product, P_s is the prevalence of contaminated units of ground beef at the point of consumption (provided by process stages), E is the expectation, or mean, of the value in brackets which is computed using Monte Carlo simulation in the iRISK tool (Food and Drug Administration, 2021b).

Uncertainty analysis was carried out by defining uncertainty in the alpha and beta dose-response parameters in the model by using a uniform distribution with the 2.5th and 97.5th percentiles reported from dose-response parameters (McCullough & Eisele, 1951; World Health Organization, Food and Agriculture Organization of the United Nations, 2002). The probability of illness equation (Eq. (3)) was also used for the uncertainty analysis by using the variability convergence process described above for 100 uncertainty iterations per convergence test. The distribution of illness estimates was then summarized and compared across convergence test batches to ensure that the variability simulations successfully converged. A change in mean risk of illness values of 5% or less qualified as model convergence (Food and Drug Administration, 2021b). The remaining model variables were described just using variability distributions as uncertainty bounds surrounding those estimates were not available.

***Salmonella* dose-response relationships**. Dose-response parameters for *Salmonella* serotype Anatum from human feeding trials and outbreak-causing *Salmonella* (serotypes Enteritidis, Typhimurium, Heidelberg, Cubana, Infantis, Newport, and Orienburg) in eggs and broiler chickens were used for low- and high-virulence serotypes, respectively (Table 1) (McCullough & Eisele, 1951; World Health Organization, Food and Agriculture Organization of the United Nations, 2002).

High- and low-virulence criteria were defined to assign dose-response relationships proportionately in the risk scenarios. To be considered high virulence, any given serotype had to meet the following criteria:

- o Listed as a top 10 serotype isolated from human illness according to the most recent CDC *Salmonella* Annual Report (Centers for Disease Control and Prevention, 2016) OR
- o Identified as an outbreak-causing serotype in ground beef products by the National Outbreak Reporting System between 2010 and 2020

Once the criteria were established, additional serotype virulence validation was required to ensure the high-virulence serotypes were not being overrepresented in the models. All serotypes that met high-virulence criteria were subjected to individual illness attribution to determine if they were overrepresented using CDC serotype reporting data (Centers for Disease Control and Prevention, 2016). *Salmonella* serotypes Montevideo, Muenchen, Dublin, and Uganda surpassed expected annual illness proportions and were characterized with the low-virulence dose-response model. The final high-virulence serotypes used in the risk assessment model were *Salmonella* Typhimurium, Newport, Infantis, I 4,[5],12:i:-, Thompson, Enteritidis, Heidelberg, and Braenderup.

Burden of MDR disease. A recent meta-analysis concluded that the risk of hospitalization and mortality are increased for MDR *Salmonella* infections when compared to susceptible *Salmonella* infections (Parisi et al., 2018). For this assessment, the increased burden of MDR disease was quantified by estimating the disability-adjusted life years (DALY) associated with MDR *Salmonella* infections based on baseline illness estimates. The DALY value corresponded to acute health outcomes as chronic manifestations were assumed not to be linked to MDR infections. Acute health outcomes were defined as moderate and severe gastroenteritis and death. Gastroenteritis was stratified by severity with moderate cases seeking medical care and severe cases being hospitalized. The calculation of the MDR and susceptible (non-MDR) DALY values required first defining the years lost due to disability (YLD) and years of life lost (YLL) which were weighted according to the increased odds of hospitalization and mortality, respectively (Parisi et al., 2018) (Table 3).

Table 3
MDR *Salmonella* DALY input data calculation

Estimate	Value	Source
Number illnesses and deaths caused by foodborne *Salmonella* infections per year	1,027,600 illnesses/year 380 deaths/year	(Scallan et al., 2015)
Mortality rate	0.0004	(Scallan et al., 2015)
Hospitalization rate (Severe GI)	0.019	
Moderate GI rate	0.224	
Moderate GI disability weight	0.015	(Scallan et al., 2015)
Severe GI disability weight	0.041	
DALY values for nontyphoidal *Salmonella*	All: 32900 DALY	(Scallan et al., 2015)
	Acute: 12800 DALY	
YLL values for nontyphoidal *Salmonella*	All: 8600 YLL	(Scallan et al., 2015)
	Acute: 8600 YLL	
YLD values for nontyphoidal *Salmonella*	All: 24300 YLD	(Scallan et al., 2015)
	Acute: 4200 YLD	
Odds Ratio adjustments for MDR acute health outcomes	Hospitalization (severe GI): 2.51 Mortality: 3.54	(Parisi et al., 2018)

YLL was calculated using the following equation (Scallan et al., 2015):

$$YLL = D \times E \quad (4)$$

Where: D is the number of deaths and E is the remaining life expectancy.

For each health state, YLD was calculated individually and then summed for total YLD estimate. The health states considered were moderate and severe gastroenteritis (GI) using the following equation (Scallan et al., 2015):

$$YLD = N \times T \times DW \quad (5)$$

Where: N is the number of incident cases, T is the duration of the health state (annualized, set to 1), DW is the disability weight which is measured on a scale of 0 to 1 ranging from least to most severe health outcomes

Finally, the acute health outcome DALY values for MDR and susceptible infections were calculated using the following equation (Scallan et al., 2015):

$$DALY = YLL + YLD \quad (6)$$

The DALY value from MDR cases could then be directly compared to the DALY value from all cases to determine what reduction of health burden would result from removing MDR serotypes from ground beef products.

Results and discussion

Overall *Salmonella* prevalence, concentration, serotype distribution, and MDR in ground beef. The FSIS dataset included sampling information for 72,169 ground beef product samples from 2010 to 2020. In total, 1,221 *Salmonella*-positive ground beef samples were observed in the FSIS data, and 1,060 (86.8%) of those samples were pathogen enumerated. *Salmonella* was enumerated with a mean concentration of −1.78 (−3.00, −0.56, 95% CI) log MPN/g in ground beef samples. Most of the enumerated samples were contaminated with very low concentrations of *Salmonella*. Only 2.4% of all production lots tested surpassed the 1 MPN/g threshold and only 0.4% of production lots surpassed 10 MPN/g. Serotype distribution varied widely in the dataset, and the top five serotypes represented were *Salmonella* serotypes Montevideo (22.0%), Dublin (7.5%), Muenchen (7.0%), Cerro (6.1%), and Anatum (5.6%). The top five high-virulence serotypes were *Salmonella* serotypes Typhimurium (5.4%), Newport (2.8%), Infantis (2.5%), I 4,[5],12:i:- (1.4%), and Thompson (0.6%). In total, 13.7% of all *Salmonella* samples met the high-virulence serotype criteria. MDR isolates accounted for 15.9% of *Salmonella*-positive ground beef samples. Most samples in the study period were resistant to at least one antimicrobial agent, and only 27.8% of *Salmonella*-positive isolates were pan-susceptible.

Annual consumption of ground beef in the US. Annual estimated beef eating occasions were collected from the USDA Economic Research Service data through personal communication with FSIS staff. An estimated 9.8×10^9 eating occasions (Mike Williams, Food Safety and Inspection Service, 2022) of ground beef were estimated in the US per year. Nearly half were estimated to be consumed at home (49.6%) and the other half in restaurants (50.4%) (Davis & Lin, 2005). Ground beef is prepared from fresh (66.7%) twice as often as frozen (33.3%) in the at-home consumption setting (Centers for Disease Control and Prevention, 2006). However, in the restaurant setting, Bogard et al. (2013) reported that 70% of restaurants cooked ground beef from fresh whereas 30% was cooked from frozen.

Cross-contamination is not yet well understood or quantified for *Salmonella* in ground beef products and was considered out of scope for this analysis. However, both the low prevalence and low enumeration values for *Salmonella* in ground beef limit the likely impact of cross-contamination on the total number of illnesses. A better characterization of cross-contamination should be prioritized in future risk assessments once empirically validated cross-contamination coefficients are established for *Salmonella* spp. in ground beef handling and cooking scenarios. Potential pathogen growth during the transportation and storage phases were not considered in these models due to data constraints (time-temperature profiles during transport and storage at home).

Estimated annual illnesses at baseline and enumeration-based scenarios. The baseline *Salmonella* risk model estimated 8,980 (6,222–14,215, 90% CI) annual illnesses due to ground beef consumption (Table 4) which accounts for approximately 1% of all domestic foodborne nontyphoidal salmonellosis cases (Scallan et al., 2011). This estimate is lower than the FSIS ground beef illness attribution estimates of 41,640 illnesses per year (Food Safety and Inspection Service, 2019). Several reasons can be identified to explain the difference in illnesses estimates. FSIS used a “top-down” approach that apportioned the number of illnesses based on outbreak attribution data (7.8% for beef). Because outbreak-related *Salmonella* cases represent only 6% of total *Salmonella* cases (Centers for Disease Control and Prevention, 2020), outbreak-derived attribution methods may be biased toward vehicles likely to be identified in outbreak investigations. This study used a “bottom-up” approach to estimate the number of illnesses likely to occur based on available routine microbiological product sampling and consumption information to evaluate specific

Table 4
Annual salmonellosis illness estimates in baseline scenario

Consumption Scenario	Annual Illnesses by Virulence Profile		
	High-virulence (90% CI)	Low-virulence (90% CI)	Total
Home, Fresh ($n = 3.2 \times 10^9$)	3360 (2360, 4480)	116 (43, 1020)	3476 (2403, 5500)
Home, Frozen ($n = 1.6 \times 10^9$)	2690 (1900, 3590)	93 (35, 819)	2783 (1935, 4409)
Restaurant, Fresh ($n = 3.5 \times 10^9$)	1250 (882, 1670)	43 (16, 379)	1293 (898, 2049)
Restaurant, Frozen ($n = 1.5 \times 10^9$)	1380 (968, 1840)	48 (18, 417)	1428 (986, 2257)
Total	8680 (6110, 11580)	300 (112, 2635)	8980 (6222, 14215)

risk reduction strategies. This QMRA approach accounts for outbreak-causing and less virulent *Salmonella* serotypes in dose-response stratification which is likely a source of risk reduction relative to the FSIS risk assessment approach which assumed that all *Salmonella* serotypes were equally likely to result in an outbreak.

Removing highly contaminated lots reduced resulting annual illnesses at each threshold level. Only five samples surpassed the 10 MPN/g enumeration threshold meaning only 0.4% of all production lots would be removed in this risk management scenario. Removal of these samples resulted in a slight reduction of initial *Salmonella* prevalence (1.46%). When lots that exceeded 10 MPN/g were assumed to be diverted from raw product sales and removed from the model, there were 7,759 (5,369–12,280, 90% CI) estimated annual illnesses which was a 13.6% illness reduction from the baseline scenario (Table 5). Decreasing the threshold limit to 1 MPN/g resulted in removing 2.4% of production lots and reduction of *Salmonella* prevalence (1.43%). When lots that exceeded 1 MPN/g were removed, there were 5,686 (3,939–8,990, 90% CI) estimated annual illnesses which represented a 36.7% illness reduction from baseline (Table 6).

To validate the earlier FSIS enumeration findings, ground beef samples intended for use in the USDA Agricultural Marketing Service (AMS) procurement programs were sampled for *Salmonella* presence using qualitative and quantitative methods from August 25, 2022 through October 31, 2022. Of 398 total samples tested, 21 samples were positive for *Salmonella* presence using qualitative methods, but none were above the LOQ using the Hygiena BAX® System SalQuant™ test kit (Hygiena, 2021). Notably, 71.4% of positive findings were observed at the end of the sampling period and were likely due to increased precipitation in cattle feedlot locations according to program managers. *Salmonella* concentrations among these samples could not be quantified supporting the finding that *Salmonella* concentrations in ground beef samples remain very low (see supplementary dataset).

Table 5
Annual salmonellosis illness estimates after removal of lots exceeding 10 MPN/g

Consumption Scenario	Annual Illnesses by Virulence Profile		
	High-virulence (90% CI)	Low-virulence (90% CI)	Total
Home, Fresh ($n = 3.2 \times 10^9$)	2,900 (2,040, 3,870)	100 (37, 879)	3,000 (2,077, 4,749)
Home, Frozen ($n = 1.6 \times 10^9$)	2,330 (1,640, 3,110)	81 (30, 706)	2,411 (1,670, 3,816)
Restaurant, Fresh ($n = 3.5 \times 10^9$)	1,080 (757, 1,440)	37 (14, 325)	1,117 (771, 1,765)
Restaurant, Frozen ($n = 1.5 \times 10^9$)	1,190 (836, 1,590)	41 (15, 360)	1,231 (851, 1,950)
Total	7,500 (5,273, 10,010)	259 (96, 2,270)	7,759 (5,369, 12,280)

Table 6
Annual salmonellosis illness estimates after removal of lots exceeding 1 MPN/g

Consumption Scenario	Annual Illnesses by Virulence Profile		
	High-virulence (90% CI)	Low-virulence (90% CI)	Total
Home, Fresh ($n = 3.2 \times 10^9$)	2,130 (1,500, 2,840)	73 (27, 643)	2203 (1527, 3483)
Home, Frozen ($n = 1.6 \times 10^9$)	1720 (1210, 2290)	59 (22, 519)	1779 (1232, 2809)
Restaurant, Fresh ($n = 3.5 \times 10^9$)	781 (550, 1040)	27 (10, 236)	808 (560, 1276)
Restaurant, Frozen ($n = 1.5 \times 10^9$)	866 (609, 1160)	30 (11, 262)	896 (620, 1422)
Total	5497 (3869, 7330)	189 (70, 1660)	5686 (3939, 8990)

Mean risk of illness varied by consumption setting. Ground beef prepared at home resulted in more annual illnesses (69.7%) than at restaurants as products were less likely to reach internal temperatures necessary to provide adequate reduction of *Salmonella* (Table 4). This finding is consistent with a study of restaurant kitchen practices where authors found that 79% of restaurants across eight states in the US employed a certified kitchen manager (CKM) with a food safety certification. Restaurants with CKMs have demonstrated better food safety practices in ground beef preparation. Specifically, they reported being more likely to take final temperatures with thermometers and less likely to serve undercooked or rare beef products to customers even when requested (Bogard et al., 2013). These consumption setting findings demonstrate that the likelihood of eating undercooked ground beef and thus acquiring salmonellosis is more likely in the home setting and is driven by consumers. However, sparce data currently exist for in-home ground beef preparation practices which could impact the generalizability of illness estimates in the home consumption setting.

Products cooked directly from frozen were also consistently associated with an increased mean risk of illness across all consumption scenarios when compared to fresh/thawed products. Products cooked from frozen accounted for 46.9% (2,921–6,666, 90% CI) of total annual illnesses despite only accounting for 31.7% of annual eating occasions. Similar to the home cooking scenario, products cooked from frozen are less likely to reach internal temperatures necessary for sufficient *Salmonella* inactivation when compared to fresh product preparation. Additional analyses were carried out to investigate the addition of a process stage to incorporate *Salmonella* inactivation from freezing. According to one study, the effect of frozen storage on decreasing *Salmonella* in beef patties ranged from 0.3 to 0.7 log CFU/g (Manios & Skandamis, 2015). When this process stage was included in the frozen risk scenario, resulting annual illnesses showed a 26.4% reduction compared to the baseline scenario. This assumption would need further confirmation as it would potentially challenge the enumeration results in FSIS ground beef pathogen sampling as samples are kept frozen before *Salmonella* enumeration at FSIS laboratories.

MDR *Salmonella* represented 15.9% of all positive *Salmonella* samples which accounted for 1,428 cases per year when applied to the baseline risk estimate. The DALY associated with a typical *Salmonella* infection in the US was estimated as 0.032 years/case with an estimated 287 DALYs per year attributable to ground beef consumption (Scallan et al., 2015). Taking only acute health burden into account (moderate and severe gastroenteritis) resulted in 112 DALY annually. After estimating relative YLL and YLD values (Table 7), susceptible and MDR infections accounted for 55.4% and 44.6% of the total DALY, respectively. These results suggest that if MDR serotypes would be detected and removed from product streams, there would be a 45% reduction in acute DALY, 21% reduction in YLD (burden of the health states), and 56% reduction in YLL (mortality). This approach assumes that MDR *Salmonella* is at least as infectious as the susceptible *Salmonella* represented in the FSIS dataset (same D-R relationships will apply) and that MDR infections do not affect postreactive sequelae complications. These assumptions were made to allow for comparisons using the limited data available but could be overestimating the burden of illness in MDR serotypes (Parisi et al., 2018).

Table 7
Annual DALY, YLL, and YLD value estimates for MDR and drug-susceptible *Salmonella* infections

Burden estimate	Drug-susceptible	MDR	Total
DALY (years)	NA*		287
Acute DALY (yrs.)	62	50	112
YLL (yrs.)	33	42	75
YLD (yrs.)	29.5	7.6	37

*Calculated in aggregate

A recent investigation of risk modeling approaches for *Salmonella* concluded that using solely dose-response relationships established in human feeding trial studies often underestimates the risk of illness because these studies used low-virulence *Salmonella* serotypes as opposed to higher virulence serotypes that are often associated with outbreaks (Oscar, 2021; Teunis et al., 2010, p.). A major limitation to using a single dose-response model is the inherent assumption that all *Salmonella* serotypes behave as a single serotype. Two-level dose-response modeling produces narrower confidence intervals and lower dispersion (heterogeneity in the ingested dose) (Teunis et al., 2010) than single parameter dose-response modeling. As such, this study used a two-level modeling approach that utilized dose-response relationships established using both human feeding trials and outbreak data.

Risk models assumed that process stages were similar among all restaurants meaning kitchen practices specific to consumption setting could only be differentiated by at-home and restaurant settings. Limited information exists detailing differences in cross-contamination practices, standard operating procedures, and cooking guidelines among consumption settings which restricts the ability to model these differences. It is possible that stratification by different types of restaurants (sit-down vs. fast food) would increase the precision of model inputs.

Sensitivity analysis of model parameters. Individual model parameter changes were tested while holding all other model inputs constant to check the sensitivity of risk estimates to each input parameter (Fig. 3). Value ranges used for each model parameter used in the sensitivity analysis are documented in Table 10. Proportion of highly virulent serotypes was the most impactful parameter in all consumption scenarios. Differences in illness estimated between high- and low-virulence serotypes were driven more by the proportion of highly virulent serotypes than the variability in relative dose-response relationships as shown in Figure 3. Realizing the importance of accurate virulence categorization in this modeling approach is central in the appropriate interpretation of model estimates. Although the nuance of every *Salmonella* serotype cannot be captured, using low- and high-virulence stratification potentially prevents over- or underestimation of risk estimates by capturing observable differences in infection virulence and human health outcomes.

Table 8
Cooking profiles and *Salmonella* log reduction for fresh and frozen ground beef cooked at home using a chance variability distribution

Probability	Temperature (°C) Achieved at Center Point	Estimated log reduction (fresh)*	Estimated log reduction (frozen)*
0.02	48.3	0.05	0.01
0.005	52.8	0.07	0.05
0.005	58.3	0.13	0.09
0.06	61.1	0.17	0.12
0.05	63.9	0.23	0.15
0.075	66.7	0.30	0.19
0.09	69.4	0.40	0.24
0.12	72.2	0.51	0.32
0.12	75.0	0.68	0.41
0.10	77.8	0.89	0.53
0.085	80.6	1.17	0.70
0.065	83.2	1.52	0.87
0.065	85.9	2.00	1.12
0.04	88.6	2.62	1.44
0.045	91.7	3.53	1.93
0.055	94.1	4.50	2.24

*Calculated using NAMI process lethality spreadsheet and D- and Z-values from ground beef (Murphy et al., 2004; North American Meat Institute, 2008).

Overall, this study found that the removal or diversion of relatively few contaminated ground beef lots containing *Salmonella* above threshold levels of 10 MPN/g and 1 MPN/g would result in a 13.6% and 36.7% reduction of annual salmonellosis illnesses, respectively. Risk to consumers is highest when cooking at home and from frozen rather than in restaurants or using fresh/thawed products. MDR *Salmonella* infections accounted for 15.9% of total annual illnesses which complicates treatment and increases the burden of illness. Removal of MDR *Salmonella* would result in a 45% reduction of acute DALY which is the burden of disease associated with the consumption of contaminated ground beef. Highly virulent serotypes account for 14% of *Salmonella*-positive ground beef samples but are responsible for nearly 97% of annual illnesses. Focusing salmonellosis reduction efforts on

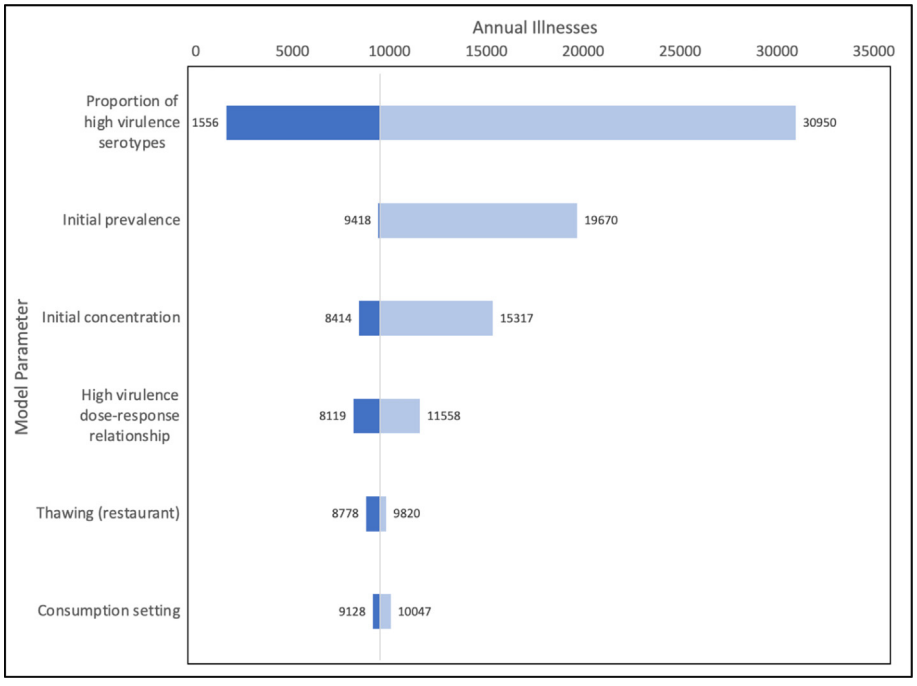


Figure 3. Tornado diagram illustrating sensitivity analysis results for model parameters.

Table 9
Cooking profiles and *Salmonella* log reduction for fresh and frozen ground beef cooked in a restaurant using a chance variability distribution

Cooking Type	Probability	Temperature (°C) Achieved at Center Point	Estimated log reduction (fresh)*	Estimated log reduction (frozen)*
Medium-rare	0.04	72.1	0.51	0.32
Medium	0.12	75.3	0.70	0.42
Medium-well	0.31	80.0	1.11	0.65
Well	0.23	82.3	1.39	0.80
Not Specified	0.30	81.7	1.31	0.76

*Calculated using NAMI process lethality spreadsheet and D- and Z-values from ground beef (Murphy et al., 2004; North American Meat Institute, 2008).

Table 10
Input parameter value ranges used in sensitivity analysis

Parameter	Initial Input	Sensitivity Analysis Value Range	Source
Proportion of high-virulence serotypes	14%	0–51.8%	Absolute minimum, Original high-virulence criteria
Initial prevalence	1.47%	1.43–3.05%	>1 MPN/g removed, (Food Safety and Inspection Service, 2020b)
Initial concentration	−1.78 (−3.00, −0.56) log MPN/g	Minimum: −1.78 (−2.88, −0.68) log MPN/g	All censored data set to 0,
		Maximum: −1.40 (−2.22, −0.58) log MPN/g	All censored data set to LOQ (0.03 MPN/g)
High-virulence dose-response relationship	α: 1.324×10^{-1},	α: Uniform (Minimum: 0.0940, Maximum: 0.1817)	(World Health Organization, Food and Agriculture Organization of the United Nations, 2002)
	β: 51.45	β: Uniform (Minimum: 43.75, Maximum: 56.39)	
Thawing (restaurant)	Frozen: 30% Fresh: 70%	Frozen: 27–61% Fresh: 39–73%	(Bogard et al., 2013)
Consumption setting	Home: 49.59% Restaurant: 50.41%	Home: 45–57% Restaurant: 43–55%	(Davis & Lin, 2005)

redirecting highly contaminated ground beef lots, MDR *Salmonella*, and highly virulent *Salmonella* serotypes from NRTE products appear to be the most effective risk prevention strategies. Model estimates will become more accurate with improved understanding of virulence categorization due to illness estimate sensitivity to this model parameter. Reliable cross-contamination coefficients in various preparation settings with ground beef and AMR-specific burden of disease metrics would bolster the interpretation of these models moving forward.

Declaration of Competing Interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Funding provided by the Beef Checkoff administered by the Foundation for Meat and Poultry Research and Education. A. Strickland was appointed to the U.S. Department of Agriculture's (USDA) Food Safety and Inspection Service (FSIS) Research Participation Program administered by the Oak Ridge Institute for Science and Education (ORISE) during the development of risk assessment models. A. Strickland is currently employed by the Food and Drug Administration within the Center of Food Safety and Applied Nutrition. C. Hedberg serves on McDonald's Food Safety Advisory Council.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jfp.2023.100093.

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