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Modeling the Risk of Colistin-Resistant Salmonella Minnesota in Cooked Chicken: A Probabilistic Microbial Assessment

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Abstract

Background

Antimicrobial-resistant *Salmonella* is an emerging food safety concern worldwide. In Saudi Arabia, published epidemiological data on antimicrobial-resistant *Salmonella Minnesota* associated with poultry products remain limited. Therefore, this study aimed to estimate the potential public health risks associated with antimicrobial-resistant *Salmonella Minnesota* in cooked chicken using a probabilistic microbial risk assessment framework.

Methods

A probabilistic microbial risk assessment model was developed using Monte Carlo simulation with 10,000 iterations. The framework integrated food consumption data, microbiological surveillance data, and a WHO-based dose–response model to estimate exposure, probability of illness, and population-level risk characterization.

Results

The modeled ingested dose of antimicrobial-resistant *Salmonella Minnesota* showed a median of 1.07 CFU/g. The estimated probability of exposure demonstrated a median value of 1.13×10^{-3}, while the modeled probability of illness showed a median value of 8.00×10^{-5}. The estimated annual foodborne illness rate showed a median of 0.20 cases per 100,000 population, ranging from 0.07 to 0.54 cases per 100,000 population across the estimated distribution. Indirect comparison using reported national *Salmonella* incidence rates between 2015 and 2023 showed general agreement between the modeled outputs and the observed epidemiological pattern.

Conclusions

This study presents a probabilistic framework for estimating the potential public health risks associated with antimicrobial-resistant *Salmonella Minnesota* in cooked chicken in Saudi Arabia. The proposed model may support preliminary risk-based surveillance and food safety assessment activities in settings where published epidemiological data remain limited.

1. Introduction

Chicken is among the most consumed worldwide it is also the main source of *Salmonella* (Siyu et al., 2025). In the last five years, Animal food consumption increased according to the increase in local production of chicken meat from 1,130,000 reaching 60% self-sufficiency level in 2022 to 71% self-sufficiency level in 2023 (MEWA, 2023). Also, Poultry ranks among the most widely consumed sources of animal protein in Saudi Arabia, with an average consumption rate estimated at 47 kg of chicken meat per person (Saudi Gazette, 2016).

The published report from the Saudi Ministry of Health in 2024 confirmed 2,289 Cases of *Salmonella*. This includes sporadic cases without outbreaks, while foodborne outbreaks in involve 833 cases from home or public sources. This is shows *Salmonella* as the most common pathogenic bacterium in Saudi Arabia and one of the most important causes foodborne illnesses (MOH, 2024).

Recent studies published in 2025 conducted in Saudi Arabia collected 212 chilled retail chickens from Riyadh and Qassim *Salmonella* was detected in 9.3% of samples, and 90% to 70% of the samples were multidrug resistant (Aljasir & Allam, 2025). Also, in 2023 39 *Salmonella* isolates were recovered from chilled chicken meat samples collected from local Saudi markets 88% of isolate were multidrug-resistant (Alzahrani et al., 2023).

On the other hand, study in 2025 focused in the criteria of usage of colistin as it used in food producing animal as the resistance is widespread along the food chain and is linked to multidrug-resistant bacterial infections in humans (Ahmed, Abouzeed, & Daw, 2025).

In 2022, Saudi Arabia announced the draft genome sequences of two strains of colistin-resistant *Salmonella enterica* serovar *Minnesota* (Mukhtar et al., 2022). Therefore, this study aimed to use quantitative risk assessment model of colistin-resistant *Salmonella Minnesota* in Cooked Chicken.

2. Method

2.1 Study Design Overview:

This study employs a Probabilistic Microbial Risk Assessment (PMRA) approach to evaluate the risk of *Salmonella Minnesota* with antimicrobial resistance. Unlike the deterministic approach, which uses fixed values for all inputs and variables, the probabilistic methodology incorporates uncertainty and variability by treating model inputs and parameters as statistical distributions (WHO,2021). As a result, the outputs are also presented as probability distributions, allowing for a more nuanced interpretation of risk that accounts for uncertainty in the data and assumptions (Zwietering & van Gerwen, 2008).

In this study, we modified the quantitative model originally developed by Pulsrikarn et al. (2022) to estimate the risk of antimicrobial-resistant *Salmonella Minnesota* ((Pulsrikarn et al., 2022). As the original model was not designed for chicken, the modifications included adjustments to inputs, variables, and equations to reflect local conditions and to enable its application for assessing the risk associated with cooked chicken products in Saudi Arabia.

As shown in Fig. 1, which provides an overview of the modeling process in probabilistic microbial risk assessment, the model incorporates three primary types of data: (1) dietary data, representing the consumption of the target food; (2) lab-based microbiological data, including the number of isolate samples and the proportion testing positive for *Salmonella*, *Salmonella Minnesota*, and colistin resistant *Salmonella Minnesota*; and (3) initial microbial load data in cooked chicken, which are estimated using values derived from the literature.

The Probabilistic approach used in this study is implemented through Monte Carlo simulation, which involves conducting a large number of iterations to reflect the variability and uncertainty in the input parameters. In each iteration, random values are sampled from predefined statistical distributions related to model input. These values are processed through the model equations to estimate outcomes. By repeating this process 10,000 times, the model generates a distribution of possible outcomes, providing more realistic assessment of microbial risk. Table 1 presents the developed equation, input data, statistical distributions, and model parameters used in this study. The table is structured to align with the risk assessment framework shown in Fig. 1, and each component is explained in the following sections.

2.2 Data Source:

With regard to the dietary data, values were obtained from the National Nutrient Consumption (NNC-V2) Model, a probabilistic model developed to estimate food consumption in Saudi Arabia, including chicken products

(Alhumaidan et al., 2024; Alhumaidan et al., 2025). The lab-based microbiological data were derived from surveillance and laboratory testing programs conducted by the Saudi Food and Drug Authority (SFDA) between 2020 and 2022. Finally, the initial microbial load data in cooked chicken were extracted from case studies published by the World Health Organization (WHO), specifically, Case Study No. 25, which includes the same food matrix targeted in this study (WHO & FAO, 2002).

2.3 Exposure Assessment:

2.3.1 Food Consumption Patterns:

Exposure assessment begins by estimating the food consumption patterns of chicken. This is achieved by extracting the statistical distribution parameters of this dietary pattern, namely the NNC_i is estimated meat groups consumption, and the probability that consumed meat being chicken meat, donated as O_i.

In Eq. 1, the NNC_i is modeled as a normal distribution characterized by the mean and standard deviation of consumption within this group. O_i is represented as a uniform distribution, defined by the minimum (min_o) and maximum (max_o) probabilities of selecting chicken as the consumed product (Eq. 2–4).

$$NNC_i \sim N\,(120{,}28)$$

1

$$O_i \sim U\,(min_o,\ max_o)$$

2

$$min_o = \frac{PF}{AF} - (\frac{PF}{AF}\ \times\ CLU)$$

3

$$max_o = \frac{PF}{AF} + (\frac{PF}{AF}\ \times\ CLU)$$

4

PF represents the number of chicken meat products within the broader meat food group, while AF denotes the total number of food items classified under this group. These values were obtained from the McCance and Widdowson's Composition of Foods Integrated Dataset (CoFID), where $PF = 102$ and $AF = 400$(Public Health England, 2021). However, since CoFID is not specific to the Saudi Arabian context and no national food composition table is currently available, an uncertainty level (CLU) of 50% was assumed to account for potential discrepancies.

2.3.2 Concentration of Salmonella:

Following this, the concentration assessment (C_i) is conducted using Eq. 5, which models the concentration of *Salmonella* after cooking for the given iteration i. This parameter is represented using a uniform distribution, reflecting the range of possible concentration values observed or estimated after the cooking process.

$$C_i \sim\ U\,(LB\,,\ UB)$$

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Where LB and UB represent the lower and upper uncertainty bounds of the concentration range, respectively. These bounds were estimated from the modeled concentration of *Salmonella* in cooked chicken (DS_i), adjusted according to the modeled food consumption amount and the uncertainty level (LU). The lower and upper bounds were estimated using Equations 6 and 7.

$$LB = \frac{DS_i}{NNC_i \times O_i} - \left(\frac{DS_i}{NNC_i \times O_i} \times LU\right)$$

6

$$UB = \frac{DS_i}{NNC_i \times O_i} + \left(\frac{DS_i}{NNC_i \times O_i} \times LU\right)$$

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Using Equations 8 and 9, the modeled concentration in cooked chicken (DS_i) was derived using the incidence coefficient of *Salmonella* in Saudi Arabia (IR_i), which was modeled using a uniform distribution based on the national incidence probability (RC) and its associated uncertainty level.

$$DS_i = 51.45 \times \left(\left(1 - IR_i\right)^{-\frac{1}{0.1324}} - 1\right)$$

8

$$IR_i \sim U\left(min_{IR},\, max_{IR}\right)$$

9

The RC was set at 7.5 per 10,000 population, based on national incidence data reported by Alamri et al. (2026). An uncertainty level (LU) of 25% was applied according to the WHO and FAO Microbiological Risk Assessment Series (WHO & FAO, 2002).

The primary aim of this approach was to estimate the concentration levels using nationally available data related to food consumption patterns and the incidence rate of *Salmonella* in Saudi Arabia. This approach was intended to generate concentration estimates that more closely reflect the expected real-world conditions within the Saudi population, rather than relying solely on hypothetical scenario-based assumptions defined concentration inputs.

2.3.3 Prevalence of Salmonella Minnesota with antimicrobial resistance:

The third component in the exposure assessment is the prevalence of the microbe, denoted as PS_i, which represents the probability of *Salmonella Minnesota* with antimicrobial resistance being present in a given sample. This was estimated as beta distribution using Eq. 10.

$$PS_i \sim Beta\left(\left(AMR \times n\right) + 1, n - \left(AMR \times n\right) + 1\right) \quad (10)$$

Where AMR the probability of detecting *Salmonella Minnesota* with antimicrobial resistance is was calculated using surveillance data from SFDA (2020–2022). The calculation followed a stepwise approach: the proportion of *Salmonella*-positive samples among all isolates (S/n), the proportion of *Salmonella Minnesota* among *Salmonella*-positive samples (SM/S), and the proportion with antimicrobial resistance among *Salmonella Minnesota* samples (SA/SM). AMR Was derived as shown in Eq. 9, which reduced as shown in Eq. 12.

$$AMR = \left(\frac{S}{n}\right) \times \left(\frac{SM}{S}\right) \times \left(\frac{SA}{SM}\right)$$

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$$AMR = \left(\frac{SA}{n}\right)$$

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2.3.4 Prevalence of Salmonella Minnesota with antimicrobial resistance:

Using the estimated values of PS_i, F_i and C_i the model proceeds to calculate the ingested dose (D_i) and the probability of exposure to antimicrobial-resistant *Salmonella Minnesota* (PE_i). These calculations are presented in Equations 13 and 14, which integrate the microbial prevalence, food consumption, and concentration levels to estimate the potential exposure per iteration.

$$D_i = O_i \times NNC_i \times C_i$$

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$$PE_i = PS_i \times (1 - Exp(-D_i))$$

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2.4 Hazard characterization and Risk characterization:

2.4.1 Probability of Illness:

In this assessment, the pathway linking food consumption to infection and illness, follows the standard structure applied in quantitative microbial risk assessment (WHO & FAO, 2002). After dietary exposure to Salmonella Minnesota is first estimated, it translated into the probability of antimicrobial-resistant *Salmonella* (PI_i) using an established dose–response relationship.

According to the internationally guidelines for microbial risk assessment issued by the World Health Organization and referenced in the Guidelines for Risk Analysis of Foodborne Antimicrobial Resistance (CXG 77-2011) developed by the Codex Alimentarius Commission, the probability of illness (PI_i) is estimated by linking the consumed dose to a dose–response model derived from real-world data (WHO & FAO, 2002).

The Dose–response models are typically developed through statistical fitting procedures that identify the best-fitting curve representing the expected relationship between ingested dose and the proportion of individuals who develop illness, based on documented outbreak data (WHO & FAO, 2002). In microbial risk assessment, the Beta-Poisson model is commonly used to describe this relationship as shown in Eq. 15.

$$PI_i = 1 - (1 + (D_i/51.45))^{-0.1324}$$

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Where the dose–response model in this equation was established for Salmonella by the WHO, and was adopted in this study (WHO & FAO, 2002). This dose-response was based on statistical fitting to human outbreak data,

incorporating information on estimated ingested doses and observed illness proportions from documented Salmonella outbreaks. The model parameters (α = 0.1324, β = 51.45) were derived through this fitting process. Accordingly, this study adopts the WHO-established Salmonella dose–response model, as it is considered appropriate for describing the dose–illness relationship and is consistent with WHO guidance and international procedures for the risk assessment of foodborne antimicrobial resistance (WHO & FAO, 2002). The resulting illness cases represent individuals who develop symptomatic infection following exposure.

2.4.2 Risk characterization Modeling

For risk characterization, two primary public health outcomes were quantified as the expected number of foodborne illness cases. These estimates require integrating two key probabilistic components: the population-level probability of exposure (PE_i), derived from the exposure assessment; the probability of illness given exposure (PI_i). Where PFI_i which represents the probability of foodborne illness based on probability of exposure level was computed using Eq. 16.

$$PFI_i = PI_i \times PE_i$$

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Because this probability reflects individual risk, an additional scaling step was required to generate estimates of total number of foodborne lines cases at the population level ($MAFI_i$). Therefore, Eq. 18 was applied to scale the individual probability by incorporating the annual number of reported foodborne outbreaks in Saudi Arabia (OB_i), as well as the proportion attributable specifically to Salmonella from poultry.

$$MAFI_i = \left(1 - \left(1 - PFI_i\right)^{OB_i}\right) \times 100{,}000$$

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Assuming an annual average of five foodborne outbreaks in Riyadh, and extrapolating this estimate across the 13 administrative regions of Saudi Arabia, the projected national burden could reach approximately 65 outbreaks per year, with 36% attributed to chicken, as reported by Alajlan et al. (2025). This extrapolation, however, does not assume that outbreaks are uniformly distributed across all regions. To incorporate uncertainty and account for regional variability, a 25% adjustment factor was applied, yielding an estimated range of 4 to 6 outbreaks per region under the modeled scenario. This was mathematically resented as in Eq. 18.

$$OB_i = U\left(\left(65 - \left(65 \times LU\right)\right), \left(65 + \left(65 \times LU\right)\right)\right) \times 0.36$$

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2.5 Handling Uncertainty and Bias in Model Inputs:

The data used in the analytical modeling include several potential sources of uncertainty, variability, and bias related to the nature of surveillance-based inputs (EFSA Scientific Committee.2018). Since risk modeling commonly relies on data that are not fully deterministic, this study adopted a probabilistic framework to represent and propagate these aspects within the model rather than relying on fixed point estimates for the input data (Costa,2008 ; Beguería ,2006).

In this model, key inputs with uncertainty included the concentration parameter (C_i), and the number of outbreak days (OB_i), both derived from epidemiological surveillance and monitoring systems. To account for uncertainty

associated with these observed values, a conservative representation was applied using uniform distributions defined as ± 25% around the reported value. Thus, the margin was defined as the uncertainty level (LU = 25%) .

In addition, the laboratory data were derived from available surveillance samples rather than from a targeted sampling design intended for precise prevalence estimation. Accordingly, the prevalence parameter was modeled using a non-informative Beta distribution. This aim is to allow the parameter to vary across its full probability range without imposing prior weighting toward specific values (Singh et a, 2015). Compared with point-estimate approaches that treat inputs as exact values, probabilistic propagation reduces overconfidence and limits structural bias, while making the resulting output range and uncertainty explicitly visible through percentiles and interval estimates (EFSA Scientific Committee, 2018).

2.6 Model performance:

Model performance could not be evaluated directly for antimicrobial-resistant Salmonella Minnesota due to limited national observational data for this specific serotype in Saudi Arabia. Therefore, model performance was assessed indirectly by comparing the predicted incidence of total Salmonella infections with the reported national incidence rate. This approach was used because Salmonella Minnesota represents a subset of total Salmonella infections. After estimating the total Salmonella incidence, the prevalence of antimicrobial-resistant Salmonella Minnesota from laboratory surveillance data was applied to estimate the resistant serotype-specific cases.

Table 1

Data and parameters for modeling microbial risk assessment for antimicrobial-resistant Salmonella Minnesota

Variable	Description	Calculation / Input	Units
Food Consumption Patterns			
NNC_i	Estimated meat groups consumption for given iteration i.	$NNC_i \sim N\,(120{,}28)$ Distribution was adopted from NNC-V2 model (Alhumaidan et al., 2024; Alhumaidan, 2025a; Alhumaidan et al., 2025b; Alhumaidan et al., 2025c).	Gram /day
O_i	Probability that consumed meat being sheep meat for given iteration i	$O_i \sim U\,(min_o, max_o)$	Fraction
min_o	Minimum possible probability value account for uncertainty level .	$min_o = \frac{PF}{AF}\,(\frac{PF}{AF}\,CLU)$	Fraction
max_o	Maximum possible probability value account for uncertainty level.	$max_o = \frac{PF}{AF}\,(\frac{PF}{AF}\,CLU)$	Fraction
CLU	Level of uncertainty for probability that consumed meat being sheep meat.	$CLU = 0.50$	Fraction
PF	Number of chicken meat product within meat food group	$PF = 102$ Extracted from the McCance and Widdowson's composition of foods integrated dataset (CoFID) (Public Health England, 2021)	Food items
AF	Number of food items within meat food group.	$AF = 400$ Extracted from the McCance and Widdowson's composition of foods integrated dataset (CoFID) (Public Health England, 2021)	Food items
Concentration of Salmonella			
C_i	Concentration of *Salmonella* after cooking	$C_i \sim U\,(LB, UB)$	CFU/gram

Variable	Description	Calculation / Input	Units
Food Consumption Patterns			
	for the given iteration i.		
LB	Lower bound of the concentration of *Salmonella* after cooking.	$LB = \frac{DS_i}{MNC_i} \times \left(\frac{DS_i}{MNC_i} \times LU\right)$	CFU/gram
UB	Upper bound of the concentration of *Salmonella* after cooking.	$UB = \frac{DS_i}{MNC_i} \times \left(\frac{DS_i}{MNC_i} \times LU\right)$	CFU/gram
DS_i	Initial concentrations in cooked chicken.	$DS_i = 51.45 \times ((1 - IR_i)^{-\frac{1}{0.1324}} - 1)$	CFU/gram
IR_i	Incidence coefficient of *Salmonella* in Saudi Arabia.	$IR_i \sim U\left(min_{IR}, max_{IR}\right)$	Fraction
min_{IR}	Minimum value for incidence coefficient of *Salmonella*.	$min_{IR} = RC - (RC \times LU)$	Fraction
max_{IR}	Maximum value for incidence coefficient of *Salmonella* .	$max_{IR} = RC - (RC \times LU)$	Fraction
RC	Probability of incidence of *Salmonella* in Saudi Arabia.	$RC = 7.5/10000$ Based on national Salmonella incidence data reported by Alamri et al. (2026).	Fraction
LU	Level of uncertainly of the initial concentrations observed.	$LU = 0.25$ Based on data from FAO and WHO Microbiological Risk Assessment Series (WHO & FAO, 2002).	Fraction
Prevalence Estimation of Salmonella Minnesota with antimicrobial resistance			
PS_i	Prevalence of sample with Positive *Salmonella* with antimicrobial resistance for	$PS_i \sim Beta\left((AMR \times n) + 1, n - (AMR \times n) + 1\right)$	Fraction

Variable	Description	Calculation / Input	Units
Food Consumption Patterns			
	the given iteration i.		
AMR	Probability of sample with Positive *Salmonella Minnesota* with antimicrobial resistance.	$AMR = \left(\frac{S}{n}\right) \times \left(\frac{SM}{S}\right) \times \left(\frac{SA}{SM}\right)$	Sample
SA	Number of samples with Positive *Salmonella Minnesota* with antimicrobial resistance by SFDA (2020–2022).	$SA = 38$	Sample
SM	Number of samples with Positive *Salmonella Minnesota* by SFDA (2020–2022).	$SM = 260$	Sample
S	Number of samples with Positive *Salmonella* by SFDA (2020–2022).	$S = 859$	Sample
n	Total number of microbial isolates samples by SFDA (2020–2022).	$n = 1032$	Sample
Ingested Dose and Probability of Exposure to Antimicrobial-Resistant Salmonella Minnesota			
PE_i	Probability of exposure for *Salmonella Minnesota* with antimicrobial resistance for the given iteration i for the given iteration.	$PE_i = PS_i \times (1 - Exp(-D_i))$	Fraction

Variable	Description	Calculation / Input	Units
Food Consumption Patterns			
D_i	Ingested Dose of *Salmonella Minnesota* for individual in Saudi Arabia for the given iteration.	$D_i = O_i \times NNC_i \times C_i$	CFU/day/person
Probability of Illness from Antimicrobial-Resistant Salmonella Minnesota			
PI_i	Probability of developing foodborne illness after exposure to antimicrobial-resistant *Salmonella Minnesota*, for the given iteration.	$PI_i = 1 - (1 + (D_i/51.45))^{-0.1324}$	Fraction
Risk characterization of Salmonella Minnesota with antimicrobial resistant			
$MAFI_i$	Annual Foodborne illness from *Salmonella Minnesota* with antimicrobial resistance for the given iteration	$MAFI_i = \left(1 - (1 - PFI_i)^{OB_i}\right) \times 100{,}000$	Illness per 100,000
PFI_i	Probability of foodborne illness based on probability of exposure level for the given iteration.	$PFI_i = PI_i \times PE_i$	Fraction
OB_i	Number of days on which Salmonella outbreak attributed to chicken occurs in the given iteration.	$OB_i = U\left((65 - (65 \times LU)), (65 + (65 \times LU))\right) \times 0.36$ Data extracted from Alajlan, Abdullah A., et al. (Alajlan et al., 2025).	Days

3. Result

3.1 Ingested Dose of Antimicrobial-resistant Salmonella Minnesota:

As shown in Fig. 2, the estimated ingested dose of antimicrobial-resistant *Salmonella Minnesota* was derived from the modeling process. The median dose was 1.07 CFU/g (0.03 log CFU/g), and the 95% confidence interval ranged from 1.05 to 1.11 CFU/g (0.02 to 0.04 log CFU/g).

3.2 Exposure Assessment and hazard characterization:

As shown in Table 2, the dietary exposure assessment modeled the ingested dose of antimicrobial-resistant Salmonella Minnesota with a median value of 1.07 CFU/g and a 95% confidence interval ranging from 1.05 to 1.11 CFU/g. The modeled probability of exposure to colistin-resistant Salmonella had a median value of 1.13×10^{-3}, with a 95% confidence interval ranging from 6.80×10^{-4} to 1.81×10^{-3}. The modeled probability of illness, based on the dose–response model, showed a median value of 8.00×10^{-5} and a 95% confidence interval ranging from 5.00×10^{-5} to 1.10×10^{-4}.

Table 2
Exposure Assessment and hazard characterization of Antimicrobial-resistant Salmonella Minnesota in Saudi Arabia

Model Variables	**Percentile**		
	2.5th	**50th**	**97.5th**
Exposure Assessment			
Ingested Dose (D_i) in CFU/g	1.05	1.07	1.11
Probability of Exposure (PE_i)	6.80×10^{-4}	1.13×10^{-3}	1.81×10^{-3}
Hazard characterization			
Probability of illnesses (PI_i)	5.00×10^{-5}	8.00×10^{-5}	1.10×10^{-4}

3.3 Risk characterization:

As shown in Table 3, the model-predicted annual foodborne illness rate attributable to antimicrobial-resistant Salmonella Minnesota in Saudi Arabia showed a median of 0.20 cases per 100,000 population. The estimated distribution ranged from 0.07 cases per 100,000 population at the 2.5th percentile to 0.54 cases per 100,000 population at the 97.5th percentile.

Table 3
Risk characterization of Antimicrobial-resistant Salmonella Minnesota in Saudi Arabia

Model Variables	**Percentile**		
	2.5th	**50th**	**97.5th**
Number of Foodborne Illness from Salmonella Minnesota			
Annual Foodborne illness per 100,000 ($MAFI_i$)	0.06725	0.20113	0.53909

3.4 Model Performance Results

The model-predicted annual total incidence rate of Salmonella exhibited a median of 4.49 cases per 100,000 individuals annually. The estimated distribution spanned from 1.56 cases per 100,000 individuals at the 2.5th percentile to 11.33 cases per 100,000 individuals at the 97.5th percentile.

The observed national total incidence rates of Salmonella, reported between 2015 and 2023, ranged from 2.34 to 7.50 cases per 100,000 individuals and were predominantly situated within the central region of the simulated distribution. This alignment suggests consistency between the model-predicted total Salmonella incidence and the reported national epidemiological data (Alamri et al., 2026).

This comparison is crucial, as estimating antimicrobial-resistant Salmonella Minnesota cases involves applying the laboratory-based prevalence of resistant isolates to the simulated total Salmonella incidence. Thus, any significant deviation in predicted total incidence directly impacts estimated c

4. Discussion

4.1 Main Finding

The main findings of this study offer probabilistic model-based estimates of foodborne exposure to antimicrobial-resistant Salmonella Minnesota linked to the consumption of cooked chicken in Saudi Arabia. The exposure assessment determined a median ingested dose of 1.07 CFU/g, while the modeled probability of exposure indicated a median value of 1.13×10^{-3}. Utilizing the WHO dose–response model, the estimated probability of illness exhibited a median value of 8.00×10^{-5}.

When these findings are translated into population-level risk characterization outcomes, the model-predicted annual foodborne illness rate attributable to antimicrobial-resistant Salmonella Minnesota revealed a median of 0.20 cases per 100,000 population, with an estimated distribution ranging from 0.07 to 0.54 cases per 100,000 population across the 2.5th and 97.5th percentiles.

Direct comparison of antimicrobial-resistant Salmonella Minnesota cases was not possible due to limited epidemiological data for this serotype in Saudi Arabia. Thus, an indirect comparison was made using total reported Salmonella incidence rates in Saudi Arabia from 2015 to 2023 (Alamri et al., 2026).

This method is valid as antimicrobial-resistant Salmonella Minnesota is a subset of the overall Salmonella burden. Estimates in this study were derived from modeled total Salmonella incidence combined with laboratory-based prevalence of resistant Salmonella Minnesota isolates.

The model-predicted annual total Salmonella incidence had a median of 4.49 cases per 100,000, while observed national incidence ranged from 2.34 to 7.50 cases per 100,000, mainly within the central region of the distribution. Although this comparison does not confirm the incidence of resistant Salmonella Minnesota directly, the agreement suggests the modeled outputs align with expected national epidemiological patterns under defined assumptions.

Given the regional heterogeneity in disease burden reported globally, developing localized, probability-based risk assessments is crucial for informing effective intervention strategies against foodborne pathogens (Jakobsen et al., 2026)

4.2 Model Application

Several strategies can be implemented to reduce the risks related to Salmonella contamination and antimicrobial resistance within the food production system. A primary approach involves regulating and ensuring the judicious use of antibiotics in livestock farming. The excessive or improper application of antimicrobials in animals raised for food is widely acknowledged as a significant contributor to the development and dissemination of antimicrobial-resistant strains of Salmonella, which can then be transmitted to humans through consumption (Ripon et al., 2023; Nair et al., 2018). Therefore, it is crucial to establish antimicrobial stewardship programs, enhance regulatory frameworks governing veterinary antibiotic usage, and encourage alternative methods for disease management as vital measures aimed at decreasing antimicrobial resistance among foodborne pathogens (Ripon et al., 2023).

Besides promoting responsible antibiotic use, enhancing hygiene practices and biosecurity throughout all stages from farm to table represents another essential intervention. Preventive actions like improved sanitation on farms, better cleanliness standards in slaughterhouses, and more effective handling procedures can substantially diminish pathogen transfer from animals to people (Morgan et al., 2023). Research modeling has indicated that while reducing antibiotic usage may change how pathogens behave within livestock populations, any possible uptick in foodborne illnesses could be countered by interventions focused on animal-to-human transmission routes alongside bolstered safety protocols along the supply chain (Morgan et al., 2023).

In addition to proper cooking techniques, enhancing consumer awareness and promoting safe food handling practices are essential components of effective food safety risk reduction. Educational efforts such as public health campaigns, community-based food safety education, and training programs for food handlers can foster adherence to recommended cooking temperatures and hygienic practices (WHO, 2002). Research has also indicated that interventions aimed at consumers and effective risk communication strategies can lower microbiological hazards related to poultry consumption by promoting safer food preparation habits (AIMS Microbiology, 2024; Poultry Science, 2024). Incorporating these educational initiatives into national food safety frameworks and health promotion efforts may improve consumer behaviors and lessen the incidence of salmonellosis. These preventive measures are particularly vital in contexts where surveillance data may be limited since encouraging proper cooking and safe handling remains a practical and cost-efficient method to reduce the risks associated with foodborne diseases (CDC, 2021; WHO, 2002).

Moreover, quantitative modeling coupled with predictive risk assessment techniques are becoming increasingly recognized as beneficial tools for assessing various intervention outcomes. Food safety risk models enable researchers to simulate scenarios involving contamination events, evaluate mitigation strategy effectiveness, and estimate potential impacts regarding foodborne diseases under differing policy environments (Foods, 2022; Fishes ,2024). Consequently, utilizing similar modeling methodologies in future investigations might yield critical insights into how regulations surrounding antimicrobials along with other control initiatives could affect Salmonella occurrence rates as well as public health implications associated with this issue. Integrating such analytical approaches into forthcoming research endeavors would aid evidence-based policymaking while contributing towards developing more robust strategies aimed at managing risks posed by foodborne pathogens effectively (One Health ,2023; Environmental Research ,2024).

The proposed model is designed to facilitate the creation of risk-based surveillance and monitoring strategies for Salmonella in poultry and associated food products. By prioritizing monitoring efforts based on public health risks, this approach enables authorities to allocate resources effectively towards the most critical stages of the food production process (WHO, 2023). Such a framework can assist in directing focused monitoring initiatives and enhancing the early detection of foodborne pathogens.

In Saudi Arabia, implementing this model holds significant importance due to limited comprehensive epidemiological data regarding salmonellosis cases. The absence of national statistics on reported infections hinders accurate assessments of disease prevalence and complicates the design of effective monitoring systems. Consequently, employing this model could aid in generating initial risk estimates while fostering the establishment of organized, risk-based surveillance programs within the nation (Environmental Development, 2025; WHO 2023).

Overall, the results of this research offer a useful foundation for enhancing food safety management and informing future public health initiatives. Utilizing the proposed model can aid in evidence-based decision-making and enhance risk-based monitoring and control strategies. Furthermore, subsequent studies could broaden the framework to incorporate additional foodborne microorganisms and various classes of antimicrobials to create priority rankings for surveillance and intervention efforts. These endeavors may ultimately fortify food safety systems and alleviate the public health challenges linked to foodborne pathogens.

4.3 Advantage and Disadvantage

The modeling structure is not limited to colistin-resistant Salmonella and can be applied as a standardized profiling tool across multiple pathogens and antimicrobial resistance patterns by updating organism-specific and resistance-specific parameters while maintaining a consistent exposure–dose–response–outcome pathway. This enables internally consistent cross-hazard comparison and risk ranking to inform surveillance prioritization and risk-based decision support.

This analysis relies on a simplifying assumption that the annual outbreak frequency and contamination levels remain constant over time. While this assumption is useful for generating a stable analytical baseline and for exploring the modeled scenario, it also represents a conservative approach that may not fully capture potential improvements or variability in real-world regulatory actions, surveillance systems, or outbreak dynamics.

5. Conclusions

This study presents a probabilistic framework for estimating the potential public health risks associated with antimicrobial-resistant *Salmonella Minnesota* in cooked chicken in Saudi Arabia. The proposed model may support preliminary risk-based surveillance.

Declarations

“The views expressed in this paper are those of the author(s) and do not necessarily reflect those of the SFDA or its stakeholders. Guaranteeing the accuracy and validity of the data is the sole responsibility of the research team.”

Consent to publication:

Not applicable.

Clinical trial number

Not applicable.

Ethics approval and consent to participate:

Not applicable.

Competing interests:

The authors have no competing interests to declare.

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Author Contribution

Authors' contributions: Conceptualization, SA,and LM; methodology, SA, LM and OA , NA , and AA; formal analysis, SA ,and OA; writing, review and editing, SA , LM ,and SM; supervision, SA and LM; project administration, SA and LM. All authors have read and agreed to the published version of this manuscript.

Data Availability

Guaranteeing the accuracy and validity of the data is the sole responsibility of the research team. Data supporting the findings of this study are available upon reasonable request. Please contact Sarah A. Alfaifi via email at safaifi@sfda.gov.sa. The model code and related computations can be accessed via the Kaggle platform at: Probabilistic Microbial Risk Model (AMR-SM)

References

1. Ahmed MO, Abouzeed YM, Daw MA. Global initiatives to phase-out colistin use in food-producing animals. Open Veterinary J. 2025;15(2):533–40. https://doi.org/10.5455/OVJ.2025.v15.i2.4.
2. Alajlan AA, Almansour A, Alhumaidan OA, Alwetaid MY, Al-Shehri AA, Alajel SM, Albaridi NA. Analysis of suspected food poisoning incidents in Riyadh, Saudi Arabia: An epidemiological perspective. Int J Microbiol. 2025;2025(1):4803121. https://doi.org/10.1155/2025/4803121.
3. Alamri SA, Alwetaid M, Alshawaish N et al. Temporal and Regional Trends of Foodborne Diseases in Saudi Arabia (2015–2023): A Nationwide Retrospective Analysis. *J Epidemiol Glob Health 16, 42 (*2026). https://doi.org/10.1007/s44197-025-00514-7.
4. Alhumaidan O. (2025a). Code for national nutrition consumption model, version 2: Model emulator. ResearchGate. https://www.researchgate.net/publication/394195653_Code_for_National_Nutrition_Consumption_Model_-Version_2_Model_emulator
5. Alhumaidan OA, Alakeel SA, Alkhunein SM, Fallata GA. Probabilistic mathematical model for dietary consumption and exposure assessment in the absence of data from national nutrition surveys: A case study on Saudi Arabia. Saudi J Health Syst Res. 2024;4:185–203. https://doi.org/10.1159/000538192.
6. Alhumaidan OA, Alakeel SA, Alkhunein SM, Fallata GA. & colleagues. (2025). Saudi Healthy Plate-2024: Framework for developing, modeling, and evaluating Saudi Arabia's dietary guidelines. (Publisher or status to be specified).
7. Alhumaidan OA, Alkhunein SM, Alakeel SA, Fallata GA, Aldhwayan MM, Alfaifi AY, Albalwi WM, AlZeer H. Saudi Healthy Plate-2024: Framework for developing, modeling, and evaluating Saudi Arabia's dietary guidelines. BMC

Nutr. 2025c;11(1):160. https://doi.org/10.1186/s40795-025-01146-7.

8. Alhumaidan O, Alakeel S, Alkhunein S, et al. Estimating dietary intake and nutrient adequacy among adults in Saudi Arabia: a population-based assessment. BMC Nutr. 2026;12:118. https://doi.org/10.1186/s40795-026-01341-0.
9. Aljasir SF, Allam SA. Prevalence and antibiotic resistance of Salmonella spp. and Campylobacter spp. isolated from retail chickens in Saudi Arabia. Microbiol Res. 2025;16(1):27. https://doi.org/10.3390/microbiolres16010027 MDPI.
10. Alzahrani KO, AL-Reshoodi FM, Alshdokhi EA, Alhamed AS, Hadlaq A, Mujallad MA, Alajel MI, S. M. Antimicrobial resistance and genomic characterization of Salmonella enterica isolates from chicken meat. Front Microbiol. 2023;14., Article 1104164. https://doi.org/10.3389/fmicb.2023.1104164.
11. Arsène MMJ, Davares AKL, Andreevna SL, Yauheniya VA, Carime BZ, Marouf R, Khelifi I. The public health issue of antibiotic residues in food and feed: Causes, consequences, and potential solutions. Veterinary World. 2022;15(3):662–71. https://doi.org/10.14202/vetworld.2022.662-671.
12. Beguería S. Validation and evaluation of predictive models in hazard assessment and risk management. Nat Hazards. 2006;37(3):315–29.
13. Cassini A, Díaz Högberg L, Plachouras D, Quattrocchi A, Hoxha A, Skov Simonsen G, Monnet DL. Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in the EU and European Economic Area in 2015: A population-level modelling analysis. Lancet Infect Dis. 2019;19(1):56–66. https://doi.org/10.1016/S1473-3099(18)30605-4.
14. Centers for Disease Control and Prevention. (2021). Salmonella Enteritidis outbreak investigation: June 2021. https://www.cdc.gov/salmonella/enteritidis-06-21/index.html
15. Costa R, editor. Predictive modeling and risk assessment. Volume 4. Springer Science & Business Media; 2008.
16. Scientific Committee EFSA, Benford D, Halldorsson T, Jeger MJ, Knutsen HK, More S, Hardy A. (2018). Guidance on uncertainty analysis in scientific assessments. Efsa J, 16(1), e05123.
17. Ghimpețeanu OM, Pogurschi EN, Popa DC, Dragomir N, Drăgotoiu D, Petcu CD. Antibiotic use in livestock and residues in food—A public health threat: A review. Foods. 2022;11(10):1430. https://doi.org/10.3390/foods11101430.
18. Havelaar AH, Kirk MD, Torgerson PR, Gibb HJ, Hald T, Lake RJ, Devleesschauwer B. World Health Organization global estimates and regional comparisons of the burden of foodborne disease in 2010. PLoS Med. 2015;12(12):e1001923. https://doi.org/10.1371/journal.pmed.1001923.
19. Iowa Department of Health and Human Services. (2025). Salmonellosis. https://hhs.iowa.gov/health-prevention/providers-professionals/center-acute-disease-epidemiology/epi-manual/reportable-diseases/salmonellosis
20. Irrazábal R, et al. Non-typhoidal Salmonella in food animals in Paraguay. Front Veterinary Sci. 2025;2., Article 1521469. https://doi.org/10.3389/fvets.2025.1521469.
21. Jakobsen LS, Agudo A, Vaes L, Al Huthiel M, Al Natour F, di Bari C, Devleesschauwer B, Nane GF, Pires SM, Thomsen ST, Redondo HG, Gibb H, Lake RJ, Havelaar AH, Roberts C, Minato Y, Ingenbleek L. WHO estimates of the global, regional, and national disease burden of nine foodborne chemicals, 2000–21: An updated data synthesis. Lancet Global Health Adv online publication. 2026. https://doi.org/10.1016/S2214-109X(26)00148-8. … WHO Foodborne Disease Burden Epidemiology Reference Group for 2021–2025.
22. Lertwatcharasarakul, et al. analyzed antimicrobial resistance trends and public health implications of Salmonella spp. reinforcing the pathogen's significance in veterinary epidemiology; 2025.

23. Ministry of Environment, Water and Agriculture. (2023). 2023 [Statistical book 2023]. Kingdom of Saudi Arabia. https://www.mewa.gov.sa/ar/InformationCenter/Researchs/Reports/GeneralReports/202023%20.pdf
24. Ministry of Health Saudi Arabia. (2024). Statistical yearbook. https://www.moh.gov.sa/Ministry/Statistics/book/Pages/default.aspx
25. Moreau MR, Edison LK, Ivanov YV, Wijetunge DSS, Hewage EMKK, Linder JE, Kariyawasam S. Comparative pathogenomics of Salmonella enterica serovar Enteritidis reveal potential host-specific virulence factors. Pathogens. 2025;14(2):128. https://doi.org/10.3390/pathogens14020128.
26. Mukhtar LE, Alhamed AS, Mujallad MI, Alshdokhi EA, Alreshoodi FM, Rashidy A, AlAkeel MS, S. I., Alajel SM. (2022). Draft genome sequence of two Salmonella enterica subspecies enterica serovar Minnesota strains harboring mcr-1.1 gene isolated from chicken meat in Saudi Arabia (Microbiology Resource Announcements, 11(11), e00787-22). Microbiology Resource Announcements. https://doi.org/10.1128/mra.00787-22
27. Popa GL, Papa MI. Salmonella spp. infection – a continuous threat worldwide. GERMS. 2021;11(1):88–96. https://doi.org/10.18683/germs.2021.1244.
28. Public Health England. (2021). Composition of foods integrated dataset (CoFID). GOV.UK. https://www.gov.uk/government/publications/composition-of-foods-integrated-dataset-cofid
29. Pulsrikarn C, Kedsin A, Boueroy P, Chopjitt P, Hatrongjit R, Chansiripornchai P, Nuanualsuwan S. Quantitative risk assessment of susceptible and ciprofloxacin-resistant Salmonella from retail pork in Chiang Mai Province in Northern Thailand. Foods. 2022;11(19):2942. https://doi.org/10.3390/foods11192942.
30. Saudi Gazette. (2016, March 14). Saudis among largest consumers of chicken. Saudi Gazette. https://saudigazette.com.sa/article/150754
31. Sheerah HA. Strengthening global health security through antimicrobial resistance control in Saudi Arabia. J Infect Public Health. 2025;18:102788. https://doi.org/10.1016/j.jiph.2025.102788.
32. Singh SK, Singh U, Yadav AS. Reliability estimation and prediction for extension of exponential distribution using informative and non-informative priors. Int J Syst Assur Eng Manage. 2015;6(4):466–78.
33. Siyu Z, Ge Z, Jianmei Z, Juan W, Lin W, Junhui L, Junwei W, Zhina Q. Quantitative risk assessment and critical control point analysis of Extended-Spectrum β-Lactamases(ESBL)Producing Salmonella in chickens from farm to fork. J Future Foods. 2025. https://doi.org/10.1016/j.jfutfo.2025.05.015.
34. Teunis PFM, Havelaar AH. Dose response for Salmonella Typhimurium and Enteritidis. Int J Food Microbiol. 2022;375:109753. https://doi.org/10.1016/j.ijfoodmicro.2022.109753.
35. van Klaveren JD, Goedhart PW, Wapperom D, van der Voet H. A European tool for usual intake distribution estimation in relation to data collection by EFSA. EFSA Supporting publications. 2012;9(6):300E.
36. Varma JK, Greene KD, Ovitt J, Barrett TJ, Medalla F, Angulo FJ. Hospitalization and antimicrobial resistance in Salmonella outbreaks, 1984–2002. Emerg Infect Dis. 2005;11(6):943–6. https://doi.org/10.3201/eid1106.041231.
37. World Health Organization, & Food and Agriculture Organization of the United Nations. Risk assessments of Salmonella in eggs and broiler chickens – 2. Microbiological Risk Assessment Series, No. Volume 2. World Health Organization & Food and Agriculture Organization of the United Nations; 2002.
38. World Health Organization. (2017). Critically important antimicrobials for human medicine (5th rev.). World Health Organization. https://iris.who.int/bitstreams/8831cd08-44cc-4741-9e30-5b1293150bda/download
39. World Health Organization. (2019). WHO integrated global surveillance on antimicrobial resistance. World Health Organization. https://iris.who.int/server/api/core/bitstreams/79d195cc-e595-44f6-90bf-6100f9cb69dc/content

40. World Health Organization. Microbiological risk assessment guidance for food. Geneva: World Health Organization. 2021. Available from: https://www.who.int/publications/i/item/9789240024892
41. Zwietering MH, van Gerwen SJC. (2008). Quantitative microbiological risk assessment. Springer. https://doi.org/10.1007/978-0-387-68776-6

Figures

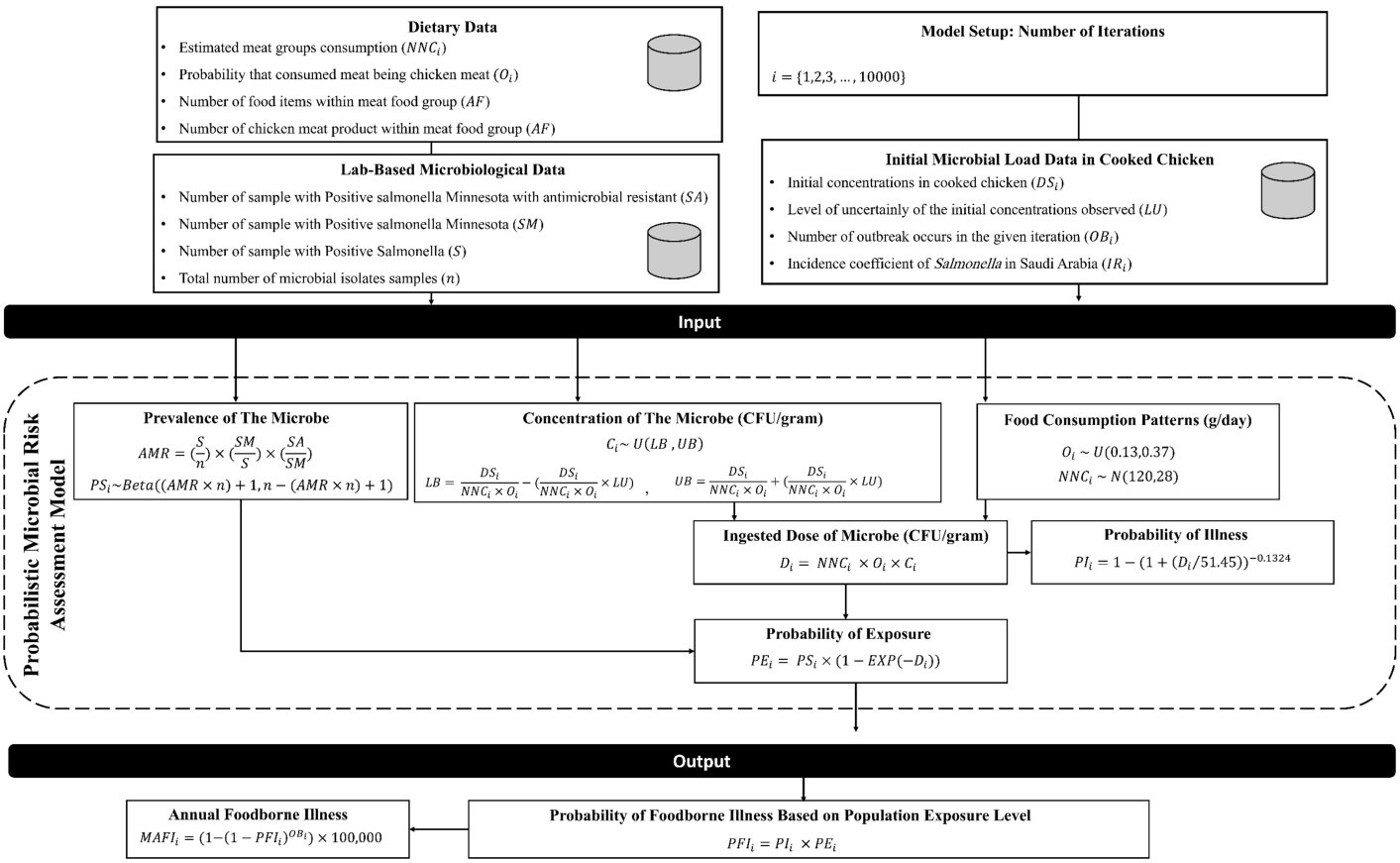


Figure 1

Overview of the Modeling Process in Probabilistic Microbial Risk Assessment

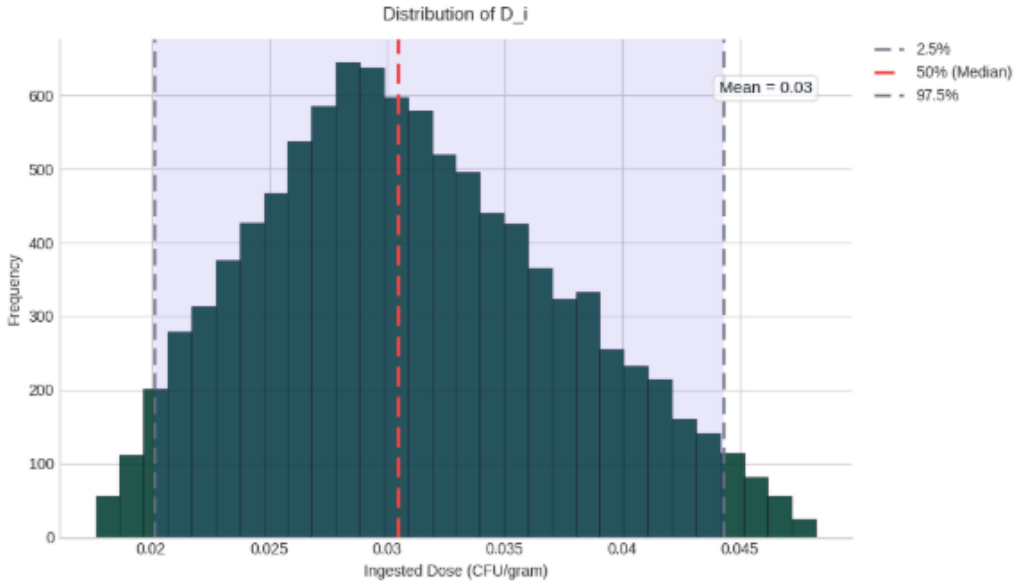


Figure 2

Ingested Dose of Antimicrobial-resistant *Salmonella Minnesota*

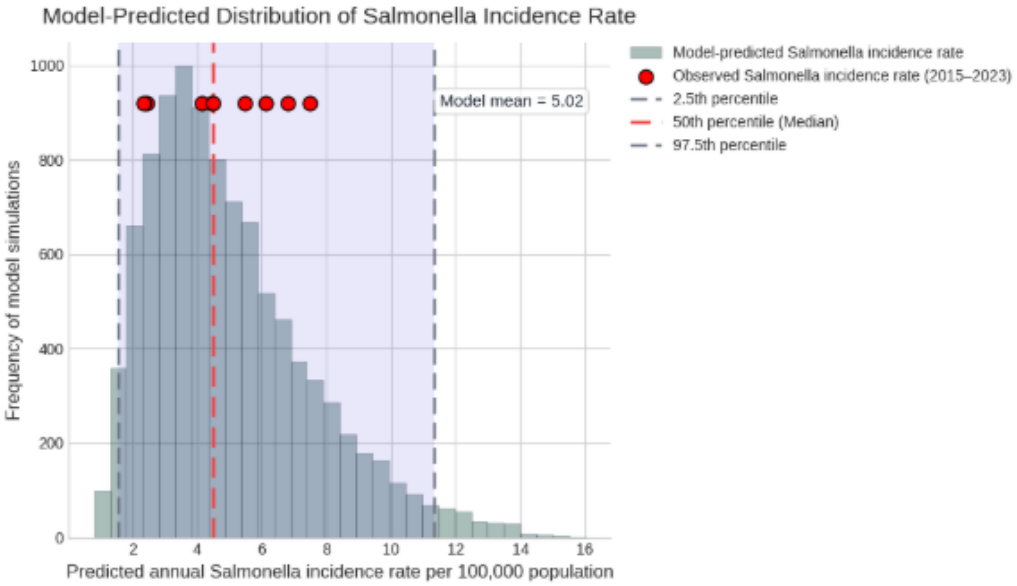


Figure 3

The model-predicted annual Salmonella incidence compared to observed rate