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Research Paper

Poultry Food Assess Risk Model for *Salmonella* and Chicken Gizzards: II. Illness Dose Step

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ABSTRACT

The Illness Dose (ID) step of a Poultry Food Assess Risk Model (PFARM) for *Salmonella* and chicken gizzards (CGs) was shown in the present study. The illness dose is the minimum dose of *Salmonella* consumed that causes an illness. It depends on the zoonotic potential (ZP) of *Salmonella*, food consumption behavior (FCB), and consumer health and immunity (CHI) or the disease triangle (DT). Zoonotic potential is the ability of *Salmonella* to survive, grow, and spread in the production chain or food and then cause illness in humans. Illness dose is predicted in PFARM using a DT, dose-response model (DRM) that was developed with human feeding trial (HFT) data and was validated with human outbreak investigation (HOI) data for *Salmonella*. The ability of the DT, DRM to predict DR data from HOI and HFT for *Salmonella* was quantified using the Acceptable Prediction Zone (APZ) method where acceptable performance occurred when the proportion of residuals in the APZ (pAPZ) was ≥0.7. United States, Centers for Disease Control and Prevention (CDC) data for human salmonellosis from 2007 to 2016 were used to simulate ZP, and only minor changes in ZP of 11 *Salmonella* serotypes were observed during this time. The performance of the DT, DRM for predicting *Salmonella* DR data from HFT and HOI was acceptable with pAPZ that ranged from 0.87 to 1 for individual serotypes of *Salmonella*. Simulation results from the DT, DRM in PFARM indicated that ID decreased ($P \leq 0.05$) and ZP increased ($P \leq 0.05$) over time in the simulated production chain because the main serotype of *Salmonella* changed from Kentucky (low ZP) to Infantis (high ZP) while FCB and CHI were held constant. These results indicated that the DT, DRM in PFARM can be used with confidence to predict ID as a function of ZP, FCB, and CHI. In other words, the DT, DRM in PFARM can be used with confidence to predict dose-response for *Salmonella* and CGs.

Salmonellosis from poultry food is a rare, random, variable, and uncertain event that occurs when by random chance multiple risk factors occur at the same time (Oscar, 2020a). The Poultry Food Assess Risk Model (PFARM) for *Salmonella* was developed to predict this "perfect storm." This is done by providing end-users of PFARM with methods for collecting and simulating data for *Salmonella* contamination (prevalence, number, and serotype) of poultry food, food consumption behavior (FCB), and consumer health and immunity (CHI) in their production chains.

In the present study, the Illness Dose (ID) step of PFARM for *Salmonella* and chicken gizzards (Fig. 1) was demonstrated. Chicken gizzards were used in this case study because they are an edible by-product of chicken processing that are known to harbor *Salmonella* (Abd-Elghany et al., 2015; Raji et al., 2021; Tshipamba et al., 2018) but have not been extensively studied. Illness dose is important because it is the denominator in the calculation of consumer response (CR) to *Salmonella* exposure from their poultry food (Fig. 1).

When a consumer is exposed to poultry foodborne *Salmonella*, they become ill when the dose consumed (DC) is ≥ to the illness dose (ID) or when the ratio of DC to ID is ≥1 (Oscar, 1998, 2004a, 2004b). The illness dose is the minimum dose of *Salmonella* consumed that causes an illness. It depends on the zoonotic potential (ZP) of *Salmonella*, FCB, and CHI or the disease triangle (DT) (Fig. 1). Zoonotic potential is the ability of *Salmonella* to survive, grow, and spread in the production chain and food and then cause illness in humans. It is calculated and simulated in PFARM using United States, Centers for Disease Control and Prevention (CDC) data for human salmonellosis (Oscar, 2017, 2019, 2020a) (Fig. 1).

In PFARM, a DT, dose-response model (DRM) that was developed with human feeding trial (HFT) and was validated with human outbreak investigation (HOI) data for *Salmonella* is used to predict ID as

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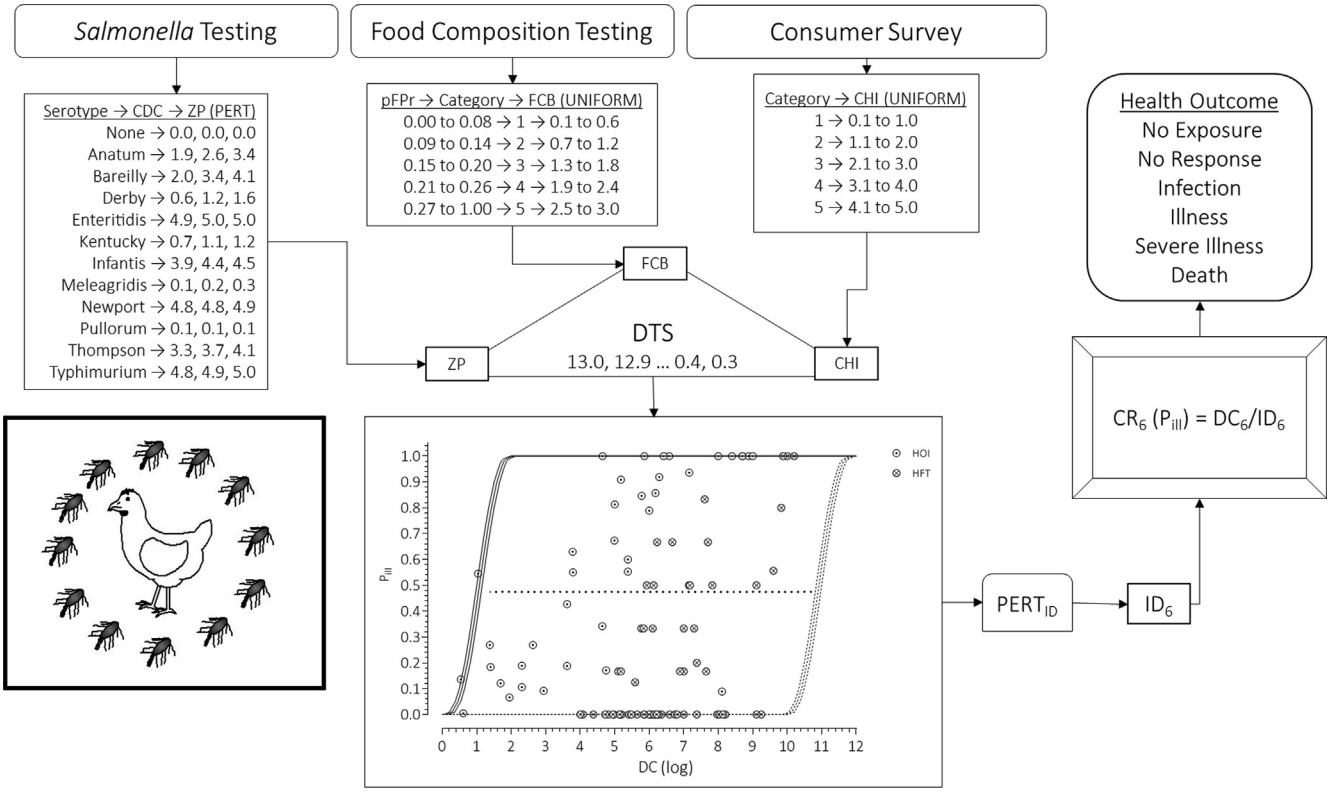

Figure 1. Diagram of the Illness Dose (ID) step of the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs). Abbreviations: CDC = U. S. Centers for Disease Control and Prevention; ZP = zoonotic potential; PERT = pert distribution (minimum, mode, maximum); pFPr = proportion of fat and protein; FCB = food consumption behavior; UNIFORM = uniform distribution (minimum, maximum); CHI = consumer health and immunity; DTS = disease triangle score; P_{ill} = probability of illness; HOI = human outbreak investigation; HFT = human feeding trial; DC = log dose consumed; CR = consumer response; and subscript 6 = output from spreadsheet 6 of PFARM (Fig. 4). See text for details.

a function of ZP, FCB, and CHI (Fig. 1). Testing of CGs for *Salmonella* (Oscar, 2022) and CDC data for human salmonellosis are used to determine ZP in the production chain of interest, whereas a consumer survey (Fig. 2) is used to determine FCB and CHI in the production chain of interest.

Although performance of the DT, DRM for predicting HFT and HOI data for *Salmonella* has been evaluated graphically or qualitatively (Oscar, 2016, 2017, 2019, 2020a), it has not been evaluated quantitatively. Therefore, in the present study, the Acceptable Prediction Zone (APZ) method and its established criteria for model performance and validation (Oscar, 2020b) were used to quantify DT, DRM performance for predicting ID as a function of ZP, FCB, and CHI. The 12 reasons for using the APZ method instead of other statistical methods to quantify model performance can be found in Oscar (Oscar, 2020b).

The DT, DRM in PFARM was developed and validated over multiple years and studies. The first DRM in PFARM was published in 1998 (Oscar). It used a rare event modeling method and two PERT distributions for ID ($PERT_{ID}$) to predict ID as a function of two risk categories (normal or high) for CHI. The next DRM in PFARM (Oscar, 2004a) was based on HFT data for *Salmonella* and used 13 $PERT_{ID}$ to predict ID as a function of virulence and prevalence of 13 *Salmonella*. This DRM was validated against the HFT data used to develop it. It showed that the dose-response curves were irregular in shape when food was contaminated with multiple subtypes of *Salmonella* and not well-predicted by a single, sigmoid-shaped dose-response curve. The next DRM in PFARM (Oscar, 2004b) introduced the concept but not the simulation method for DT as only one $PERT_{ID}$ was used to predict ID as a function of ZP, FCB, and CHI. However, in the next study (Oscar, 2011), eight $PERT_{ID}$ were used to predict ID as a function of DT for the first time.

Two advances in the next study (Oscar, 2016) were the use of CDC data to assign *Salmonella* to two risk categories for virulence and the use of HOI data to qualitatively validate DT, DRM performance against an independent set of data. This was followed by a study (Oscar, 2017) in which criteria for assigning *Salmonella*, food, and consumers to five risk categories per DT factor were introduced. In addition, the Disease Triangle Score (DTS) concept for finding which $PERT_{ID}$ to use to predict ID as a function of DT was introduced. Here, DTS ranged from 2.5 to 12.5 in increments of 0.5 for 21 $PERT_{ID}$. Predictions of this DT, DRMs were validated qualitatively against HOI (independent data) and HFT (dependent data) data for the first time.

In the next study (Oscar, 2019), the composite virulence concept for simulating portions contaminated with multiple *Salmonella* serotypes was introduced, which led to expansion of the DT, DRM from 21 to 101 $PERT_{ID}$. This was done by changing DTS to increments of 0.1 from 2.5 to 12.5. The final study (Oscar, 2020a) before the current study introduced a formula for calculating the virulence of *Salmonella* serotypes from CDC data, and expanded DTS to 1.1 to 12.5 in increments of 0.1 for 115 $PERT_{ID}$. Thus, through a series of studies over an extended period, the DT, DRM in PFARM was developed, improved, and validated; yet, it still has limitations.

Therefore, in the present study, the DT, DRM in PFARM was improved by the following: 1) changing the term virulence to ZP; 2) using 10 instead of 1 year of CDC data to simulate ZP; 3) introducing the proportion of fat and protein in the meal to better simulate FCB; 4) changing DTS to 0.3 to 13.0 in increments of 0.1 for 128 $PERT_{ID}$ to better predict ID as a function of DT; 5) developing a consumer survey to collect data for CHI and FCB including meal preparation practices (MPPs); 6) developing a method to simulate consumer survey data in PFARM; 7) using the APZ method to quantitatively evaluate and val-

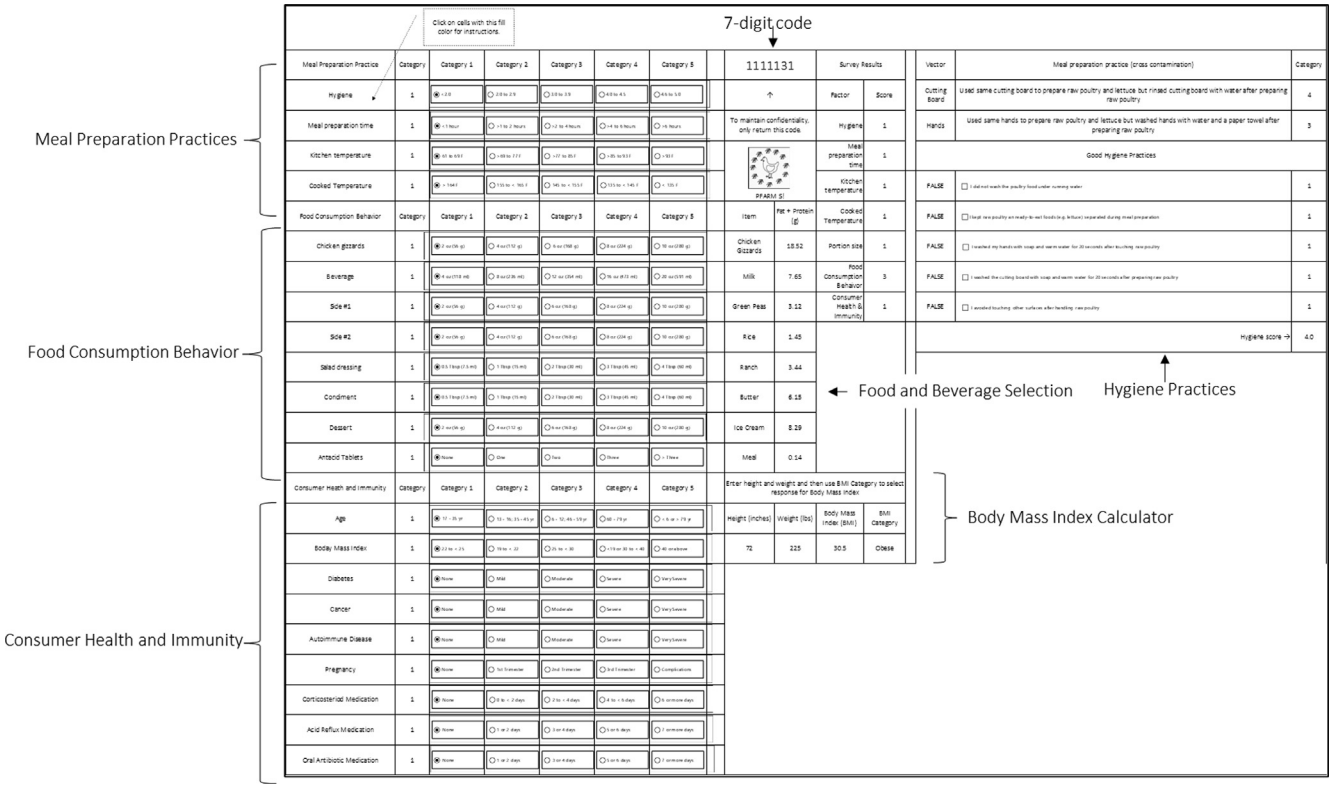

Figure 2. Overview of the consumer survey for meal preparation practices (MPPs), food consumption behavior (FCB), and consumer health and immunity (CHI) for simulation of these variables in the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs). See text for details and Table 1 for survey queries, which are not visible in this figure.

idate DT, DRM performance using established criteria for model performance and validation; and 8) using $PERT_{ZP}$ to better simulate strain variation of *Salmonella* and variability and uncertainty of ZP.

To demonstrate the ID step of PFARM, "What if" scenario analysis using computer-generated consumer survey results ($n = 100$) and *Salmonella* contamination (prevalence, number, and serotype) data ($n = 100$) from the Initial Contamination (IC) step of PFARM for *Salmonella* and CGs (Oscar, 2022) were simulated over time in a single production chain using a running window of 60 consecutive samples. The idea was to simulate a current practice in the poultry industry, namely, the use of a running window of *Salmonella* test samples to find unsafe production chains.

A data gap in the present study was information about FCB and CHI in the simulated production chain at the time of testing CGs for *Salmonella*. Consumer survey data were not collected because the survey tool was developed after the data for *Salmonella* Pr, N, and ZP of CGs were collected.

Even if the survey tool had been developed before the collection of *Salmonella* Pr, N, and ZP data for CGs, it still would have been valuable to simulate the current "What if" scenario. By holding FCB and CHI constant over time in the production chain, it made it easier to evaluate the effect of ZP on ID. In contrast, if FCB and CHI had changed over time in the production chain, the effect of ZP on ID could have been missed.

Materials and methods

Human subject data. Published data from HOI and HFT that were used in this study are exempt from Institutional Review Board (IRB) requirements (Anonymous, 2022). Likewise, because the consumer survey data used in the current study were computer-generated and not from human subjects, they were also exempt from IRB requirements.

Nomenclature: In the present study, outputs from spreadsheet 6 (6!) of PFARM (Fig. 3) are shown using their abbreviation followed a subscript that references the spreadsheet name (e.g., ID_6).

Consumer survey. OPTION BUTTON (FORM CONTROL), GROUP (FORM CONTROL), and CHECK BOX (FORM CONTROL) functions of Excel (Office 365, MicroSoft Corp.) were used to create a consumer survey (Fig. 2) that had three sections: 1) MPP; 2) FCB; and 3) CHI. Survey responses were summarized as a 7-digit code where code digits corresponded to 1) hygiene; 2) meal preparation time; 3) kitchen temperature; 4) cooked temperature; 5) portion size; 6) FCB; and 7) CHI. The 7-digit code was entered into spreadsheet D (D!) of PFARM (Fig. 4) and was the only information that would be returned by the respondent and the only information needed to simulate consumer survey results in PFARM.

Each query in the main body of the survey had five option buttons that corresponded to five risk categories from 1 (low) to 5 (high) (Table 1). The category value selected (hygiene, meal preparation time, kitchen temperature, cooked temperature, portion size) or calculated (FCB, CHI) was used as the lookup value in the VLOOKUP function of Excel that returned a UNIFORM distribution from the array spreadsheet (A!) in PFARM for the simulated variable. The UNIFORM distribution was randomly sampled by @Risk (version 8.2, Decision Tools Suite, Palisade Corp.) to provide a value for the variable that was used to simulate individual meals in the production chain. In this way, consumer survey results were simulated in PFARM.

The recommended data collection plan in PFARM (Oscar, 2022) is to collect one poultry food sample at the start of meal preparation and at least one completed consumer survey per sampled household in the production chain of interest. This plan and the consumer survey were developed after the completion of testing CGs for *Salmonella* in the pre-

A) Not exposed

Consumption (Dose-Response)		
Food Consumption Behavior	FCB	1.5
Consumer Health and Immunity	CHI	1.5
Serotype	S	
Zoonotic Potential	ZP	#VALUE!
Disease Triangle Score	DTS	#VALUE!
Dose Consumed	DC	0
Illness Dose	ID	#VALUE!
Consumer Response	CR	0.00E+00
PFARM 6!		No Exposure

B) Exposed

Consumption (Dose-Response)		
Food Consumption Behavior	FCB	1.9
Consumer Health and Immunity	CHI	1.0
Serotype	S	Enteritidis
Zoonotic Potential	ZP	5.0
Disease Triangle Score	DTS	7.9
Dose Consumed	DC	3
Illness Dose	ID	234,108
Consumer Response	CR	1.28E-05
PFARM 6!		No Response

Figure 3. Spreadsheet 6 (6!) of the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs). Simulation results are for a single meal of CGs that: A) did not result in consumer exposure to Salmonella; or B) did result in consumer exposure to Salmonella. See text for details.

Data Input						
Sample size	56	g	PFARM D!			
Mean Portion size	168	g				
Lot size	1,000	kg				
Portions	5,952	iterations				
Salmonella Testing	Minimum	Mode	Maximum	Unit		
Native Microflora	2.500	4.500	7.000	log/g		
Salmonella	0.000	0.417	2.788	log/sample		
Code	0	1	2	3	4	5
Serotype	None	Kentucky	Infantis	Enteritidis	Typhimurium	Thompson
Prevalence	63.3	23.3	1.7	5.0	5.0	1.7
Zoonotic Potential	0.0	1.1	4.3	5.0	4.9	3.7
Consumer Survey	5	1	2	3	4	5
Hygiene	3	1	4	3	3	3
Meal preparation time	2	2	2	4	4	2
Kitchen temperature	2	2	3	3	3	2
Cooked Temperature	3	4	3	4	3	3
Portion size	3	3	3	5	3	3
Food Consumption Behaivor	3	4	4	3	1	3
Consumer Health & Immunity	2	3	3	2	4	2

Figure 4. Data input spreadsheet (D!) of the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs). The Salmonella testing results for weeks 1 to 6 of the study and computer-generated survey results for the first 5 of 100 consumer surveys simulated are shown. See text for details.

sent study. Therefore, to demonstrate the current PFARM, survey results were computer-generated as follows.

First, it was assumed that the probability of occurrence of categories 1, 2, 3, 4, and 5 for all seven consumer survey variables were 5, 15, 60, 15, and 5%, respectively. Next, a DISCRETE distribution from @Risk was defined:

$$= \text{RiskDiscrete}(\{1,2,3,4,5\},\{5,15,60,15,5\})$$

and then copied and pasted across a 7 by 100 block of cells in D! (Fig. 4) to create 100 computer-generated consumer surveys for demonstration purposes.

Next, the RANDBETWEEN(1,100) function of Excel was used to randomly find the consumer survey to simulate for each meal or iteration of PFARM. Here, the randomly selected consumer survey number from 1 to 100 was used as the LOOKUP value in the HLOOKUP function of Excel that returned the proper 7-digit code from the computer-generated consumer survey array. For example, in Figure 4, the randomly selected consumer survey was #5, which had a 7-digit code of 3323332.

Disease triangle score. In the ID step of PFARM (Fig. 1), DT was simulated using a DTS that was equal to the sum of ZP (0.1–0.5 in 0.1 increments), FCB (0.1–3.0 in 0.1 increments), and CHI (0.1–5.0 in 0.1 increments) (Oscar, 2017, 2019, 2020a). This resulted in 128 PERT_{ID} (Fig. 1). When a consumer was not exposed to *Salmonella,* there was no value for ZP and DTS was not calculated. For example, in Figure 3A, the simulated meal of CGs was not contaminated with *Salmonella* at consumption and thus, a DTS could not be calculated. The dose of *Salmonella* consumed and response of the consumer are determined in the DC and CR steps of PFARM, respectively, as shown in Figure 1.

Zoonotic potential. The ZP of a *Salmonella* serotype was calculated using CDC data (Anonymous) as follows (Oscar, 2017, 2019, 2020a)

$$\text{ZP} = 5.1 - 0.1r \text{ IF } r \le 20$$

Table 1
Queries in the consumer survey spreadsheet (S!) of the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs) shown in Figure 2

Section	Query	Category 1	Category 2	Category 3	Category 4	Category 5
Meal Preparation Practices	Hygiene	<2.0	2.0 to 2.9	3.0 to 3.9	4.0 to 4.5	4.6 to 5.0
	Meal preparation time	<1 h	>1 to 2 h	>2 to 4 h	>4 to 6 h	>6 to 8 h
	Kitchen temperature	61 to 69F	>69 to 77F	>77 to 85F	>85 to 93F	>93F
	Cooked temperature	>165 F	155 to <165F	145 to <155F	135 to <145F	<135 F
Food Consumption Behavior	Chicken gizzards	2 oz (56 g)	4 oz (112 g)	6 oz (168 g)	8 oz (224 g)	10 oz (280 g)
	Beverage	4 oz (118 ml)	8 oz (236 ml)	12 oz (354 ml)	16 oz (473 ml)	20 oz (591 ml)
	Side #1	2 oz (56 g)	4 oz (112 g)	6 oz (168 g)	8 oz (224 g)	10 oz (280 g)
	Side #2	2 oz (56 g)	4 oz (112 g)	6 oz (168 g)	8 oz (224 g)	10 oz (280 g)
	Salad dressing	0.5 Tbsp (7.5 ml)	1 Tbsp (15 ml)	2 Tbsp (30 ml)	3 Tbsp (45 ml)	4 Tbsp (60 ml)
	Condiment	0.5 Tbsp (7.5 ml)	2 Tbsp (15 ml)	3 Tbsp (30 ml)	4 Tbsp (45 ml)	5 Tbsp (60 ml)
	Dessert	2 oz (56 g)	4 oz (112 g)	6 oz (168 g)	8 oz (224 g)	10 oz (280 g)
	Antacid Tablets	None	One	Two	Three	>Three
Consumer Health and Immunity	Age	17–35 yr	13–16; 35–45 yr	6–12; 46–59 yr	60–79 yr	<6 or >79 yr
	Body Mass Index	22 to <25	19 to <22	25 to <30	<19 or 30 to <40	40 or above
	Diabetes	None	Mild	Moderate	Severe	Very Severe
	Cancer	None	Mild	Moderate	Severe	Very Severe
	Autoimmune Disease	None	Mild	Moderate	Severe	Very Severe
	Pregnancy	None	1st Trimester	2nd Trimester	3rd Trimester	Complications
	Corticosteroid Medication	None	0 to <2 days	2 to <4 days	4 to <6 days	6 or more days
	Acid Reflux Medication	None	1 to <2 days	3 to <4 days	5 to <6 days	6 or more days
	Oral Antibiotic Medication	None	2 to <2 days	4 to <4 days	6 to <6 days	6 or more days
Hygiene	Cutting Board (Category 1)	Used separate cutting boards to prepare raw poultry and lettuce				
	Cutting Board (Category 2)	Used same cutting board to prepare raw poultry and lettuce but washed cutting board with soap and water after preparing raw poultry				
	Cutting Board (Category 3)	Used same cutting board to prepare raw poultry and lettuce but washed cutting board with water and a paper towel after preparing raw poultry				
	Cutting Board (Category 4)	Used same cutting board to prepare raw poultry and lettuce but rinsed cutting board with water after preparing raw poultry				
	Cutting Board (Category 5)	Used same cutting board to prepare raw poultry and lettuce but did not wash cutting board after preparing raw poultry				
	Hands (Category 1)	Used separate hands to prepare raw poultry and lettuce				
	Hands (Category 2)	Used same hands to prepare raw poultry and lettuce but washed hands with soap and water after preparing raw poultry				
	Hands (Category 3)	Used same hands to prepare raw poultry and lettuce but washed hands with water and a paper towel after preparing raw poultry				
	Hands (Category 4)	Used same hands to prepare raw poultry and lettuce but rinsed hands with water after preparing raw poultry				
	Hands (Category 5)	Used same hands to prepare raw poultry and lettuce but did not wash hands after preparing raw poultry				
Good Hygiene Practices	True or False	I did not wash the poultry food under running water				
	True or False	I kept raw poultry and ready-to-eat foods (e.g. lettuce) separate during meal preparation				
	True or False	I washed my hands with soap and water for 20 seconds after touching raw poultry				
	True or False	I washed the cutting board with soap and warm water for 20 seconds after preparing raw poultry				
	True or False	I avoided touching other surfaces after handling raw poultry				
Body Mass Index	Height (inches)	Enter number				
	Weight (lbs)	Enter number				

$$ZP = 3.1 * (c/c_{20}) \text{ IF } r > 20$$

where r was serotype ranking for cases of salmonellosis from 1 to 20, c was cases of salmonellosis for that serotype, and c_{20} was cases of salmonellosis for the 20th ranked serotype, which changed from year-to-year (Table 2). Thus, if the serotype was ranked in the top 20, the first equation was used; otherwise, the second equation was used.

PERT (minimum, mode, maximum) distributions were used to simulate strain variation and variability and uncertainty of ZP ($PERT_{ZP}$) for individual serotypes of *Salmonella* (Fig. 1). The $PERT_{ZP}$ were based on 10 years of CDC data for the reasons presented below. In addition, this method and its assumptions were evaluated with HOI (Table 3) and HFT data (Table 4) and the APZ method as described below.

Composite ZP was used to simulate portions contaminated with multiple serotypes of *Salmonella* (Oscar, 2022):

$$ZP_{composite} = \Sigma(N_i/N_{total}) * ZP_i$$

where N_i was number of the ith serotype, N_{total} was total number of *Salmonella*, and ZP_i was ZP of the ith serotype. Portions consisted of 1, 2, 3, 4, or 5 servings of 56 g, which was the size of sample analyzed for *Salmonella* contamination (Oscar, 2022). Thus, portion sizes of 56, 112, 168, 224, and 280 g were simulated and included in the consumer survey (Table 1).

Consumer health and immunity. The consumer survey (Fig. 2) for CHI (Table 1) queried age, health (body mass index, pregnancy, diabetes, cancer, autoimmune disease), gastric acid production (hypochlorhydria), and medications (corticosteroids, acid blockers, oral antibiotics). Because it was not known how these factors interacted to affect CHI, the highest-risk category among queried variables was used to simulate CHI. In this way, a fail-safe prediction of CHI was made.

The CHI category, which was selected randomly from a DISCRETE distribution from computer-generated survey results as described above, was used as the lookup value in the VLOOKUP function of Excel that returned a UNIFORM distribution for CHI from A! in PFARM where 1 was CHI from 0.1 to 1.0; 2 was CHI from 1.1 to 2.0; 3 was CHI from 2.1 to 3.0; 4 was CHI from 3.1 to 4.0; and 5 was CHI from 4.1 to 5.0 (Fig. 1).

The UNIFORM distribution was then randomly sampled by @Risk, and the selected value for CHI was used to calculate DTS for the simulated meal. In this way, survey results for CHI were simulated in PFARM. For example, in Figure 3B, the randomly selected value of CHI_6 for the simulated meal was 1.0 and the DTS_6 was 7.9.

Values used to simulate CHI were developed in a previous study (Oscar, 2017) and this simulation method and its assumptions were

Table 2
U. S. Centers for Disease Control and Prevention (CDC) data for salmonellosis that was used to simulate zoonotic potential (ZP) of Salmonella serotypes in the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs)[a]

	Anatum			Bareilly			Derby			Enteritidis			Infantis			Kentucky		
Year	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	ZP
2007	204	>20	2.2	237	>20	2.6	143	>20	1.6	6,056	2	4.9	517	12	3.9	95	>20	1.0
2008	219	>20	1.9	222	>20	2.0	140	>20	1.2	7,197	1	5.0	633	12	3.9	93	>20	0.8
2009	227	>20	2.6	282	19	3.2	131	>20	1.5	7,122	1	5.0	626	12	3.9	73	>20	0.9
2010	227	>20	2.6	339	19	3.2	132	>20	1.5	8,896	1	5.0	807	10	4.1	94	>20	1.1
2011	282	20	3.1	429	17	3.4	113	>20	1.2	7,546	1	5.0	901	9	4.2	101	>20	1.1
2012	402	17	3.4	890	10	4.1	110	>20	1.1	7,095	1	5.0	1,106	7	4.4	113	>20	1.2
2013	253	>20	3.0	347	17	3.4	81	>20	1.0	6,815	1	5.0	1,310	7	4.4	92	>20	1.1
2014	282	>20	2.8	381	16	3.5	104	>20	1.1	8,895	1	5.0	1,357	7	4.4	93	>20	0.9
2015	261	>20	2.1	418	17	3.4	79	>20	0.6	9,150	1	5.0	1,057	8	4.3	87	>20	0.7
2016	257	20	3.1	412	16	3.5	77	>20	0.9	7,830	1	5.0	1,281	6	4.5	63	>20	0.8
	Meleagridis			Newport			Pullorum			Thompson			Typhimurium			20th Ranked		
Year	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	ZP	*c*	*r*	Serotype
2007	27	>20	0.3	3,554	3	4.8	0	>20	0.1	406	17	3.4	6,152	1	5.0	285	20	Hadar
2008	9	>20	0.1	3,828	3	4.8	0	>20	0.1	411	18	3.3	6,485	2	4.9	351	20	Schwarzengrund
2009	16	>20	0.2	3,815	3	4.8	0	>20	0.1	473	13	3.8	6,087	2	4.9	266	20	Hadar
2010	13	>20	0.1	5,046	3	4.8	0	>20	0.1	480	14	3.7	6,104	2	4.9	271	20	Poona
2011	16	>20	0.2	5,185	3	4.8	0	>20	0.1	534	14	3.7	6,120	2	4.9	282	20	Anatum
2012	20	>20	0.2	5,077	3	4.8	0	>20	0.1	818	12	3.9	5,702	2	4.9	301	20	Berta
2013	13	>20	0.2	3,706	3	4.8	0	>20	0.1	627	13	3.8	5,745	2	4.9	259	20	Berta
2014	10	>20	0.1	4,437	3	4.8	0	>20	0.1	626	12	3.9	5,041	2	4.9	307	20	Agona
2015	5	>20	0.0	4,731	3	4.8	0	>20	0.1	723	14	3.7	4,943	2	4.9	394	20	Paratyphi B var. L(+) tartrate+
2016	16	>20	0.2	4,728	2	4.9	0	>20	0.1	792	10	4.1	4,581	3	4.8	257	20	Anatum

[a] Abbreviations: c = cases of salmonellosis; r = epidemiological rank of the serotype; and ZP = zoonotic potential.

quantitatively evaluated in the present study using HOI (Table 3) and HFT (Table 4) data and the APZ method as described below.

This method for simulating CHI is best understood by looking at the output distribution for CHI_6 in PFARM (Fig. 5A), which was a hybrid of the DISCRETE and UNIFORM distributions used to generate it. The hybrid distribution can vary in shape from a UNIFORM distribution to a NORMAL distribution to a LOGNORMAL distribution that is skewed to the right or left depending on results of the consumer survey in PFARM that defines the distribution of consumers among risk categories for CHI.

Food consumption behavior. *Salmonella* must pass through the gastric acid barrier of the stomach to cause illness. The composition of the meal affects the ability of *Salmonella* to do this. Dietary fat protects *Salmonella* from gastric acid (Greenwood & Hooper, 1983), whereas dietary protein and antacid medication buffer gastric acid and protect *Salmonella* from inactivation by low pH (Birk et al., 2012; Mennah-Govela & Bornhorst, 2021; Smith, 2003). Therefore, the consumer survey (Fig. 2) for FCB (Table 1) queries for amount and types of food (i.e., chicken gizzards, sides, condiments, and dessert), beverage, and antacid consumed. Pull-down menus are used to select food and beverage items from a list in the A! of PFARM.

Fat and protein content of food (e.g., chicken gizzards) and beverage items were mostly obtained from the USDA, Food Data Central database (Anonymous) and the rest from other food composition databases. Results were used to calculate the proportion of fat and protein (pFPr) in food or beverage items used in the consumer survey and in HFT or found in HOI.

The pFPr was used to identify the FCB category where 1 was pFPr from 0 to 0.08; 2 was pFPr from 0.09 to 0.14; 3 was pFPr from 0.15 to 0.20; 4 was pFPr from 0.21 to 0.26; and 5 was pFPr from 0.27 to 1 (Fig. 1). The pFPr ranges per category of risk were determined by trial and error and were validated using the APZ method. In the consumer survey, a pFPr for the meal was calculated based on the amount of food and beverage item consumed and their fat and protein contents. In addition, if antacid tablets were consumed with the meal, the pFPr of the meal was increased by 0.04 per antacid tablet consumed to simulate an increased risk of successful passage of *Salmonella* through the gastric acid barrier of the stomach.

The FCB category, which was selected randomly from a DISCRETE distribution from computer-generated survey results as described above, was used as the lookup value in the VLOOKUP function of Excel that returned a UNIFORM distribution for FCB from A! in PFARM where 1 was FCB from 0.1 to 0.6, 2 was FCB from 0.7 to 1.2, 3 was FCB from 1.3 to 1.8, 4 was FCB from 1.9 to 2.4, and 5 was FCB from 2.5 to 3.0 (Fig. 1).

The identified UNIFORM distribution for FCB was randomly sampled by @Risk, and the selected value was used to calculate DTS for the meal. For example, in Figure 3B, the randomly selected value for FCB_6 was 1.9 and DTS_6 was 7.9.

This simulation method for FCB and its assumptions were evaluated quantitatively using HOI (Table 3) and HFT (Table 4) data and the APZ method as described below. This simulation method can be best understood by looking at the output distribution for FCB_6 in PFARM (Fig. 5B). Here, the outcome of simulating FCB in two steps was a probability distribution that was a hybrid of the DISCRETE and UNIFORM distributions used to generate it. The hybrid distribution can vary in shape from a UNIFORM distribution to a NORMAL distribution to a LOGNORMAL distribution that is skewed to the right or left depending on results of the consumer survey in PFARM that determines the distribution of meals among risk categories for FCB.

Illness dose. To simulate ID in PFARM (Fig. 1), DTS for the simulated meal is used to calculate $PERT_{ID}$ (Oscar, 2017, 2019, 2020a):

$$ID_{min} = 0.787 * (13 - DTS)$$

$$ID_{mode} = 0.787 * (13 - DTS) + 1$$

$$ID_{max} = 0.787 * (13 - DTS) + 2$$

where ID_{min} was minimum ID (log); ID_{mode} was most likely ID (log), and ID_{max} was maximum ID (log).

The values for ZP, FCB, and CHI used to calculate DTS were rounded to one decimal place resulting in 128 $PERT_{ID}$ for simulating dose-response. The number of $PERT_{ID}$ can be increased by a factor of 10 for each movement of the decimal used for rounding of ZP, FCB, and CHI. For example, rounding ZP, FCB, and CHI to two decimal places yields 1,280 $PERT_{ID}$ for simulating dose-response, three decimal

Table 3
Human outbreak investigation (HOI) data for evaluating the performance of the disease triangle, dose-response model (DT, DRM) for Salmonella in the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs) shown in Figure 1a

Serotype	Population[b]	Vehicle	pFPr	DC	Exposed	Ill	$P_{ill\ obs}$	$P_{ill\ pred}$	Residual	APZ	ZP_{min}	ZP_{mode}	ZP_{max}	CHI_{min}	CHI_{max}	FCB_{min}	FCB_{max}	DTS_{min}	DTS_{max}	pFPr Source
Enteritidis	C	bavarois	0.13	5.00	123	100	0.813	0.813	0.000	1.000	4.9	5.0	5.0	0.1	4.0	0.7	1.2	5.7	10.2	myfitnesspal.com
Enteritidis	A	beef/bean/ sesame	0.15	2.94	10,552	967	0.092	0.092	0.000	1.000	4.9	5.0	5.0	0.1	5.0	1.3	1.8	6.3	11.8	laurasleanbeef.com
Enteritidis	C	cake	0.24	2.63	5,103	1,371	0.269	0.269	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.9	2.4	6.9	11.4	fdc.nal.usda.gov
Enteritidis	C	cake	0.24	5.78	13	11	0.846	0.846	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.9	2.4	6.9	11.4	fdc.nal.usda.gov
Enteritidis	C	chicken/egg/ rice	0.09	3.62	16	3	0.188	0.188	0.000	1.000	4.9	5.0	5.0	0.1	4.0	0.7	1.2	5.7	10.2	fdc.nal.usda.gov
Enteritidis	A	chicken/egg/ rice	0.09	3.62	117	50	0.427	0.427	0.000	1.000	4.9	5.0	5.0	0.1	5.0	0.7	1.2	5.7	11.2	fdc.nal.usda.gov
Enteritidis	C	cream sauce	0.16	6.00	38	30	0.789	0.789	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.3	1.8	6.3	10.8	fdc.nal.usda.gov
Enteritidis	A	dessert bun	0.08	0.61	18,571	92	0.005	0.000	0.005	0.980	4.9	5.0	5.0	0.1	5.0	0.1	0.6	5.1	10.6	fdc.nal.usda.gov
Enteritidis	C	egg	0.26	1.04	363	198	0.545	0.000	0.545	0.000	4.9	5.0	5.0	0.1	4.0	1.9	2.4	6.9	11.4	fdc.nal.usda.gov
Enteritidis	A	egg salad	0.33	1.38	156	42	0.269	0.269	0.000	1.000	4.9	5.0	5.0	0.1	5.0	2.5	3.0	7.5	13.0	fdc.nal.usda.gov
Enteritidis	A	Hollandaise	0.62	4.65	39	39	1.000	1.000	0.000	1.000	4.9	5.0	5.0	0.1	5.0	2.5	3.0	7.5	13.0	fdc.nal.usda.gov
Enteritidis	C	ice cream	0.15	6.58	5	5	1.000	1.000	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.3	1.8	6.3	10.8	fdc.nal.usda.gov
Enteritidis	A	ice cream	0.15	1.95	452	30	0.066	0.066	0.000	1.000	4.9	5.0	5.0	0.1	5.0	1.3	1.8	6.3	11.8	fdc.nal.usda.gov
Enteritidis	A	macaroni salad	0.21	4.64	152	52	0.342	0.342	0.000	1.000	4.9	5.0	5.0	0.1	5.0	1.9	2.4	6.9	12.4	fdc.nal.usda.gov
Enteritidis	C	mayonnaise	0.76	4.75	2,907	498	0.171	0.171	0.000	1.000	4.9	5.0	5.0	0.1	4.0	2.5	3.0	7.5	12.0	fdc.nal.usda.gov
Enteritidis	C	natto/eggs	0.16	5.86	9	9	1.000	1.000	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.3	1.8	6.3	10.8	nutritionix.com
Enteritidis	C	omelet	0.26	5.18	11	10	0.909	0.909	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.9	2.4	6.9	11.4	fdc.nal.usda.gov
Enteritidis	C	omelet	0.26	5.38	103	57	0.553	0.553	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.9	2.4	6.9	11.4	fdc.nal.usda.gov
Enteritidis	A	peanut dressing	0.17	1.40	2,267	418	0.184	0.083	0.101	0.596	4.9	5.0	5.0	0.1	5.0	1.3	1.8	6.3	11.8	fdc.nal.usda.gov
Enteritidis	A	peanut dressing	0.17	0.54	1,320	179	0.136	0.000	0.136	0.456	4.9	5.0	5.0	0.1	5.0	1.3	1.8	6.3	11.8	fdc.nal.usda.gov
Enteritidis	C	prawn/egg	0.22	4.99	104	70	0.673	0.673	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.9	2.4	6.9	11.4	nutritionix.com
Enteritidis	A	rice dish	0.07	6.18	7	6	0.857	0.857	0.000	1.000	4.9	5.0	5.0	0.1	5.0	0.1	0.6	5.1	10.6	fdc.nal.usda.gov
Enteritidis	C	seared beef	0.27	5.38	5	3	0.600	0.600	0.000	1.000	4.9	5.0	5.0	0.1	4.0	2.5	3.0	7.5	12.0	fdc.nal.usda.gov
Enteritidis	C	spaghetti salad	0.16	7.16	78	73	0.936	0.995	-0.059	0.882	4.9	5.0	5.0	0.1	4.0	1.3	1.8	6.3	10.8	fdc.nal.usda.gov
Enteritidis	C	spinach/peanut	0.18	1.69	5,320	644	0.121	0.000	0.121	0.516	4.9	5.0	5.0	0.1	4.0	1.3	1.8	6.3	10.8	omnivorescookbook.com
Enteritidis	C	thin omelet	0.26	3.78	886	558	0.630	0.630	0.000	1.000	4.9	5.0	5.0	0.1	4.0	1.9	2.4	6.9	11.4	fdc.nal.usda.gov
Enteritidis	C	tiramisu	0.30	8.11	7,873	697	0.089	1.000	-0.911	0.000	4.9	5.0	5.0	0.1	4.0	2.5	3.0	7.5	12.0	nutritionix.com
Enteritidis	C	yam/soup	0.01	6.29	123	113	0.919	0.919	0.000	1.000	4.9	5.0	5.0	0.1	4.0	0.1	0.6	5.1	9.6	fdc.nal.usda.gov
Infantis	A	ham	0.27	6.42	8	8	1.000	1.000	0.000	1.000	3.9	4.4	4.5	0.1	5.0	2.5	3.0	6.5	12.5	fdc.nal.usda.gov
Typhimurium	A	chiffonade	0.00	3.79	60	33	0.550	0.550	0.000	1.000	4.8	4.9	5.0	0.1	5.0	0.1	0.6	5.0	10.6	myfitnesspal.com
Typhimurium	C	ice cream	0.15	8.88	2	2	1.000	1.000	0.000	1.000	4.8	4.9	5.0	0.1	4.0	1.3	1.8	6.2	10.8	fdc.nal.usda.gov
Typhimurium	C	ice cream	0.15	8.70	1	1	1.000	1.000	0.000	1.000	4.8	4.9	5.0	0.1	4.0	1.3	1.8	6.2	10.8	fdc.nal.usda.gov
Typhimurium	A	ice cream	0.15	8.70	2	2	1.000	1.000	0.000	1.000	4.8	4.9	5.0	0.1	5.0	1.3	1.8	6.2	11.8	fdc.nal.usda.gov
Typhimurium	B	ice cream	0.15	9.00	1	1	1.000	1.000	0.000	1.000	4.8	4.9	5.0	4.1	5.0	1.3	1.8	10.2	11.8	fdc.nal.usda.gov
Typhimurium	B	ice cream	0.15	8.40	1	1	1.000	1.000	0.000	1.000	4.8	4.9	5.0	4.1	5.0	1.3	1.8	10.2	11.8	fdc.nal.usda.gov
Typhimurium	B	ice cream	0.15	8.00	1	1	1.000	1.000	0.000	1.000	4.8	4.9	5.0	4.1	5.0	1.3	1.8	10.2	11.8	fdc.nal.usda.gov
Typhimurium	C	water	0.00	2.31	7,572	805	0.106	0.000	0.106	0.576	4.8	4.9	5.0	0.1	4.0	0.1	0.6	5.0	9.6	
Typhimurium	A	water	0.00	2.31	1,216	230	0.189	0.068	0.121	0.516	4.8	4.9	5.0	0.1	5.0	0.1	0.6	5.0	10.6	

[a]ZP = zoonotic potential; CHI = consumer health and immunity; FCB = food consumption behavior; DC = dose consumed; DTS = disease triangle score; *n* = number of exposures; min = minimum; max = maximum; F = fat; Pr = protein; g = grams; and pFPr = proportion of fat and protein.
[b]A = high-risk consumers; B = high-risk consumer; C = no high-risk consumer(s).

Table 4
Human feeding trial (HFT) data for evaluating performance of the disease triangle, dose-response model (DT, DRM) for Salmonella in the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs) shown in Figure 1a

Serotype	Strain	*n*	Food	ZP_{min}	ZP_{mode}	ZP_{max}	CHI_{min}	CHI_{max}	FCB_{min}	FCB_{max}	DTS_{min}	DTS_{max}	pAPZ
Anatum	I	8	eggnog[b]	1.9	2.6	3.4	0.1	4.0	0.7	1.2	2.7	8.6	1.00
Anatum	II	8	eggnog	1.9	2.6	3.4	0.1	4.0	0.7	1.2	2.7	8.6	1.00
Anatum	III	3	eggnog	1.9	2.6	3.4	0.1	4.0	0.7	1.2	2.7	8.6	1.00
Meleagridis	I	11	eggnog	0.1	0.2	0.3	0.1	4.0	0.7	1.2	0.9	5.5	1.00
Meleagridis	II	5	eggnog	0.1	0.2	0.3	0.1	4.0	0.7	1.2	0.9	5.5	1.00
Meleagridis	III	4	eggnog	0.1	0.2	0.3	0.1	4.0	0.7	1.2	0.9	5.5	1.00
Pullorum	I	4	eggnog	0.1	0.1	0.1	0.1	4.0	0.7	1.2	0.9	5.3	1.00
Pullorum	II	3	eggnog	0.1	0.1	0.1	0.1	4.0	0.7	1.2	0.9	5.3	1.00
Pullorum	III	4	eggnog	0.1	0.1	0.1	0.1	4.0	0.7	1.2	0.9	5.3	1.00
Pullorum	IV	5	eggnog	0.1	0.1	0.1	0.1	4.0	0.7	1.2	0.9	5.3	1.00
Bareilly		4	eggnog	2.0	3.4	4.1	0.1	4.0	0.7	1.2	2.8	9.3	1.00
Derby		5	eggnog	0.6	1.2	1.6	0.1	4.0	0.7	1.2	1.4	6.8	1.00
Newport		3	eggnog	4.8	4.8	4.9	0.1	4.0	0.7	1.2	5.6	10.1	1.00

[a]ZP = zoonotic potential; CHI = health and immunity; FCB = food consumption behavior; DTS = disease triangle score; *n* = number of subjects; min = minimum; max = maximum; and pAPZ = proportion of residuals in the acceptable prediction zones.
[b]Composition was 4.19 g of fat and 4.55 g of protein per 100 g per USDA, FoodData Central, code 11531000. Proportion of fat and protein (pFPr) was 0.087, which is a category of 2 in PFARM for *Salmonella* and CGs.

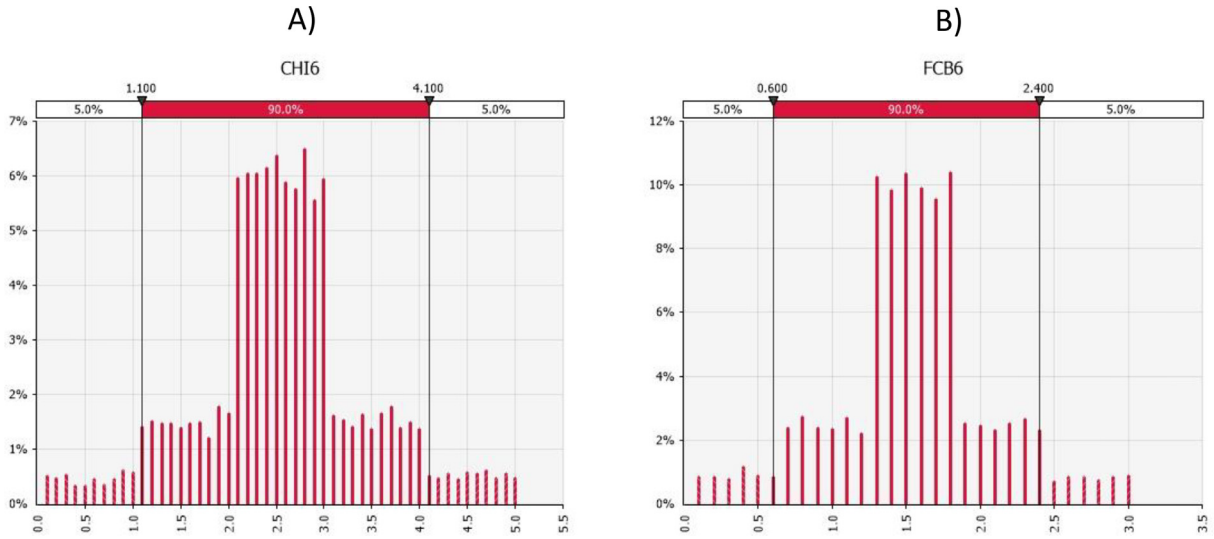

Figure 5. Output distributions for A) consumer health and immunity (CHI_6); and B) food consumption behavior (FCB_6) from simulation of DISCRETE and UNIFORM input distributions for these variables in spreadsheet 6 (6!) of the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs).

places yields 12,800 $PERT_{ID}$ for simulating dose-response, and so forth. Thus, smaller differences among DT interactions can be simulated in PFARM.

The identified $PERT_{ID}$ was then randomly sampled by @Risk to provide an ID_6 for the simulated meal (Fig. 1). For example, in Figure 3B, DTS_6 was 7.9; thus, ID_{min} was 4.0137 log, ID_{mode} was 5.0137 log, and ID_{max} was 6.0137 log. The randomly selected value of ID_6 from this $PERT_{ID}$ for the simulated meal was 5.3694 log or 234,108.

Although the simulated meal (Fig. 3B) was contaminated with *Salmonella* Enteritidis, which is the highest-risk serotype (ZP = 5.0), the meal was consumed by a low-risk consumer (CHI = 1.0) with a low-risk meal (FCB = 1.9) and the dose of *Salmonella* consumed was low (N_6 = 3 cells). Thus, PFARM predicted a health outcome of "No Response" for this meal, which could mean that the consumed cells of *Salmonella* Enteritidis failed to survive passage through the gastric acid barrier of the stomach and(or) survived passage through the stomach but failed to initiate an infection in the lower gastrointestinal tract that led to an illness in the consumer.

Use of $PERT_{ID}$ to simulate ID for *Salmonella* has been validated for goodness-of-fit using HFT data for individual strains and serotypes of *Salmonella* (Oscar, 2004a) and was further validated in the present study as described next.

Acceptable prediction zones method. The APZ method (Oscar, 2005a, 2005b, 2020b) was used to quantify performance of the DT, DRM in PFARM. Here, predictions of the probability of illness (P_{ill}) as a function of DC (log N) were compared to observed P_{ill} for serotypes and strains of *Salmonella* from HOI (Teunis et al., 2010) and HFT (Oscar, 2004a). To do this, minimum (min) and maximum (max) DTS for observed DT were calculated for HOI (Tables 3) and HFT (Table 4) data. Next, coordinates (X = DC and Y = P_{ill}) for $PERT_{ID}$ corresponding to DTS_{min} and DTS_{max} were used to establish DR curve boundaries of fully acceptable APZ (Figs. 6 and 7). The coordinates (DC, P_{ill}) for plotting the *Salmonella* DR curves in Figures 6 and 7 were obtained from @Risk using the DEFINE DISTRIBUTION (PERT) function.

Next, if observed P_{ill} for the DC of the simulated DT was in the fully acceptable APZ or between the DR curves for DTS_{min} and DTS_{max}, a residual of zero and an APZ value of 1 were assigned. However, if the observed P_{ill} for the DC of the simulated DT was outside the fully acceptable APZ, a residual was calculated:

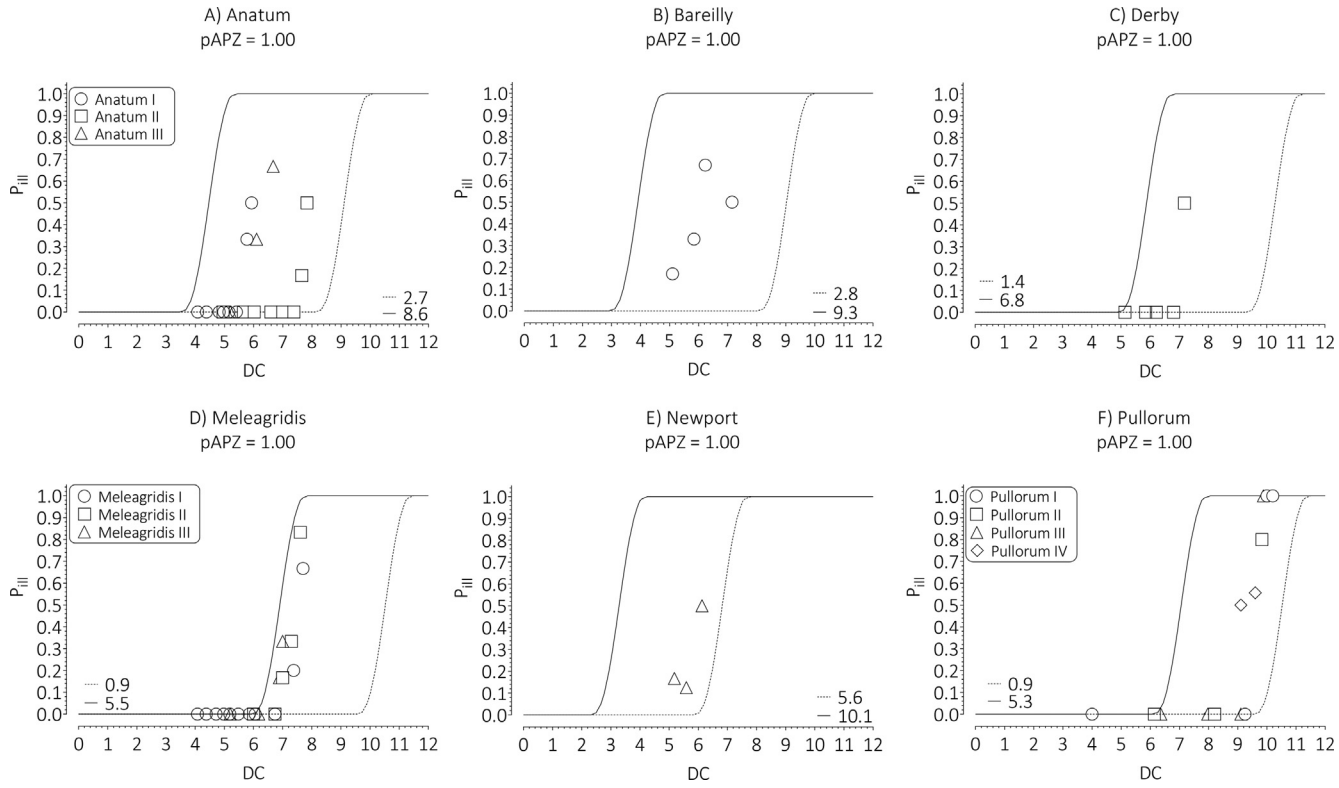

Figure 6. Acceptable prediction zone (APZ) analysis of the disease triangle, dose-response model (DT, DRM) in the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs). Data are from human feeding trials (HFTs) for strains and serotypes of Salmonella: A) Anatum; B) Bareilly; C) Derby; D) Meleagridis; E) Newport; and F) Pullorum from Table 4. Abbreviations: P_{ill} = probability of illness; DC = log dose consumed; and pAPZ = proportion of residuals in the acceptable prediction zones. Legends show the disease triangle scores (DTSs) for the dose-response (DR) curves that defined the boundaries of the fully acceptable prediction zone.

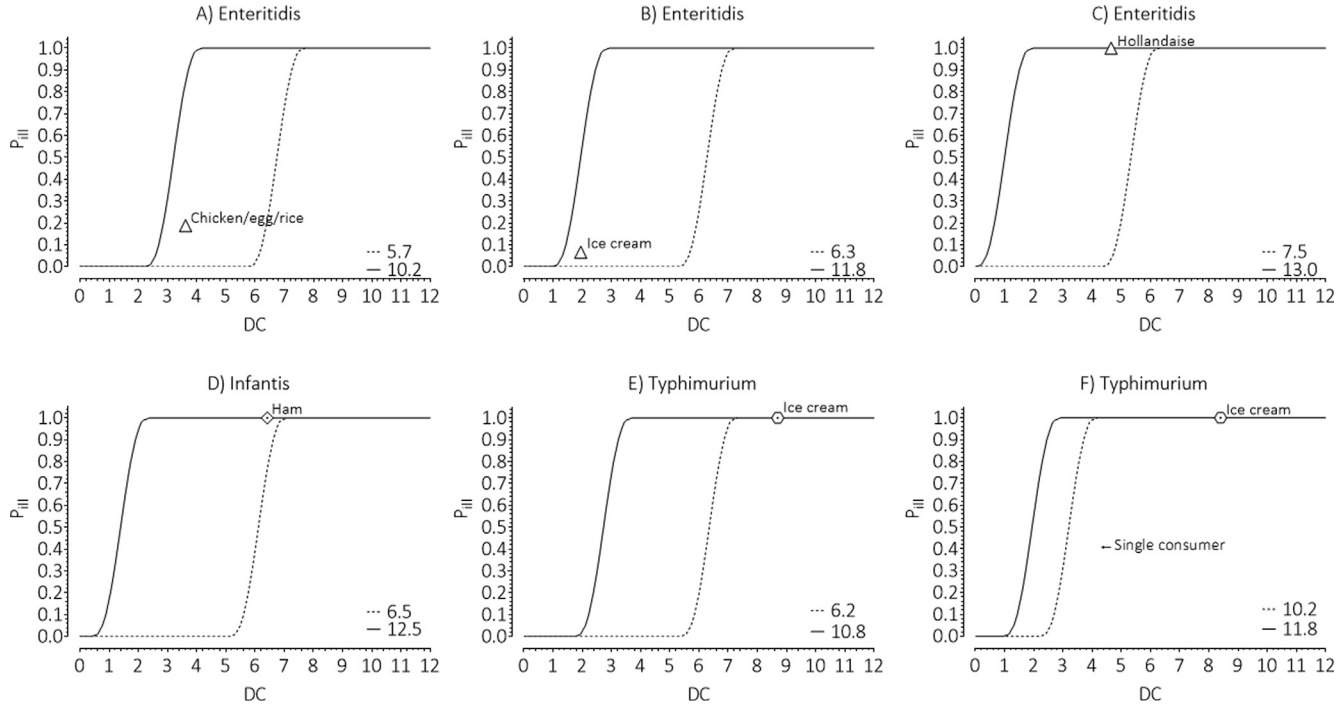

Figure 7. Acceptable prediction zone (APZ) analysis of the disease triangle, dose-response model (DT, DRM) in the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs). Data are from human outbreak investigations (HOIs) for Salmonella serotypes Enteritidis (panels A to C), Infantis (panel D), and Typhimurium (panels E and F) from Table 3. Abbreviations: P_{ill} = probability of illness and DC = log dose consumed. Legends show disease triangle scores (DTSs) for dose-response (DR) curves that defined the boundaries of the fully acceptable prediction zone.

$= P_{ill\ obs} - P_{ill\ pred}$

where $P_{ill\ obs}$ was the observed P_{ill} and $P_{ill\ pred}$ was the predicted P_{ill} from the closest boundary of the fully acceptable APZ.

The DT, DRM made a fail-safe prediction (negative residual) when $P_{ill\ pred}$ was $>P_{ill\ obs}$ and it made a fail-dangerous prediction (positive residual) when $P_{ill\ pred}$ was $<P_{ill\ obs}$. These predictions (outside the fully acceptable APZ) were considered partly acceptable if the absolute residual was ≤0.5 in the fail-safe direction or ≤0.25 in the fail-dangerous direction (Oscar, 2020b). An APZ value (>0 to <1) was assigned to these residuals based on their linear distance from the closest boundary of the fully acceptable APZ, while an APZ value of 0 was assigned for residuals outside the fully and partly acceptable APZ.

Finally, the proportion of residuals in the APZ (pAPZ) was calculated as the sum of the APZ values divided by the number of prediction cases. When the pAPZ was ≥0.70, the DT, DRM was considered to provide predictions with acceptable bias and accuracy of the test data (Oscar, 2005a, 2005b, 2020b).

Human outbreak investigation data. *Salmonella* serotype, DC, P_{ill}, consumer, and food and beverage vehicle data and information from HOI (Table 3) were from Teunis et al. (2010). Consumer populations were reported as having no information available or as including or not including young or old individuals. In PFARM, very young or old individuals are in risk category 5 (Table 1). Thus, the assumed risk category range was 1 to 5 (CHI = 0.1–5) for populations with very young and old individuals and no information, 5 (CHI = 4.5–5) for a very young or old individual, and 1–4 (CHI = 0.1–4) for populations that did not include very young or old individuals and for individuals that were not very young or old.

The FCB category depended on pFPr of the food or beverage vehicle identified in the HOI (Table 3). They ranged from category 1 (FCB = 0.1–0.6) for water (pFPr = 0) to 3 (FCB = 1.3–1.8) for ice cream (pFPr = 0.15) to 5 (FCB = 2.5–3.0) for hollandaise (pFPr = 0.62) (Fig. 1; Table 3). Thus, differences in fully acceptable APZ (DTS_{min} to DTS_{max}) among HOI were from differences in ZP, FCB, and CHI (Table 3). The HOI data were not used to develop the DT, DRM in PFARM and thus were independent data for validation.

Human feeding trial data. *Salmonella*, DC, and P_{ill} data were from Oscar (2004a) who obtained them from the original HFT (McCullough & Eisele, 1951a, 1951c, 1951d) and used them to develop the DT, DRM in PFARM, and thus, they were the dependent data used for validation.

Subjects were healthy men, which corresponded to categories 1–4 (CHI = 0.1–4.0) in PFARM. The FCB category for eggnog was 2 (FCB = 0.7–1.2) based on a pFPr of 0.087 (Anonymous). Thus, differences in fully acceptable APZ (DTS_{min} to DTS_{max}) among HFT were from differences in ZP only as FCB and CHI were the same for all HFT (Table 4).

Scenario analysis. Data for *Salmonella* contamination of CGs were collected at a rate of 10 samples (56 g) per week for 10 consecutive weeks (Oscar, 2022). Data were simulated in moving windows of 60 consecutive samples resulting in five time periods or scenarios: 1) 1–6 weeks; 2) 2–7 weeks; 3) 3–8 weeks; 4) 4–9 weeks; and 5) 5–10 weeks.

Running windows were not used to simulate the computer-generated consumer survey results. Instead, all 100 computer-generated consumer surveys were simulated in each scenario. Although this deviated from the PFARM plan, which would have simulated the 100 surveys in running windows of 60 to coincide with the food sampling and testing plan, it was done for the reasons stated above.

The five scenarios were simulated with @Risk settings of Latin Hypercube sampling, Mersenne Twister generator, initial seeds of 1, 2, 3, or 4, and 5,952 iterations. Different initial seeds were used to obtain replicate simulations of each scenario for statistical analysis.

The recommended approach in PFARM is to simulate a fixed amount of poultry food, which is determined by the end-user. In the present study, 1,000 kg of CGs was simulated for demonstration purposes.

In PFARM, the iterations or meals simulated depend on the amount of poultry food simulated and the mean portion size. In the present study, the mean portion size, which was calculated in PFARM from the consumer survey results for portion size, was 168 g (Fig. 4). Thus, 5,952 meals were simulated.

Finally, the portion size was assigned at the start of meal preparation so that all 1,000 kg of CGs was simulated from the start of meal preparation to consumption. This simulation method was used because it provides more accurate results than methods that simulate one-gram portions until consumption when the amount of poultry food simulated increases 100-fold or more (Oscar, 2021).

Statistical analysis. To determine if ZP of *Salmonella* serotypes (n = 11) was stable over time in the United States, CDC data (Anonymous) (Table 2) were evaluated in running windows of 5 years: 1) 2007 to 2011; 2) 2008 to 2012; 3) 2009 to 2013; 4) 2010 to 2014; 5) 2011 to 2015; and 6) 2012 to 2016 to provide replicate values of ZP for statistical analysis. Effect of time on ZP from CDC data was analyzed within *Salmonella* serotypes by one-way analysis of variance (ANOVA). When ANOVA was significant ($P \leq 0.05$), mean ZP among time periods within a *Salmonella* serotype were compared using Tukey's multiple comparison test at $P \leq 0.05$.

To decide if and how ID_6 and ZP_6 changed over time in the simulated production chain, a two-step approach was used. In step one, a nonparametric test (Kruskal-Wallis or K-W) was used to determine K-W mean ranks of output distributions in replicate simulations. In the K-W test (Steel & Torrie, 1980), values of ID_6 and ZP_6 from all scenarios within a replicate simulation or initial seed were combined, sorted from smallest to largest, and ranked from first to last. When values were identical, rank was equal to the average of shared ranks. The K-W statistic (H) was as follows:

$$H = \frac{12}{T(T+1)} \sum_{i=1}^{k} \frac{R_i^2}{n_i} - 3(T+1)$$

where n_i was number of observations in the ith distribution, T was total number of observations in all distributions, and R_i was sum of ranks for the ith distribution.

The H statistic was chi-square distributed with $k-1$ degrees of freedom, where k was the number of distributions. When H was significant ($P \leq 0.05$), K-W mean ranks among time periods within a replicate simulation were compared using Dunn's multiple comparison test at $P \leq 0.05$. The K-W mean rank was equal to the sum of ranks divided by the number of observations in the distribution.

In step two, K-W mean ranks from replicate simulations (n = 4) for ID_6 or ZP_6 were combined and evaluated by ANOVA, as described above. The ANOVA/Tukey's and K-W/Dunn's tests were performed in Prism (version 9.2, GraphPad Software Inc.). In PFARM, statistical tests are used to provide an objective interpretation of simulation results.

Results

Analysis of variance results for zoonotic potential. Mean ZP of *Salmonella* serotypes Anatum (Fig. 8A), Bareilly (Fig. 8B), Meleagridis (Fig. 8D), and Newport and Pullorum (Table 2) did not change ($P > 0.05$) from 2007 to 2016. However, mean ZP of serotype Derby (Fig. 8C) was lower ($P \leq 0.05$) from 2012 to 2016 than from 2007 to 2011 but was the same for all other comparisons. These serotypes were those fed in the HFT (Table 4).

Mean ZP of *Salmonella* serotypes Kentucky (Fig. 9A), Thompson (Fig. 9C), Typhimurium (Fig. 9D), and Enteritidis (Table 2) did not change ($P > 0.05$) from 2007 to 2016. However, mean ZP of serotype

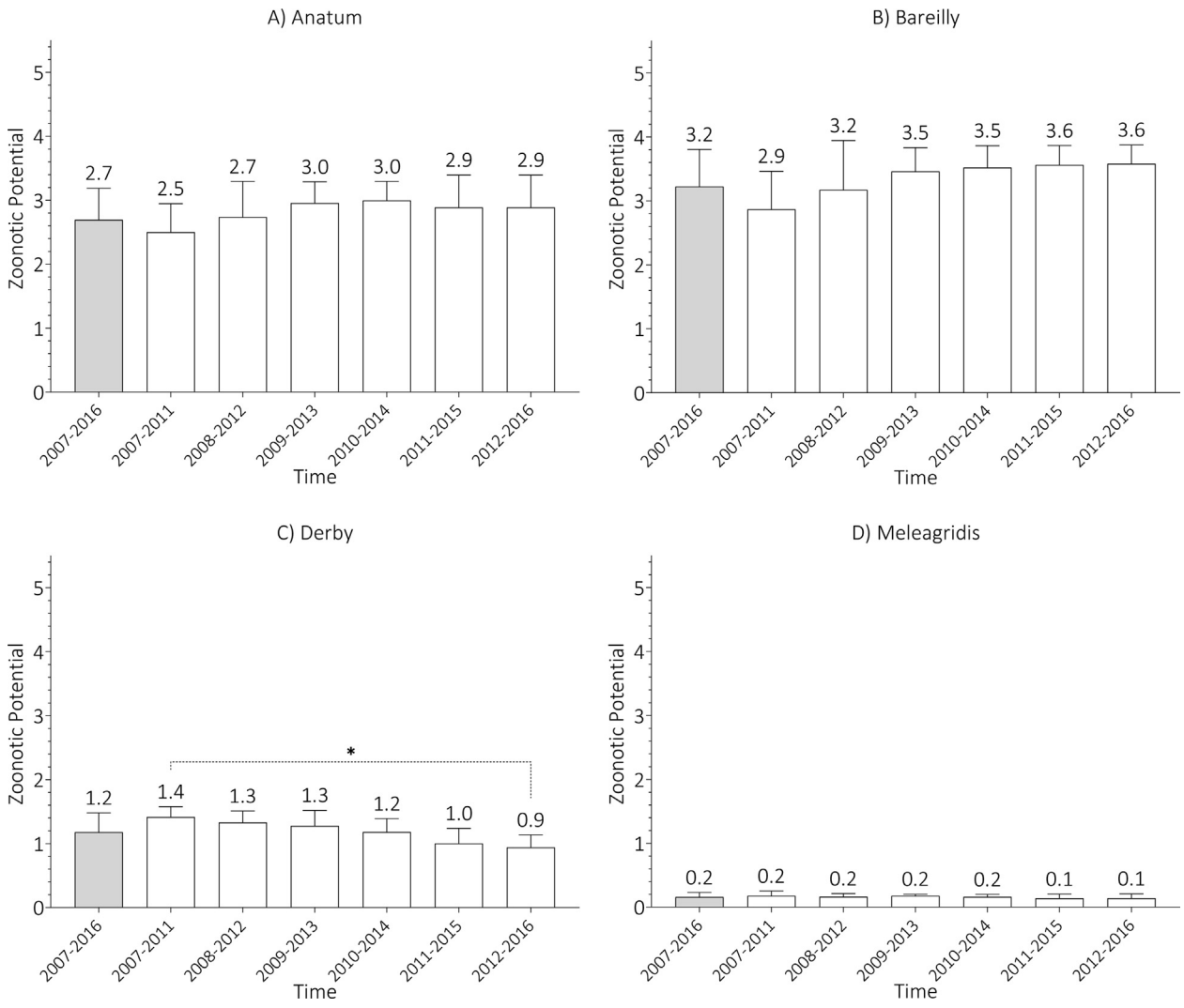

Figure 8. Effect of time on zoonotic potential (ZP) of Salmonella serotypes: A) Anatum; B) Bareilly; C) Derby; and D) Meleagridis. Bars are means ± standard deviations for five consecutive years of ZP data from the U. S. Centers for Disease Control and Prevention (Table 2). Bars connected by a dashed line with * are different at $P \leq 0.05$ per one-way analysis of variance (ANOVA) followed by Tukey's multiple comparison test at $P \leq 0.05$.

Infantis (Fig. 9B) was higher ($P \leq 0.05$) from 2012 to 2016 than from 2007 to 2011 but was the same for all other comparisons. These serotypes were isolated from CGs in the present study (Fig. 4) or were identified in HOI (Table 3).

Regardless of *Salmonella* serotype (Figs. 8 and 9 and Table 2), mean overall ZP from 2007 to 2016 was not different ($P > 0.05$) from any 5-year period. Thus, $PERT_{ZP}$ based on CDC data from 2007 to 2016 (Table 2) were used to simulate ZP of *Salmonella* in the DT, DRM of PFARM using a $PERT_{ID}$ for strain variation of ZP within a serotype (Fig. 1).

Acceptable prediction zone analysis of human outbreak investigation data. Table 3 summarizes HOI data for P_{ill} and DC that were used to evaluate performance of the DT, DRM in PFARM for independent data using the APZ method. Of 38 HOI data for P_{ill} and DC, 29 were in fully acceptable APZ (APZ values = 1), 7 were in partly acceptable APZ (APZ values from >0 to <1), and 2 were outside the APZ (APZ values = 0) (Table 3). The pAPZ were 0.87 for serotype Enteritidis, 1.00 for serotype Infantis, 0.90 for serotype Typhimurium, and 0.88 for all three serotypes combined. Thus, the DT, DRM in PFARM provided acceptable predictions (pAPZ ≥ 0.7) of independent data for P_{ill} and DC from HOI.

Selected examples of APZ analyses for HOI data are shown in Figure 7. Figure 7A to C shows results for serotype Enteritidis where in all cases, $P_{ill\ obs}$ was in the fully acceptable APZ, which differed in width among food vehicles and consumer populations. The lone HOI data for serotype Infantis are presented in Figure 7D where $P_{ill\ obs}$ was in the fully acceptable APZ. Finally, Figure 7E and 7F for serotype Typhimurium shows how the fully acceptable APZ was wider for a population of consumers than for an individual consumer, respectively. In both cases, $P_{ill\ obs}$ was in the fully acceptable APZ.

Data in partly acceptable APZ where APZ values ranged from >0 to <1 (Table 3) were serotype Enteritidis in dessert bun (APZ = 0.98), peanut dressing (APZ = 0.596 and 0.456), spaghetti salad (APZ = 0.882), and spinach/peanut (APZ = 0.516), and serotype Typhimurium in water (APZ = 0.576 and 0.516). Data outside APZ where APZ was 0 were serotype Enteritidis in egg and tiramisu (Table 3).

Acceptable prediction zone analysis of human feeding trial data. Table 4 summarizes HFT data for P_{ill} and DC that were used to develop and to validate performance of the DT, DRM in PFARM for dependent data using the APZ method. In all cases, observed HFT data for $P_{ill\ obs}$ were in fully acceptable APZ for pAPZ of 1.00 (Fig. 6). Thus,

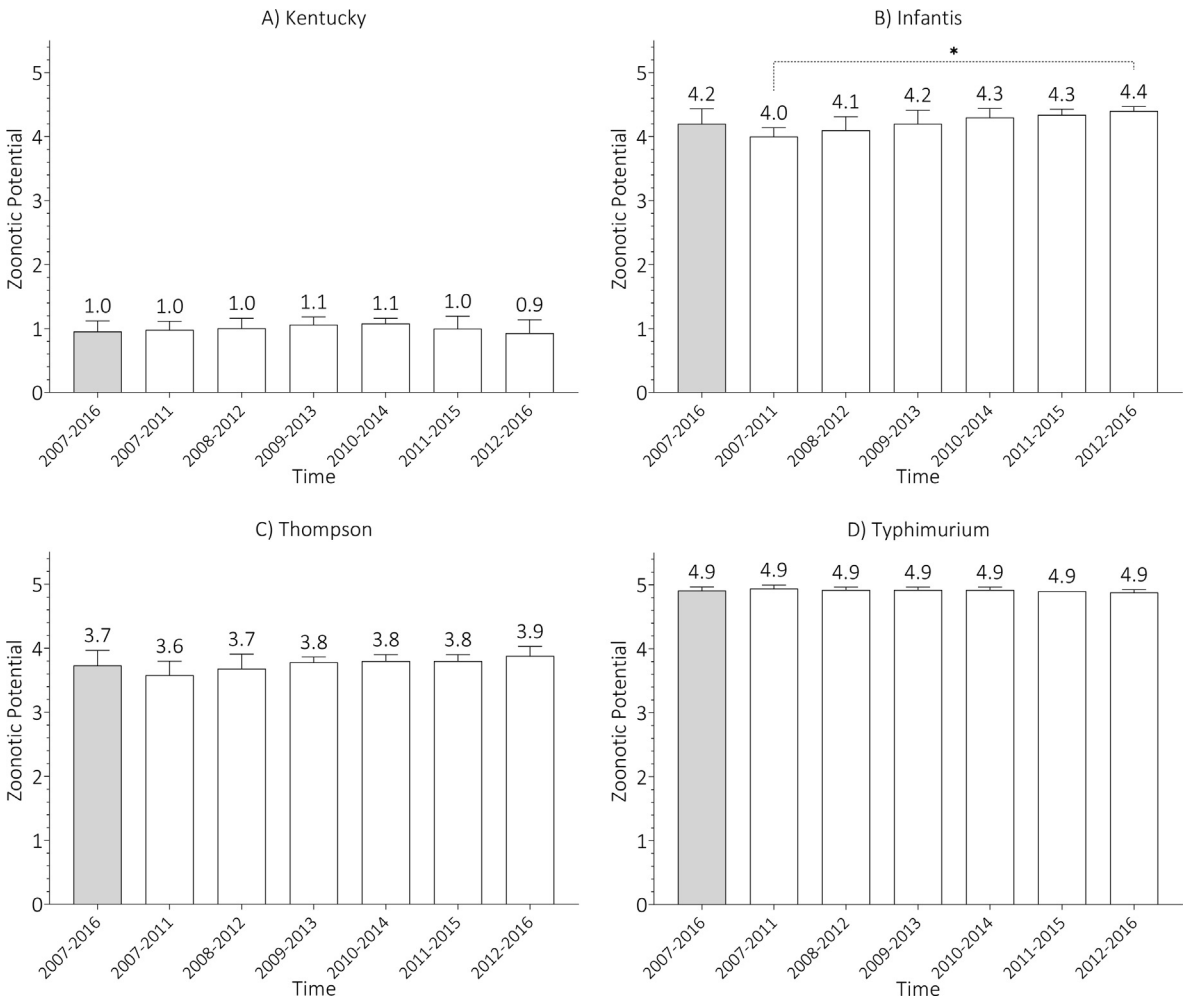

Figure 9. Effect of time on zoonotic potential (ZP) of Salmonella serotypes: A) Kentucky; B) Infantis; C) Thompson; and D) Typhimurium. Bars are means ± standard deviations for five consecutive years of ZP data from the U. S. Centers for Disease Control and Prevention (Table 2). Bars connected by a dashed line with * are different at $P \leq 0.05$ per one-way analysis of variance (ANOVA) followed by Tukey's multiple comparison test at $P \leq 0.05$.

the DT, DRM in PFARM provided acceptable predictions (pAPZ ≥ 0.7) of the dependent $P_{ill\ obs}$ data from HFT.

Scenario analysis for illness dose. Replicate simulations and K-W tests showed that ID_6 changed ($P \leq 0.05$) over time in the simulated production chain (Fig. 10). However, the pattern of change of K-W mean ranks for ID_6 over time differed among replicate simulations.

To resolve this, K-W mean ranks for ID_6 among replicate simulations were evaluated by ANOVA, which confirmed that ID_6 changed ($P \leq 0.05$) over time in the simulated production chain (Fig. 11A). Here, ID_6 was highest in periods 1, 2, and 3, and lowest in periods 4 and 5.

Scenario analysis for zoonotic potential. Replicate simulations and K-W tests showed that ZP_6 changed ($P \leq 0.05$) over time in the simulated production chain (Fig. 12). However, the pattern of change of K-W mean ranks for ZP_6 over time differed among replicate simulations.

To resolve this, K-W mean ranks for ZP_6 among replicate simulations were evaluated by ANOVA, which confirmed that ZP_6 changed ($P \leq 0.05$) over time in the simulated production chain (Fig. 11B). Here, ZP_6 was highest in periods 4 and 5, and lowest in periods 1, 2, and 3.

Scenario analysis summary. Results of the scenario analysis showed that ID_6 decreased over time in the simulated production chain and was lower in periods 4 and 5 than in periods 1, 2, and 3 where it was similar (Fig. 11A). Because MPP, FCB, and CHI were held constant over time in the simulations, the change in ID_6 over time in the simulated production change could be attributed to the change in ZP_6 over time in the simulated production chain. Here, ZP_6 was higher in periods 1, 2, and 3 than in periods 4 and 5 where it was similar (Fig. 12B). This occurred because the main *Salmonella* serotype changed from Kentucky, which had a low ZP, in periods 1, 2, and 3 to Infantis, which had a high ZP, in periods 4 and 5.

This change in the main serotype is shown in Figure 12, which highlights a novel feature of PFARM; namely, the ability to use ZP to identify which serotype is present in CG meals at consumption. Also visible in Figure 12 are meals that are contaminated with two or more serotypes of *Salmonella* at consumption. They are most easily observed as stray data points between serotype Thompson and serotype Kentucky.

Discussion

When a person ingests a dose of *Salmonella* from a meal, their peak response falls on a continuum from no response (no fecal shedding or symptoms) to infection (fecal shedding but no symptoms) to illness (fecal shedding and symptoms) to severe illness (hospital) to death (McCullough & Eisele, 1951a, 1951b, 1951c, 1951d). Where on this continuum, the peak response falls depends on an interaction between *Salmonella*, consumer, and food or DT.

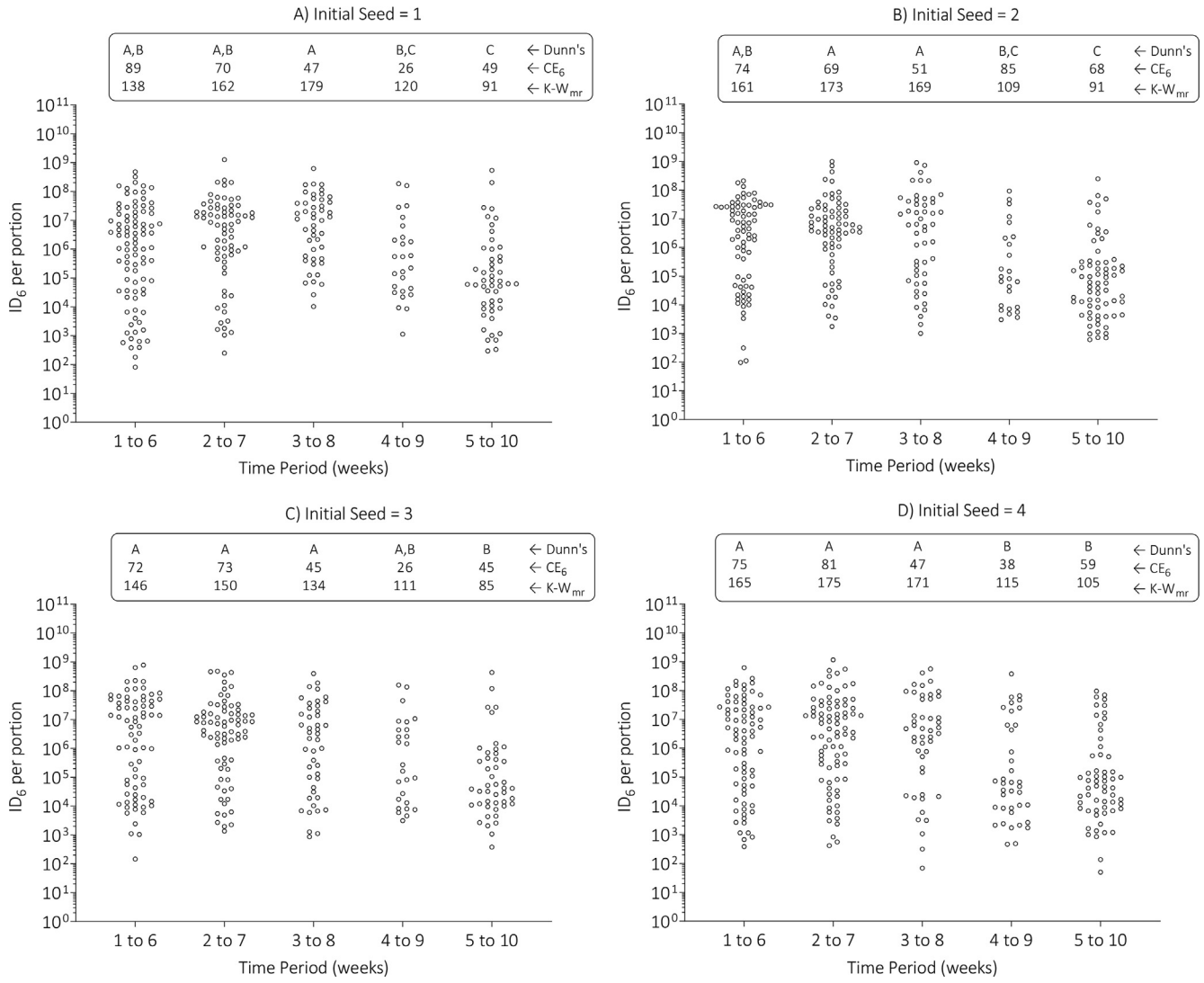

Figure 10. Scenario analysis from the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs) for the effect of time on illness dose (ID_6) in the simulated production chain. Time periods with different capital letters within an initial seed or replicate simulation differ at $P \leq 0.05$ per Kruskal-Wallis (K-W) test followed by comparison of K-W mean ranks ($K\text{-}W_{mr}$) using Dunn's multiple comparison test at $P \leq 0.05$. Abbreviation: CE_6 = number of consumer exposures.

To simulate *Salmonella* DR, it is important to simulate DC and ID. In the present study, this was accomplished using a DT, DRM in PFARM that was developed with HFT data (Oscar, 2004a) and validated with HOI (independent) and HFT (dependent) data for *Salmonella*. The DT, DRM in PFARM predicts ID as a function of DT or ZP, FCB, and CHI. The ID is important because it is the denominator in the equation that determines CR where DC is the numerator (Fig. 1). Because of data and knowledge gaps, assumptions were made to simulate ID as a function of DT or ZP, CHI, and FCB. However, these assumptions were evaluated quantitatively in the present study for the first time using HOI and HFT data for individual strains and serotypes of *Salmonella* and the APZ method (Oscar, 2020b). Results showed that the DT, DRM provided acceptable (pAPZ ≥ 0.70) predictions of *Salmonella* DR and by inference ID as a function of DT or ZP, CHI, and FCB.

Although HFT data used in this study (McCullough & Eisele, 1951a, 1951b, 1951c, 1951d) had limitations (see below), they were valuable in development of the DT, DRM in PFARM. Of note, in a previous study (Oscar, 2004a), they were used to develop a DRM that used $PERT_{ID}$ to predict P_{ill} as a function of DC and *Salmonella* serotype and strain prevalence and virulence. Simulation of that DRM showed that when food is contaminated with multiple strains or serotypes of *Salmonella* with different ZP, the DR curve is nonsigmoid in shape and not well-predicted by traditional methods that use sigmoid-shaped DRM (Holcomb et al., 1999; Rose & Gerba, 1991; Teunis et al., 1999). Subsequently, that DRM was expanded to include CHI and FCB using the DTS concept (Oscar, 2017, 2019, 2020a).

Important limitations of HFT data (McCullough & Eisele, 1951a, 1951b, 1951c, 1951d) used to develop the DT, DRM in PFARM are lack of low doses of *Salmonella*, lack of high-risk subjects, as subjects were healthy men, and lack of high-risk food, as eggnog used to deliver *Salmonella* was a category 2 beverage with a pFPr of 0.087. However, in subsequent studies (Oscar, 2017, 2019, 2020a), these limitations of HFT data for DT, DRM in PFARM were addressed by validating it against data for lower doses of *Salmonella* from HOI with high-risk consumers (very young and old) and high-risk foods (pFPr from 0.27 to 1.00) resulting in a complete validation of the DT, DRM. Thus, both HFT and HOI data were important in the development and validation of the DT, DRM in PFARM.

In addition to Pr, N, and ZP (serotype), the previous history and physiological state of *Salmonella* are important to consider in the ID

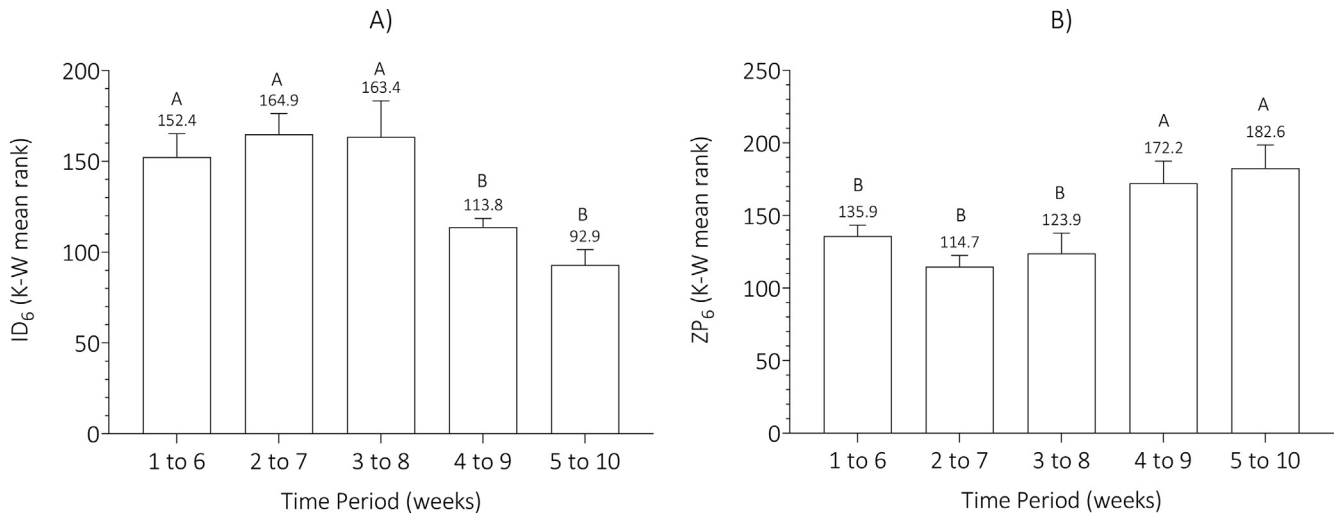

Figure 11. One-way analysis of variance (ANOVA) results for the effect of time on A) the Kruskal-Wallis mean rank ($K\text{-}W_{mr}$) statistic from the K-W test for illness dose (ID_6); and B) the $K\text{-}W_{mr}$ statistic from the K-W test for zoonotic potential (ZP_6) of Salmonella on chicken gizzards (CGs) at consumption. Bars are means ± standard deviations for four replicate simulations of the scenario. Bars with different capital letters within a panel differ per ANOVA ($P \leq 0.05$) followed by Tukey's multiple comparison test at $P \leq 0.05$.

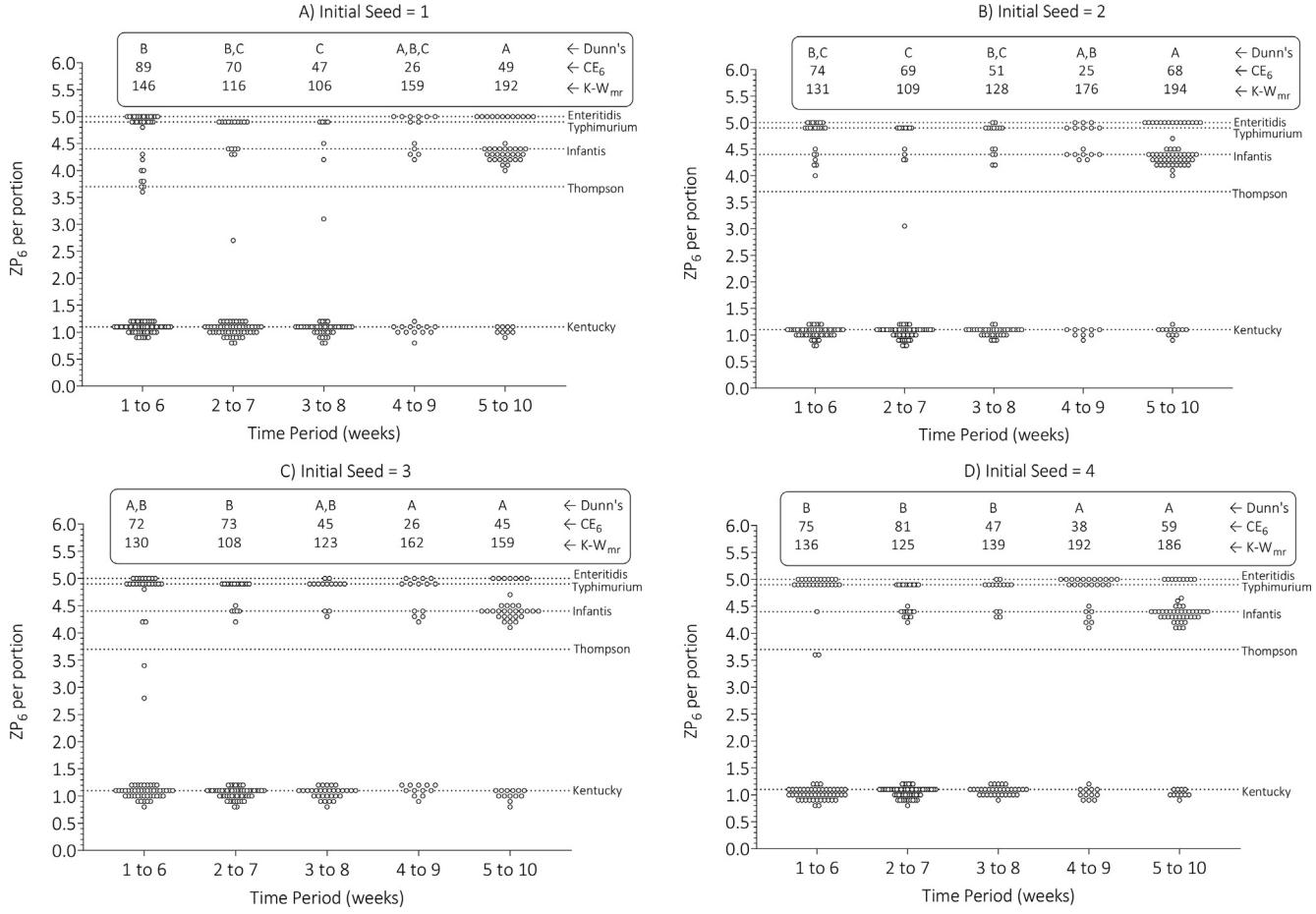

Figure 12. Scenario analysis from the Poultry Food Assess Risk Model (PFARM) for Salmonella and chicken gizzards (CGs) for the effect of time on zoonotic potential (ZP_6) in the simulated production chain. Time periods with different capital letters within an initial seed or replicate simulation differ at $P \leq 0.05$ per Kruskal-Wallis (K-W) test followed by comparison of K-W mean ranks ($K\text{-}W_{mr}$) using Dunn's multiple comparison test at $P \leq 0.05$. Abbreviation: CE_6 = number of consumer exposures.

step of PFARM. Prior exposure to low pH can induce acid tolerance making it easier for *Salmonella* to survive passage through the gastric acid barrier in the stomach (Foster & Hall, 1990; Fratamico, 2003; Garcia-del Portillo et al., 1993; Gawande & Bhagwat, 2002). On the other hand, freezing and thawing, cooking, low pH, low water activity (high salt or sugar), and other stresses encountered in the production

chain or food can injure *Salmonella* and make it harder for them to survive passage through the stomach and cause illness (Chen & Griffiths, 1996; Clark & Ordal, 1969; Ellison et al., 1991; Mackey & Derrick, 1982; Wang et al., 2017; Zheng et al., 2015). To simulate the effects of strain variation, previous history, physiological state, and other variables on ZP of *Salmonella* serotypes, $PERT_{ZP}$ and $PERT_{ID}$ were used in the ID step of PFARM (Fig. 1). In this way, all imagined scenarios for the effects of genotype and phenotype of *Salmonella* on dose-response were captured and simulated in the DT, DRM of PFARM.

In the ID step of PFARM, it is also important to consider host factors that affect *Salmonella* DR (Coleman et al., 2017). Some important host factors are age, physiological state (pregnancy), preexisting health conditions like diabetes (Hohmann, 2001; Telzak et al., 1991), immunocompetence (Havelaar & Swart, 2014; McCullough & Eisele, 1951b), and medications like steroids and antacids (Oscar, 2019). Effects of host factors (CHI) on *Salmonella* DR in PFARM are simulated using a combination of probability distributions. First, a DISCRETE distribution is used to simulate the distribution of consumers among five risk categories of CHI from low to high. Second, UNIFORM distributions are used to simulate the variability and uncertainty of CHI within a risk category (Fig. 1). Because it was not known how host factors interact to affect CHI, a worst-case scenario approach was used instead of a composite CHI approach. Here, the CHI factor with the highest risk was used to simulate CHI. This resulted in a fail-safe prediction of CHI.

Like host factors, food factors (FCB) affect outcome of the DT on *Salmonella* DR. Important food factors are fat level (Barmpalia-Davis et al., 2009; Greenwood & Hooper, 1983; Juneja & Eblen, 2000; Tammings et al., 1976; Zhu et al., 2012), protein level (Mennah-Govela & Bornhorst, 2021; Tan et al., 2014), native microflora (Bielke et al., 2003; Callaway et al., 2008; Carter et al., 2017; Moye et al., 2019; Nair & Kollanoor-Johny, 2017; Totton et al., 2012), pH (Alvarez-Ordonez et al., 2009; Foster & Hall, 1990; Fratamico, 2003; Garcia-del Portillo et al., 1993; Gawande & Bhagwat, 2002), buffering capacity (Mennah-Govela & Bornhorst, 2021), and antacid medication (Smith, 2003). Effects of food factors (FCB) on *Salmonella* DR in PFARM were simulated using a combination of probability distributions. First, a DISCRETE distribution was used to simulate distribution of FCB among five categories of risk from low to high. Second, UNIFORM distributions were used to simulate the variability and uncertainty of FCB within a risk category (Fig. 1). A survey was developed to determine FCB in the consumer population as a function of the pFPr of the meal. Contribution of FCB to DTS was 60% of that from ZP and CHI, giving it less weight in determining outcome of the DT on *Salmonella* DR. This assumption was tested and validated in the present study using HOI and HFT data and the APZ method (Oscar, 2020b).

As discussed above and further discussed here because of its importance, the DT, DRM in PFARM was developed with HFT data and validated with HOI and HFT data because both types of data were important. First, HOI data were important because they included high-risk *Salmonella* serotypes (Enteritidis, ZP_{mode} = 5.0; Typhimurium, ZP_{mode} = 4.9; Infantis, ZP_{mode} = 4.4), high-risk consumers (very young and old; CHI category 5 = 4.1 to 5.0), and high-risk food (category 5 = pFPr = 0.27 to 1.00 = FCB of 2.5 to 3.0), and provided $P_{ill\ obs}$ at low doses (<3 log) of *Salmonella* for serotypes (Enteritidis, Typhimurium, Infantis) isolated from CGs in the IC step of this PFARM study (Oscar, 2022).

Second, HFT data were important because they were collected under controlled conditions and informed design of the DT, DRM in PFARM (Oscar, 2017, 2019, 2020a), provided data for one top five (Newport, ZP_{mode} = 4.8) and one top 20 human clinical isolate (Bareilly, ZP_{mode} = 3.4), and provided $P_{ill\ obs}$ at higher doses (>6 log) of *Salmonella* and for low-risk serotypes of *Salmonella* (Derby, ZP_{mode} = 1.2; Meleagridis; ZP_{mode} = 0.2; and Pullorum, ZP_{mode} = 0.1) that were similar to serotype Kentucky (ZP_{mode} = 1.1), which was the main serotype isolated from CGs in the IC step of this PFARM study (Oscar, 2022). Thus, together HOI and HFT data allowed the development and validation of a more complete DT, DRM in PFARM that simulated a broad range of DT, DTS, and ID for *Salmonella* that covered a broad spectrum of the possible DC, P_{ill}, and DR curves for *Salmonella*.

Poultry FARM can be used to find the proportion of consumers in a population that become ill or PFARM can be used to find P_{ill} for a single consumer. To determine population P_{ill}, the results of surveys from multiple consumers are simulated together, whereas to determine individual P_{ill}, the results of one or more surveys from one consumer are simulated. In the validation and scenario phases of the present study, population P_{ill} was simulated because HOI and HFT data and computer-generated survey data were for multiple subjects and consumers, respectively, and not just one subject or consumer except for four HOI cases for serotype Typhimurium.

A DTS in the DT, DRM of PFARM corresponds to one $PERT_{ID}$ with a range of 2.0 log and one DR curve. In previous PFARM (Oscar, 2017, 2019, 2020a), DTS ranged from 1.1 to 12.5 in increments of 0.1 for a total of 115 $PERT_{ID}$. In the current DT, DRM in PFARM, DTS ranged from 0.3 to 13.0 in increments of 0.1 for a total of 128 $PERT_{ID}$ with a range of 2.0 log. This small change was made to better simulate ID as a function of DT or ZP, CHI, and FCB.

Although a DTS in PFARM represents a single $PERT_{ID}$ and DR curve, multiple combinations of ZP, CHI, and FCB result in the same DTS. For example, a DTS of 9.5 could be from a ZP of 4.5, a CHI of 3.0, and an FCB of 2.0 or it could be from a ZP of 3.5, a CHI of 3.0, and an FCB of 3.0 etc. Thus, multiple DT scenarios result in the same $PERT_{ID}$ and DR curve.

The DT, DRM in PFARM simulates in two directions: horizontal and vertical. In the horizontal direction, it simulates multiple *Salmonella* serotypes, consumers, and meals, whereas in the vertical direction, it simulates a single meal or DT. The DTS is used to simulate in the horizontal direction, whereas a $PERT_{ID}$ is used to simulate in the vertical direction. The $PERT_{ID}$ has a range of 2-log, which simulates the variability and uncertainty of the simulated meal or DT. The randomly selected ID from the $PERT_{ID}$ is used to simulate individual DR as a discrete event: illness or no illness. When DC ≥ ID or when the ratio of DC to ID is ≥1, an illness occurs; otherwise, no illness occurs.

In contrast, other DRMs use one to three DRM like the exponential or beta-Poisson (Holcomb et al., 1999; Latimer et al., 2001; Oscar, 2004a; Rose & Gerba, 1991; Teunis et al., 2010) to simulate *Salmonella* DR in the vertical direction only (one DRM) and in the vertical and to a limited extent in the horizontal direction (two or three DRMs). However, the use of only one to three DRMs to simulate the HOI and HFT data in Figure 1 would result in an inaccurate (pAPZ < 0.7) prediction of these data. Therefore, in the present study, the DT, DRM, which had 128 DR curves, was used instead. In addition, the current DT, DRM is the only *Salmonella* DRM that has been quantitatively evaluated and validated using the established criteria for model performance in the APZ method (Oscar, 2020b).

The DT, DRM in PFARM is a robust method that can be changed to incorporate new data and knowledge without major changes in its methods and assumptions. For example, if the CDC ranking of *Salmonella* changes from serotype to strain based on whole genome sequencing, the calculation of ZP for strains would be similar because it is based on the ranking and not what is being ranked. Likewise, if the ranking of a *Salmonella* serotype changed because of a new food production practice like a serotype-specific vaccine (Saenz et al., 2022), no change in the DT, DRM would be needed. Rather, the DT, DRM would capture and simulate this change in ZP of the serotype. This occurred in the present study for serotypes Derby and Infantis. However, in the present study, changes in food production practices from 2007 to 2016 did not significantly change ZP of nine of 11 *Salmonella* serotypes examined because ZP was stable over time.

Additionally, as new consumer (CHI) and food (FCB) factors emerge and are identified that impact *Salmonella* DR, new queries can be added to the consumer survey in PFARM without a need for

major changes in the way they are simulated in the DT, DRM. For example, the consumer survey in PFARM could query for a new preexisting health condition like COVID-19 without altering how (worst-case approach) CHI is simulated in the DT, DRM of PFARM. For FCB, a query could be added for probiotics and an adjustment factor like that used for antacids could be added to the calculation of pFPr for the meal and simulation of FCB in the DT, DRM. Thus, by developing a robust method (DT, DRM) for simulating *Salmonella* DR, PFARM is well-positioned to handle future changes in data and knowledge for ZP, CHI, and FCB.

Simulation of individual consumers in the DT, DRM of PFARM was demonstrated in the present study with HOI data for *Salmonella* Typhimurium in the validation analysis phase. In the validation analysis, there were four cases that corresponded to individual consumers (3 were very young or old and 1 was not). In all cases, the consumer became ill ($P_{ill\ obs} = 1$) from the estimated dose of *Salmonella* in the food vehicle, which was ice cream, and in all cases, the DT, DRM in PFARM correctly predicted ($P_{ill\ pred} = 1$) their response. These cases are important because they show the individual DR is a discrete event: the consumer becomes ill or not after ingesting a dose of *Salmonella*. In other words, individual $P_{ill\ obs}$ is 0 or 1.

In previous PFARM (Oscar, 2017, 2019, 2020a), CDC data were used to simulate differences in virulence among serotypes of *Salmonella*. However, the virulence term does not consider that the CDC data also reflect DC, which in turn reflects the ability of a *Salmonella* serotype to survive, grow, and spread in the production chain and food. Therefore, rather than abandon the use of CDC data to simulate differences in illness potential among serotypes of *Salmonella*, the term virulence was changed in the current study to the term zoonotic potential (ZP) to better reflect the totality of the PFARM serotype ranking based on CDC data. Here, ZP is the ability of a *Salmonella* serotype to survive, grow, and spread in the production chain and food and then cause illness in humans.

An important addition to PFARM in this study was the use of a nonparametric test (K-W) to evaluate simulation results involving outputs (ID_6, ZP_6) that were not normally distributed. Although the K-W/Dunn's test did not provide unambiguous results by itself, when combined with ANOVA/Tukey's, it provided a clearer interpretation of PFARM simulation results for ID_6 and ZP_6.

The next steps in PFARM for *Salmonella* and CGs are DC and CR. In the DC step of PFARM, two pathways of consumer exposure to *Salmonella* will be simulated: 1) from undercooked CGs; and 2) from cross-contamination and growth of *Salmonella* from CGs on a ready-to-eat food (i.e., lettuce). In the CR step of PFARM, ID_6 from this study will be combined with DC_6 from the DC step of PFARM to predict CR (no exposure, no response, infection, illness, hospitalization, death) over time in the simulated production chain (Fig. 1). Thus, completion of the ID step of PFARM for *Salmonella* and CGs in this study, including validation of the DT, DRM for predicting ID as a function of DT or ZP, FCB, and CHI, was an important step toward the goal of assessing risk and severity of salmonellosis from CGs in the simulated production chain. When applied to multiple production chains, the current PFARM can be used to identify those that pose the highest risk to public health.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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