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Comparing the Effect of Various Contamination Levels for *Salmonella* in Chicken Meat Preparations on the Probability of Illness in Belgium

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ABSTRACT

At the urging of competent national authorities, a limited risk assessment on *Salmonella* in chicken meat preparations in Belgium was undertaken following a retail-to-table approach. The input distribution of *Salmonella* was based on surveillance data in Belgium. To analyze the relative impact of reducing the risk of salmonellosis associated with a decrease in the *Salmonella* contamination level, different distributions based on the actual situation but limiting the number of portions containing *Salmonella* at 1 CFU per 1, 10, and 25 g of meat were used in the quantitative microbial risk assessment model. The quantitative microbial risk assessment model also was run several times with a theoretical fixed input of *Salmonella* assuming all portions possessed the same fixed contamination level set at 1,000, 100, 10, and 1 CFU/g of meat and 1 CFU per 10, 25, 100, and 1,000 g of meat. With regard to the initial contamination level, the results indicate, both by the narrowing of the current distribution and by the fixed input, that especially the higher levels of contamination (>1 CFU/g) contribute to the increased risk for salmonellosis.

For many years, *Salmonella* has been an established foodborne pathogen. In Belgium, this pathogen was the primary cause of bacterial gastroenteritis as reported by the public health services; 9,543 clinical isolates of *Salmonella* (ca. 91 cases of salmonellosis per 100,000 inhabitants), of which 6,075 were *Salmonella* Enteritidis, were reported to the National Reference Centre in 2004 *(10)*. The Belgian control program has been focused on *Salmonella* Enteritidis and consists of vaccination of breeding animals and other measures focused on the breeding sector. Since 2005, the number of reported cases of *Salmonella* infection has dramatically decreased to 4,846, mainly due to a reduction of *Salmonella* Enteritidis infections (2,202 cases reported in 2005) *(11)*. For other *Salmonella* serotypes implicated in infections (of which *Salmonella* Typhimurium has been the predominant serovar since 2005), no significant changes in reports have been noticed *(5)*. In the summer of 2005, a national outbreak of *Salmonella* Ohio infection caused by the consumption of pork occurred in Belgium. Red meat (such as beef, pork, and lamb) has been linked to *Salmonella* infection outbreaks *(38)*. However, cases of salmonellosis also have been attributed to broiler chicken meat and derived products *(3)*. In a national survey conducted from 2000 to 2003, poultry (almost exclusively chicken) remained the most contaminated meat type in Belgium; *Salmonella* contamination was found in ca. 9.5% of broiler carcasses, ca. 13.0% of breast fillets, and ca. 25.6% of meat products *(18)*.

As a control measure for prevention of foodborne salmonellosis, a safety criterion of zero *Salmonella* per 10 g (of five samples, none can be positive for *Salmonella*) for ground meat and meat preparations of poultry and other animals intended to be eaten after heat treatment was set in European Union (EU) legislation *(13)*. The limit will be lowered on 1 January 2010 to zero *Salmonella* in 25 g for products made from poultry meat. However, because *Salmonella* is a heat-sensitive microorganism, the risk of infection should be considerably reduced in ground meat and meat preparations intended to be eaten after heat treatment *(28)*. Therefore, discussion has focused on to what extent the presence of *Salmonella* in 10 g of food, especially in this category of fresh meat, represents a risk to public health and to what extent a further reduction to zero *Salmonella* in 25 g may contribute to the protection of the consumers' health.

At the urging of the Federal Public Service Health, Food Chain Safety and Environment, a working group of the Belgian Health Council has undertaken a limited quantitative microbial risk assessment (QMRA) following a retail-to-table approach for *Salmonella* in chicken meat preparations (CMPs) intended to be eaten after heat treatment. These preparations include a range of consumer

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products such as chicken meat reduced to fragments or minced, sold as such, or marinated, stuffed, or seasoned. From a questionnaire on consumption habits taken from 3,000 Belgian consumers in 2004 and 2005 *(8),* the consumption of CMPs was estimated as 0.9 kg per year per inhabitant (ca. 5.5% of the total volume of all types of meat preparations). Based on a 100-g portions, this amount corresponds to 90 million portions consumed per year in Belgium (10^7 inhabitants). At present in Belgium, there is no epidemiological evidence of cases of salmonellosis linked to consumption of chicken meat preparations; however, attributing illness to food is not an easy task *(2, 14)*. The QMRA was requested by the risk managers because of the high prevalence of *Salmonella* in chicken meat preparations in Belgium *(18)* and because consumption of undercooked meat is a risk factor for salmonellosis *(9)*. To analyze the relative impact of a decrease in the *Salmonella* contamination level on the risk of salmonellosis associated with chicken meat preparations, the QMRA model was run for different distributions based on the actual situation but limiting the number of portions with *Salmonella* at the levels of 1 CFU per 1, 10, and 25 g of meat. The QMRA model also was run several times with a theoretical fixed input of *Salmonella* assuming all portions possessed the same fixed contamination level. The objective was to use this limited risk assessment as one of the supportive factors in the discussion of risk-based microbiological criteria for *Salmonella* in meat and meat preparations intended to be eaten after heat treatment.

MATERIALS AND METHODS

Definition of the food type. This study focused on only CMPs because it is the most contaminated meat type in Belgium. According to EU legislation, a ''meat preparation'' refers to fresh meat, including meat that has been reduced to fragments, that has added foodstuffs, seasonings, or other additives or has undergone processes insufficient to modify the internal muscle fiber structure of the meat and thus eliminate the characteristics of fresh meat. Minced meat is, according to EU legislation, boned meat that has been minced into fragments and contains less than 1% salt. In reality, all minced chicken meat products brought to the retail market in Belgium contain more than 1% salt and are catalogued as meat preparations. Thus, CMPs include such items as sausages and hamburgers of raw minced chicken meat, satays of chicken meat (pieces of poultry meat mounted on a wooden stick separated by onion or pepper slices), stuffed chicken fillets, and marinated chicken wings. CMPs are intended to undergo a heat treatment before consumption.

Data collection. Data on the prevalence of *Salmonella* in CMPs were derived from the National Belgian surveillance of zoonotic agents executed by the competent national authorities (Federal Agency for Safety of the Food Chain) in Belgium to comply with the Directive 92/117/CEE of the European Council. Sample collection and microbiological analysis were performed as described by Ghafir et al. *(18)*. The following prevalence data were available: 21% (44 of 210) positive samples (*Salmonella* presence in 10 g of meat) in 2001, 21% (17 of 81) positive samples (presence in 25 g) in 2002, 29.3% (29 of 99) positive samples (presence per 25 g) in 2003, and 18.5% (62 of 335) positive samples (presence in 1 g) in 2004.

Description of the model. The QMRA follows a retail-to-table approach. The necessary data and scientific backup for assumptions in the QMRA were mainly derived from information from the Food and Agriculture Organization (FAO) and the World Health Organization (WHO) *(16)* with other information from national reports and international literature.

The QMRA was constructed in an Excel spreadsheet (Microsoft, Redmond, WA) and was simulated using @RISK (Palisade, Ithaca, NY), an Excel add-in program. An overview of the QMRA is shown in Figure 1. The QMRA is divided in seven modules: module 1, arrival at retail level; module 2, storage at retail level; module 3, transport; module 4, storage at consumer level; module 5, consumer handling (undercooking and cross-contamination); module 6, consumption; and module 7, illness. As shown in Figure 1, the outputs of one module are used as inputs for the following module. The detailed model and an overview of assumptions made and references to reports or publications are given in Table 1.

With regard to *Salmonella* growth, the growth model used in the QMRA model was developed by Oscar *(34)*. He assumed that *Salmonella* will only grow at temperatures above 10°C. The model takes time, temperature, and sodium chloride concentration into account:

$$\text{Logarithmic growth per hour} = \exp[-6.2251 - 0.0114\cdot\text{Slt} + 0.3234\cdot T + 0.002\cdot(\text{Slt} \times T) - 0.0085\cdot\text{Slt}^2 - 0.0045\cdot T^2]$$

where T is the temperature (degrees Celsius) and Slt is the salt (sodium chloride) concentration (percentage). The salt concentration was fixed at 2%. In the present growth model, the lag phase of *Salmonella* was not taken into account. Everywhere in the QMRA where growth was calculated, the growth was limited to 10^9 CFU/100 g.

Description of the model: module 1, arrival at retail level. The first module describes the contamination level and prevalence of *Salmonella* in raw CMPs in Belgium. As mentioned above (''Data collection''), data were derived from the National Belgian surveillance program. No quantitative data (enumeration of *Salmonella* in the food type) were available, but presence-absence testing was done for different sample weights from different years in the surveillance plan. As such the available data set was limited

It was assumed that the level of *Salmonella* in raw CMPs is log normally distributed; lognormal distributions are used for representing quantities expressed as orders of magnitude *(41)*. Based on the prevalence data of *Salmonella* in CMPs, 75% of the CMPs contained 1.39 ln CFU/100 g or less, 79% contained 2.30 ln CFU/100 g, and 81.5% contained 4.61 ln CFU/100 g. A normal distribution through these three data points was constructed with the function RiskNormalAlt. This function allows construction of a normal distribution, but percentiles are used instead of specifying the mean and standard deviation. From this distribution, 550 samples were taken, and a normal distribution was fit to these data points to determine the mean and standard deviation of this normal distribution: −3.5 and 6.65 ln CFU/100 g, respectively.

This normal distribution was used to calculate the number of *Salmonella* cells in a raw CMP of 100 g (N_{rCMP}). It was assumed that a portion of 100 g was consumed. The prevalence of *Salmonella* in a raw CMP (P_{rCMP}) was manually determined from the distribution for N_{rCMP}. The prevalence of contaminated CMPs was calculated as described by Uyttendaele et al. *(40)*.

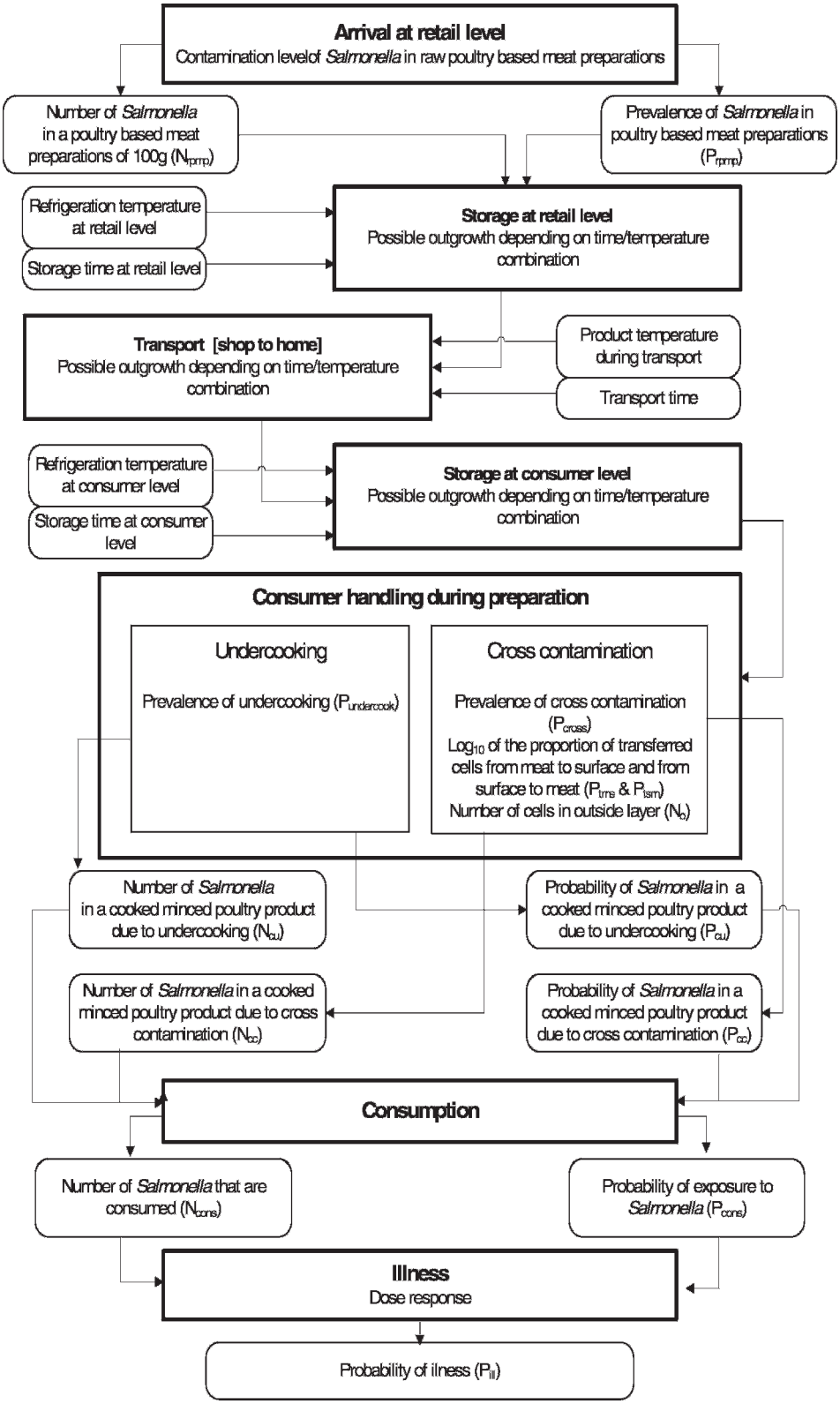

FIGURE 1. *Overview of the quantitative risk assessment model.*

Description of the model: module 2, storage at retail level. A survey of 65 retail storage temperatures in Brussels, Belgium (data provided by the Belgian Federal Agency for the Security of the Food Chain) was available. This information was incorporated nonparametrically by using a discrete uniform distribution. A discrete uniform distribution is a special case of the discrete distribution where all possible values have the same probability of occurrence *(41)*. The maximum recorded temperature was 8°C, which is below the growth model's minimum level for *Salmonella* growth (10°C) *(34)*.

Based on contacts with 11 companies during a Belgian nationwide study *(21)*, information was obtained from the poultry meat processing industry with regard to shelf life of CMPs. It became clear that most CMPs upon production are immediately

TABLE 1. *Detailed overview of the quantitative risk assessment model and its assumptions*

Module	Variable	Description	Unit	Distribution or model	Assumptions and references
Arrival at retail level	N_{rCMP}	Level of *Salmonella* in a raw CMP[a] of 100 g	CFU/100 g	exp(Normal(μ; σ))	Level of *Salmonella* in minced poultry meat and CMPs is log normally distributed
	P_{rCMP}	Prevalence of *Salmonella* in CMPs		Fixed value depending on the distribution of N_{rCMP}	$P_{rp} = (A + 0.1 \times B + 0.01 \times C)/100$, where A is the percentage of CMPs that contains ≥1 CFU/100 g, B is the percentage that contains between 1 CFU/100 g and 1 CFU/1,000 g, and C is the percentage that contains between 1 CFU/1,000 g and 1 CFU/10,000 g *(37)*
Storage at retail level	T_r	Storage temp at retail level	°C	DUniform	Source: Federal Agency for the Safety of the Food Chain
	t_r	Storage time at retail level	h	Pert(1, 48, 120)	Expert opinion
	Lg_r	Logarithmic growth during retail		If($T_r < 10$; 0; $t_r \times Lg/h_r$)	Lg/h_r is the logarithmic growth per hour calculated using a published growth model *(34)*
	N_r	No. of cells at the end of retail	CFU/100 g	$10^{\log(N_{rCMP}) + Lg_r}$	
Transport from retail to home	T_t	Temp during transport from retail to home	°C	Pert(4, 10, 25)	*(28)*
	t_t	Time required for transport from retail to home	h	Gamma(5.24; 8.17)/60	*(28)*
	Lg_t	Logarithmic growth during transport		If($T_t < 10$; 0; $t_t \times Lg/h_t$)	Lg/h_t is the logarithmic growth per hour calculated using a published growth model *(34)*
	N_t	No. of cells at the end of transport	CFU/100 g	$10^{\log(N_r) + Lg_t}$	
Storage at consumer level	T_c	Storage temp at consumer level	°C	Cumulative	Belgian Food Consumption Survey *(8)*
	t_c	Storage time at consumer level	h	Exponential	Taking into account the practical shelf life of the product *(28)*
	Lg_c	Logarithmic growth during consumer level		If($T_c < 10$; 0; $t_c \times Lg/h_c$)	Lg/h_c is the logarithmic growth per hour calculated using a published growth model *(34)*
	N_c	No. of cells at the end of consumer level	CFU/100 g	$10^{\log(N_t) + Lg_c}$	
Consumer handling: undercooking	$T_{cooking}$	Temp of product during cooking	°C	Pert(60; 64; 65)	*(16)*
	$t_{cooking}$	Time of cooking	min	Pert(0.5; 1; 1.5)	*(16)*
	$P_{undercook}$	Probability of undercooking		Pert(0.05; 0.1; 0.15)	*(16)*
	$O_{undercook}$	Occurrence of undercooking, where 0 indicates undercooking and 1 indicates no undercooking		Binomial(1; $1 - P_{undercook}$)	When this binomial distribution generates a 0, undercooking occurs, whereas 1 indicates that no undercooking occurred
	D	Decimal reduction time	min	$10^{-0.139 \cdot T_{cooking} + 8.58}$	*(16)*
	L_r	Logarithmic reduction		If($O_{undercook} = 1$; ''inactivation''; $t_{cooking}/D$)	
	N_{cu}	Level of *Salmonella* in a heated CMP due to undercooking	CFU/100 g	If($L_r =$ ''inactivation''; 0; max(0; $N_c - 10^{L_r}$))	When the binomial distribution (for O_{cross}) shows that no cross-contamination occurs, the no. of *Salmonella* cells in a cooked CMP will be 0; however, when cross-contamination occurs, N_{cc} will be equal to N_{tsm}

TABLE 1. *Continued*

Module	Variable	Description	Unit	Distribution or model	Assumptions and references
	P_{cu}	Probability of *Salmonella* in a heated CMP due to undercooking		$P_{rCMP} \times P_{undercook}$	
Consumer handling: cross-contamination	P_{cross}	Prevalence of cross-contamination		Pert(0.25; 0.5; 0.76)	The results of different studies *(7, 40, 41)* on consumer behavior integrated in a Pert distribution
	O_{cross}	Occurrence of cross-contamination, where 0 indicates no cross-contamination and 1 indicates cross-contamination		Binomial(1; P_{cross})	When this binomial distribution generates a 0; no cross-contamination occurs, whereas 1 indicates that cross-contamination occurred
	$Prop_{tms}$	Logarithm of the proportion of cells transferred from meat to surface		Pert(-6; -2; -1)	Logarithm of the proportion of cells transferred from a meat product to a surface was represented by a Pert distribution with a minimum of -6, a mode of -2, and a maximum of -1 *(15)*
	N_o	No. of cells in outside layer	CFU/100 g	$N_c \times 0.15$	*Salmonella* cells in the 15-g outer contact side of a P-GM-MP can give rise to transmission; this assumption is based on calculations of the outer contact side; a homogenous distribution of the cells is assumed
	N_{tms}	No. of cells transferred from meat to surface	CFU/100 g	$N_o \times$ power(10, $Prop_{tms}$)	
	$Prop_{tsm}$	Logarithm of the proportion of cells transferred from surface to meat		Pert(-6; -2; -1)	Logarithm of the proportion of cells transferred from a meat product to a surface was represented by a Pert distribution with a minimum of -6, a mode of -2, and a maximum of -1 *(15)*
	N_{tsm}	No. of cells transferred from surface to meat	CFU/100 g	$N_{tms} \times$ power(10, $Prop_{tsm}$)	
	N_{cc}	Level of *Salmonella* in a heated CMP due to cross-contamination	CFU/100 g	If($O_{cross} = 0$; 0; N_{tsm})	When the binomial distribution (for O_{cross}) shows that no cross-contamination occurs, the no. of *Salmonella* cells in a cooked CMP will be 0; however, when cross-contamination occurs, N_{cc} will be equal to N_{tsm}
	P_{cc}	Probability of *Salmonella* in a heated CMP due to cross-contamination		$P_{rCMP} \times P_{cross}$	
Consumption	N_{cons}	No. of *Salmonella* cells consumed	CFU/100 g	$N_{cu} + N_{cc}$	Each consumer eats a 100-g portion
	P_{cons}	Probability of exposure		$P_{cu} + P_{cc} - P_{cu} \times P_{cc}$	Exposure is due to combination of cross-contamination and undercooking
Illness	$P_{ill/D}$	Probability of illness from the dose		$1 + (1 - N_{cons}/\beta)^{\alpha}$	α and β are selected from a second-order data set *(15)*
	P_{ill}	Probability of illness		$P_{ill/D} \times P_{cons}$	

[a] CMP, chicken (poultry) meat preparation.

sent to retail outlets (or in the worst case sent after overnight storage under refrigeration), which are supplied nearly every day. The maximum shelf life of these CMPs is 5 days. Thus, the retail storage time could best be described as Pert(1;48;120).

Description of the model: module 3, transport. The temperature during transport is largely unknown. Expert opinion from within an EU-funded project proposed a minimum of 4°C, but the effective temperatures during transport most likely range from 10 to 25°C *(31)*. For the transport time, a Gamma distribution with parameters 5.24 and 8.17 was used *(31)*. This distribution was based on British data. A heat transfer coefficient correcting for the slow transfer of heat from the environment to the mass of the portion (holding the *Salmonella*) was not included.

Description of the model: module 4, storage at consumer level. In the Belgian Food Consumption Survey of 2004 *(8),* the temperatures of home refrigerators of respondents were recorded. These data were available as a cumulative distribution, which was incorporated in the model as a nonparametric distribution. The average value of this distribution was 6.7°C, with a standard deviation of 2.8°C. For the storage time at consumer level, an exponential distribution was used based on the day of purchase and the use-by date *(31)*. However, it was assumed that the consumer will not eat the product when it is already spoiled. Depending on the temperatures at which the product was stored in the chain, the practical shelf life was calculated and used as a maximum for the shelf life. To calculate the practical shelf life of the product, a simple development from the Arrhenius reaction rate equation can be used to calculate relative spoilage rates:

$$\text{Relative spoilage rate} = (1 + 0.1T)^2$$

where T is the temperature (degrees Celsius) *(17)*. The shelf life at the reference temperature of 4°C was set at the shelf life indicated by the producer, and in this way the practical shelf life at each temperature could be calculated.

Description of the model: module 5, consumer handling. The present study has included two pathways for this module in the model: (i) cross-contamination of a meal due to unsafe food handling procedures and (ii) the survival of *Salmonella* due to undercooking of the CMP.

The consumer module for undercooking was implemented according to the model used in the FAO-WHO *(16)* risk assessment of *Salmonella* on broiler meat. In general, the bacteria are killed completely by the cooking process. However, there is a chance of undercooking, Pert(0.05; 0.1; 0.15). When undercooking occurs, there will be a reduction of *Salmonella* with a decimal reduction time $D = 10^{-0.139 \cdot T_{\text{cooking}} + 8.58}$ (min). The temperature in the center of the product during cooking was derived from the FAO-WHO study on *Salmonella (16).*

In addition to undercooking, consumers also can cause cross-contamination. In the present study, cross-contamination was taken into account as described by Uyttendaele et al. *(40)*. The prevalence of cross-contamination was described by a Pert distribution using data from different studies *(7, 43, 44)*. To determine whether cross-contamination occurs, a binomial distribution was used. When cross-contamination occurs for CMPs, the pathogen cells are first transferred from the meat product to a surface (e.g., knife or cutting board), and those cells are transferred again from the contaminated surface to another food or back to the meat after it is cooked. However, not all the pathogen cells present in the meat product are transferred; only those cells on the outer layer of the product can be transferred. Based on calculations of the outer contact side of a hamburger and a sausage, it was assumed that only cells on the 15-g outer contact side of a 100-g CMP can give rise to transmission of the pathogen, and not all cells on the outer layer are transferred. Therefore, the FAO-WHO model *(15)* was used. After cooking, a transfer will occur again from the contaminated surface to the meat product. This transfer is calculated in the same way as the transfer from the meat to the surface.

The possible transfer of *Salmonella* from a CMP to a ready-to-eat salad by cross-contamination as described by a model for *Campylobacter* in the chicken meat chain (carcasses to chicken fillets) *(6)* was not taken into account. Although there are some data available about the parallel consumption of poultry meat and ready-to-eat salad in Belgium, this association with ready-to-eat salad especially relates to poultry carcasses or chicken breast fillets and not to CMPs, the type of product included in the present study.

Description of the model: module 6, consumption. It was assumed that each consumer eats a 100-g CMP portion. The number of *Salmonella* cells consumed is the sum of the number of *Salmonella* cells in a cooked CMP (N_{cons}) due to undercooking and due to cross-contamination. The probability of exposure (P_{cons}) is calculated based on the probability of *Salmonella* being present in a heat-treated CMP due to undercooking and/or cross-contamination.

Description of the model: module 7, illness. When the consumer is subjected to a certain dose of *Salmonella,* there is a certain chance that this consumer will become ill. This relationship is described by a dose-response model. The model used here is the same as that used by the FAO-WHO *(16)*. It is based on a relative large collection of *Salmonella* outbreak data, which could be best described by a Beta-Poisson model: $1+(1-N_{\text{cons}}/\beta)^{\alpha}$, where α and β are selected from a second order data set.

Effect of *Salmonella* contamination level in minced poultry meat and meat preparations on the probability of illness. To analyze the relative impact of reducing the risk of salmonellosis associated with a decrease in the *Salmonella* contamination level, the QMRA model was run for different distributions based on the actual situation (situation 1) but limiting the number of portions that contain *Salmonella* at 1 CFU/g (situation 2), 1 CFU/10 g (situation 3), and 1 CFU/25 g (situation 4). Table 2 shows the characteristics of the distribution describing the contamination level of *Salmonella* in raw CMPs. For situations 2 through 4, the mean of the distribution that represents the natural logarithm of the *Salmonella* level in CMPs (C_{rCMP}) was the same as for situation 1, but the standard deviation was lower (Table 2). This option was taken because it was assumed that by taking control measures (e.g., setting criteria) especially the higher (nonconforming) levels of contamination would be eliminated without changing the overall mean level of contamination. The QMRA model was run several times with a theoretical fixed input of *Salmonella,* assuming all portions possessed a contamination level set at 10^9, 10^8, 10^7, 10^6, 10^5, 10^4, 10^3, 100, 10, 4, 1, and 0.1 CFU/100 g. For these simulations, a prevalence of *Salmonella* in CMPs (P_{rCMP}) of 1 was used, indicating that every CMP is contaminated with *Salmonella*.

Simulation settings and modifications. To run the simulations, Latin Hypercube sampling was used and 10^5 iterations were carried out. The random generator seed was fixed at 1. This fixed value was used because, providing the model is not changed, the same simulation results can be exactly repeated. More importantly, one or more distributions can be changed within the model and a

TABLE 2. *Characteristics of the normal distributions of the natural logarithm of level of* Salmonella *in chicken meat preparations*

Characteristic	Situations:			
	1 (actual)[a]	2	3	4
Mean (ln CFU/100 g)	−3.50	−3.50	−3.50	−3.50
Standard deviation (ln CFU/100 g)	6.65	3.48	2.50	2.10
99th percentile	1,580 CFU/g	1 CFU/g	1 CFU/10 g	1 CFU/25 g

[a] The current situation in Belgium.

second simulation can be run to determine whether these changes have an effect on the model's output. It is then certain that any observed change in the result is due to changes in the model and not a result of the randomness of the sampling *(41)*.

RESULTS

To determine the effect of lowering the numbers of *Salmonella* present in CMPs, different situations were simulated (Table 3). Situation 1 is the current situation in Belgium. To analyze the effect of reducing the high levels of *Salmonella* without affecting the mean concentration, situations 2 through 4 were simulated corresponding to a limitation (<1%) of the *Salmonella* contamination level of CMPs to >1 CFU/g, >1 CFU/10 g, and >1 CFU/25 g, respectively. The option was taken not to simulate an effect of complete absence per 1, 10, or 25 g because it was assumed that even if in microbiological criterion were imposed, differences in hygiene levels among food business operators would remain and some suppliers of CMPs would be unable to comply, thus bringing to the market a limited number (assumed <1%) of nonconforming CMPs.

The different outputs of the QMRA model for the current situation (situation 1) of *Salmonella* distribution in CMPs is shown in Table 4 for the various percentiles. The mean probability of illness is 1.26E−3, indicating that overall per 1,000 portions of CMPs consumed (assuming consumption after heat treatment), approximately one person becomes ill. It is clear that exposure to *Salmonella* (>1 cell per portion) and an increased probability of illness is limited to a small percentage of the population of CMP consumers: between the 98th (P_{98}) and 100th (P_{100}) percentiles. Although only a small percentage of the population of CMP consumers is affected, given the magnitude of the population (an estimated 90 million CMP portions consumed per year by inhabitants in Belgium), the small percentage reflects a significant number of exposures and risk for salmonellosis in Belgium.

Refrigeration temperature at retail is well maintained and controlled in Belgium (maximum recorded temperature was 8°C, which is below the growth model's 10°C minimum for *Salmonella* growth), as reflected in Table 4 as $N_{rCMP} = N_r$. Therefore, temperature abuse enabling *Salmonella* growth occurs only during transport and storage at the consumer's home.

Comparison of the probability (P) and numbers of cells (N) introduced because of cross-contamination (cc) and undercooking (cu) for these higher percentiles (P_{95} through $P_{99.5}$, Table 4) indicates that although the probability of undercooking (13 to 14%) is lower than the probability of cross-contamination (20 to 22%), the number of *Salmonella* cells remaining after preparation due to undercooking (ca. 100 to 1,000 cells) is higher than the number introduced due to cross-contamination (ca. 1 to 5 cells). Kusumaningrum et al. *(23)* found that the probability of *Campylobacter* cross-contamination was higher than that for *Salmonella* because both the prevalence and levels of *Campylobacter* spp. on chicken carcasses are higher than those of *Salmonella*.

Using the QMRA model described in Figure 1 and Table 1, the relative impact of reducing the levels of *Salmonella* present at retail in CMPs and the accompanying risk reduction for salmonellosis was studied. Table 5 provides the mean values of the various outputs in the QMRA model for the current situation and the scenario analysis simulating a *Salmonella* distribution in which the distribution of the contamination level is controlled to restrict the higher numbers of *Salmonella*: situation 2, <1 CFU/g; situation 3, <1 CFU/10 g; and situation 4, <1 CFU/25 g. The cumulative probability of the number of

TABLE 3. *Percentage of raw poultry–based meat preparations (CMP) contaminated with* Salmonella *above a certain level for the different tested situations (Sit)*

Salmonella level (CFU/100 g)	% contaminated CMPs			
	Sit 1 (actual)[a]	Sit 2	Sit 3	Sit 4
1.00E−08	98.75	100.00	100.00	100.00
1.00E−07	97.10	99.99	100.00	100.00
1.00E−06	93.94	99.85	100.00	100.00
1.00E−05	88.57	98.92	99.93	99.99
1.00E−04	80.45	94.93	98.89	99.67
1.00E−03	69.56	83.58	91.39	94.75
1.00E−02	56.59	62.42	67.09	70.03
1.00E−01	42.85	36.54	31.54	28.41
1.00E−00	29.94	15.75	8.02	4.78
1.00E+01	19.15	4.79	1.00	0.29
1.00E+02	11.15	1.00	0.06	0.1
1.00E+03	5.89	0.14	0.00	0
1.00E+04	2.80	0.01	0.00	0.00
1.00E+05	1.20	0.00	0.00	0.00
1.00E+06	0.46	0.00	0.00	0.00
1.00E+07	0.16	0.00	0.00	0.00
1.00E+08	0.05	0.00	0.00	0.00
1.00E+09	0.01	0.00	0.00	0.00
1.00E+10	0.00	0.00	0.00	0.00
1.00E+11	0.00	0.00	0.00	0.00
1.00E+12	0.00	0.00	0.00	0.00

[a] The current situation in Belgium.

Salmonella cells consumed per person is shown in Figure 2. The probability of illness for different distributions of *Salmonella* in CMPs is shown in Figure 3. Controlling the maximum level of *Salmonella* contamination significantly reduces the mean probability of illness to 1.66E−4 for situation 2, 8.65E−5 for situation 3, and 7.06E−5 for situation 4, corresponding to a reduction of risk by a factor 7.58, 14.56, and 17.84, respectively, compared with the current situation 1. The important risk reduction from situation 1 to situation 2 can be explained by the fact that the 99th percentile of the distribution of *Salmonella* concentration in CMP drops from 1,580 CFU/g for situation 1 to 1 CFU/g for situation 2 (1,000-fold reduction) (Table 2), whereas between situations 2 and 3 and situations 3 and 4 the reductions of the higher contamination level (99th percentile) are less drastic (10-fold and 2.5-fold, respectively). As a consequence, in this scenario analysis the reduction of mean probability of illness by further reducing the contamination levels from <1 CFU/10 g (situation 3) to <1 CFU/25 g (situation 4) is small. Because exposure to the higher numbers of *Salmonella* (and corresponding a high probability of illness) is limited to a small percentage of the population of CMP consumers (between 98th and 100th percentile), it was expected that the impact of a distribution with reduction of higher contamination levels would have the highest impact on the exposure (Fig. 2) and corresponding reduction of the risk (Fig. 3) noted for the highest percentiles (P_{95} to P_{100}). The highest levels of contamination, albeit with a low prevalence, are usually those determining the majority of cases.

The present QMRA model is based on data that were available in Belgium and in published national and international reports; however, the data on the local situation in Belgium and on this particular product (CMPs) were rather scarce. Data on the concentration of *Salmonella* in CMPs was semiquantitative; only presence-absence testing of three sample sizes was performed. As a consequence, only three data points were available to fit the normal distribution. As an alternative theoretical approach, the QMRA model of *Salmonella* in CMPs was run with various fixed inputs of *Salmonella,* i.e., assuming all portions possessed a contamination level of 1,000 CFU/g, 100 CFU/g, 10 CFU/g, 1 CFU/g, 1 CFU/10 g, 1 CFU/25 g, 1 CFU/100 g, or 1 CFU/1,000 g. Table 6 shows the different percentiles of the number of consumed cells for the different fixed inputs. When the concentration of *Salmonella* in the CMP decreases, the percentage of the population exposed to one or more cells also decreases. The mean probability of the different outputs in the QMRA model for the different fixed outputs are shown in Table 7. These results show a similar change in the number of cells along the food chain considered in this study.

The mean probability of illness and the 99th and 99.9th percentiles of the probability of illness (P_{99} and $P_{99.9}$) for the various fixed levels of *Salmonella* in CMPs are shown in Figure 4. These probabilities of illness should not in any way be used as the basis for an absolute risk estimate of the national population because the input is not a distribution but only a theoretical fixed value allocated to all portions at the time of production and release to retail markets. The

TABLE 4. *Statistics of the outputs of the different modules of the model for the current situation in Belgium (situation 1)*[a]

Percentile	N_{rCMP}	N_r	N_f	N_c	N_{cc}	P_{cc}	N_{cu}	P_{cu}	N_{cons}	P_{cons}	P_{ill}
10	5.97E−06	5.97E−06	6.48E−06	7.85E−06	0.00E+00	1.09E−01	0.00E+00	7.47E−02	0.00E+00	1.93E−01	0.00E+00
25	3.39E−04	3.39E−04	3.69E−04	4.57E−04	0.00E+00	1.26E−01	0.00E+00	8.59E−02	0.00E+00	2.11E−01	0.00E+00
50	3.01E−02	3.01E−02	3.27E−02	4.32E−02	0.00E+00	1.47E−01	0.00E+00	1.00E−01	0.00E+00	2.33E−01	0.00E+00
75	2.68E+00	2.68E+00	2.93E+00	4.16E+00	3.00E−08	1.70E−01	0.00E+00	1.14E−01	4.15E−08	2.56E−01	2.48E−11
90	1.52E+02	1.52E+02	1.67E+02	2.73E+02	3.30E−05	1.89E−01	0.00E+00	1.25E−01	5.53E−05	2.75E−01	3.43E−08
95	1.71E+03	1.71E+03	1.86E+03	3.52E+03	1.12E−03	2.00E−01	0.00E+00	1.31E−01	3.13E−03	2.86E−01	1.82E−06
97	8.20E+03	8.20E+03	8.89E+03	1.88E+04	**9.26E−03**	**2.06E−01**	**0.00E+00**	**1.34E−01**	**6.93E−02**	2.92E−01	**4.23E−05**
98	2.59E+04	2.59E+04	2.85E+04	6.83E+04	**4.31E−02**	**2.09E−01**	**0.00E+00**	**1.36E−01**	**1.72E+00**	2.97E−01	**9.67E−04**
99	1.59E+05	1.59E+05	1.72E+05	5.45E+05	**4.91E−01**	**2.15E−01**	**1.12E+02**	**1.39E−01**	**2.22E+02**	3.04E−01	**4.66E−02**
99.5	8.36E+05	8.36E+05	8.85E+05	3.65E+06	**4.24E+00**	**2.20E−01**	**2.78E+03**	**1.42E−01**	**3.79E+03**	3.09E−01	**1.02E−01**
99.9	2.54E+07	2.54E+07	2.65E+07	4.19E+08	4.77E+02	2.27E−01	4.38E+05	1.45E−01	4.51E+05	3.20E−01	1.76E−01
99.95	9.59E+07	9.59E+07	1.08E+08	1.00E+09	2.84E+03	2.29E−01	2.35E+06	1.46E−01	2.35E+06	3.24E−01	1.93E−01
99.99	1.00E+09	1.00E+09	1.00E+09	1.00E+09	9.23E+04	2.32E−01	1.82E+08	1.48E−01	1.82E+08	3.30E−01	2.21E−01
Mean	2.95E+05	2.95E+05	3.08E+05	1.15E+06	3.45E+01	1.49E−01	9.79E+04	1.00E−01	9.79E+04	2.34E−01	1.26E−03
SD[b]	1.37E+07	1.37E+07	1.40E+07	3.04E+07	3.06E+03	2.99E−02	8.79E+06	1.89E−02	8.79E+06	3.14E−02	1.20E−02

[a] Each parameter is explained in Table 1. Bold values indicate the contribution of cross-contamination versus undercooking on number of *Salmonella* cells consumed and the probability of illness.
[b] SD, standard deviation.

TABLE 5. *Mean values of the different outputs of the model for the different simulated situations (2, 3, and 4) related to the current situation (1)*[a]

Situation	N_{rCMP}	N_r	N_f	N_c	N_{cc}	P_{cc}	N_{cu}	P_{cu}	N_{cons}	P_{cons}	P_{ill}
1	2.95E+05	2.95E+05	3.08E+05	1.15E+06	3.45E+01	1.49E−01	9.79E+04	1.00E−01	9.79E+04	2.34E−01	1.26E−03
2	1.16E+01	1.16E+01	1.25E+01	3.58E+05	9.05E+00	8.88E−02	4.23E+03	1.00E−01	4.24E+03	1.80E−01	1.66E−04
3	6.69E−01	6.69E−01	7.29E−01	3.43E+05	7.73E+00	5.23E−02	3.27E+03	1.00E−01	3.28E+03	1.47E−01	8.65E−05
4	2.73E−01	2.73E−01	2.98E−01	3.29E+05	7.53E+00	3.75E−02	3.12E+03	1.00E−01	3.13E+03	1.34E−01	7.06E−05

[a] Each parameter is explained in Table 1.

probabilities of illness noted in Figure 4 are high (0.001 to 1) because all portions are assumed to be contaminated, whereas in a real-life situation there is a distribution of contamination levels in which the majority of samples are *Salmonella* free (<1 CFU per each 100-g portion) and only a small number of portions carry *Salmonella* at various levels. From Figure 4, a gradual decrease in the mean probability of illness was noted upon reduction of the levels of *Salmonella* in the scenario analysis with fixed values. A turnover in the trend for stepwise enhanced decrease in the mean probability of illness can be noted at the fixed value of ca. 1 CFU/g. The $P_{99.9}$ value indicates that a small percentage of the population of CMP consumers, regardless of the *Salmonella* levels initially present, will constitutively be exposed to a high risk of salmonellosis. This constitutively high probability of illness for a small percentage of the population of CMP consumers can probably be explained by the fact that even if very low levels of *Salmonella* are present (e.g., 1 CFU/100 g) (parameters in the mathematical QMRA model are all situated at the tails of the distributions noted in Table 1) these few cells may multiply to higher numbers due to temperature abuse. Combined with potential for cross-contamination and undercooking, these initial low levels can lead to exposure to high levels of *Salmonella* and subsequent high probability of illness. Although only a small percentage of the population of CMP consumers is implicated in this exposure ($P_{99.9}$ to P_{100} percentile), this restricted number of cases contribute to the overall mean probability of illness, which is probably why the mean probability of illness reduces only gradually and to a very limited extent even when the *Salmonella* contamination is low (<1 CFU/g). In contrast, the probability of illness for the majority of the population of CMP consumers (P_{99} percentile) significantly decreases when the contamination level drops below 1 CFU/g (Fig. 4).

DISCUSSION

Several QMRA studies related to *Salmonella* in meat and poultry are available *(24)*. Some have included an examination of the entire production-to-consumption food chain *(32, 35),* whereas others have covered in detail only those stages closest to the point of consumption *(4, 19)*. Some studies involved only the case study of *Salmonella* in meat for development and comparison of modeling approaches for risk assessment *(30, 36)*. The focus of many QMRA studies was directed to *Salmonella* in broiler chickens *(27)* and eggs *(25, 29)* and in live pigs and pork *(37)*. To our knowledge, this is the first QMRA for *Salmonella* in CMPs.

The current QMRA study is based upon a limited data set from the current situation of *Salmonella* in CMPs with a mean probability of illness of 1.28E−3 and with 90 million CMPs consumed, which would result in an annual 115,000 illnesses. If these numbers were correct, epidemiological links probably would have been established. The lack of reported links indicates that the burden of salmonellosis due to CMP was overestimated in the present study, possibly

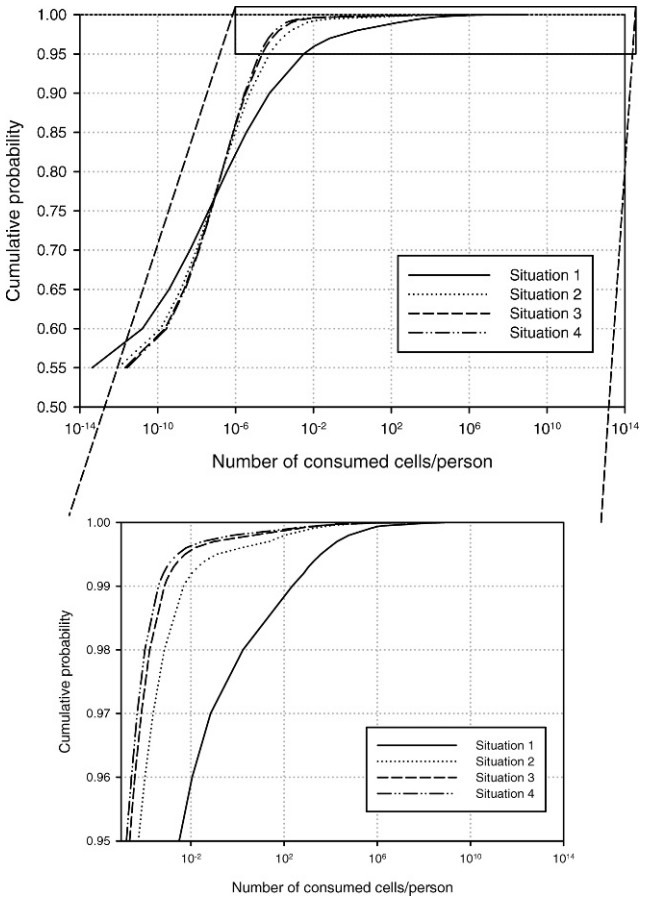

FIGURE 2. *Cumulative probability of the number of* Salmonella *cells that are consumed per person in chicken meat preparations with different levels of* Salmonella.

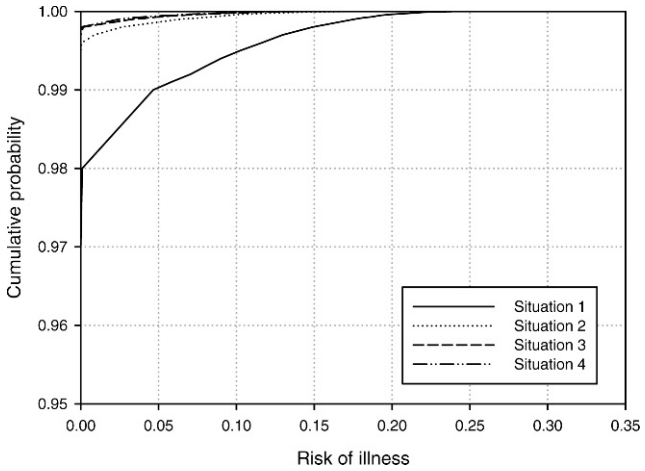

FIGURE 3. *Probability of illness based on different levels of* Salmonella *in chicken meat preparations.*

because of several assumptions that have been made. For example, the focus was placed on CMPs made with minced meat, whereas CMPs also can include portioned meat (with or without skin) *(21)* where *Salmonella* is present at the surface of the meat and thus undercooking becomes less important as a risk factor. The simple approach to modeling temperature transfer and growth (not taking into account the lag phase of *Salmonella*) also may result in an overestimate of the risks. Accurate risk assessment requires the input of appropriate data. In this retail-to-table approach, quantitative data on *Salmonella* contamination levels were lacking. Because of the low prevalence and often heterogeneous distribution of *Salmonella* in the food and when present the often low contamination levels, it is a challenge to develop a representative sampling plan and detection methodology. Recently, *Salmonella* was enumerated on chicken breast fillets using a combination of prior enrichment of pooled samples and subsequent enumeration of *Salmonella* in positive samples using a most-probable-number assay *(39)*. Appropriate planning and resources allocation is essential for accurate modeling.

Another difficulty in the present QMRA is the lack of information available for the Belgian situation with regard to module 5 on consumer handling (including undercooking and cross-contamination). Therefore, module 5 was based on the FAO-WHO study on *Salmonella* in broiler chickens and eggs *(16)*. However, the present study deals with *Salmonella* in CMPs, which may be subjected to other types of mishandling.

The lack of data to establish a risk assessment for other hazards in other foods also has been reported by others *(1, 4, 12, 22, 26, 33, 35)*. This issue is one of the most important problems associated with quantitative risk assessment because predictions of quantitative risk are only as good as the data used to develop and define them *(35)*.

The uncertainty associated with the outcome of the present QMRA due to the lack of adequate data and assumptions may detract from its usefulness for food safety management. However, although the risk estimate in the present study is highly uncertain (and most probably an overestimate), more important than an absolute measure of risk is the relative change in the magnitude of risk outcomes resulting from changing some parameters in the QMRA model *(24)*. This type of scenario analysis was applied in the current study comparing in a relative manner the risk associated with various input distributions of *Salmonella* contamination in CMPs. By narrowing the standard deviation of the current distribution, it becomes apparent that especially the higher levels of contamination contribute to the increased risk for salmonellosis. This finding was confirmed by Straver et al. *(39),* who used process risk modeling to determine that more than two-thirds of annual predicted salmonellosis cases due to chicken breasts were caused by the small fraction of fillets containing more than 3 log CFU at retail (0.8% of fillets).

The QMRA model with a fixed input also revealed that especially the higher levels of contamination contribute to the increased risk for salmonellosis. The probability of illness for the majority of the population of CMP consumers (99th percentile) dropped drastically for fixed levels of contamination below 1 CFU/g. Nevertheless, a high probability of illness remained for a small proportion of the population of CMP consumers. This finding also was confirmed by Straver et al. *(39),* who found that a low contamination level (1 to 10 CFU per portion of chicken breast fillet) accounts for a small percentage of illnesses (1 to 2%). Thus, reduction of the higher levels of contamina-

TABLE 6. *Number of* Salmonella *cells consumed for different fixed inputs of contamination level*[a]

	Salmonella contamination levels:											
Percentile	10^7 CFU/g	10^6 CFU/g	10^5 CFU/g	10^4 CFU/g	10^3 CFU/g	10^2 CFU/g	10 CFU/g	1 CFU/g	1 CFU/10 g	1 CFU/25 g	1 CFU/100 g	1 CFU/1,000 g
25	0	0	0	0	0	0	0	0	0	0	0	0
50	2.46E−01	3.06E−02	3.12E−03	3.12E−04	3.12E−05	3.12E−06	2.32E−07	0	0	0	0	0
75	**1.05E+04**	**1.36E+03**	**1.45E+02**	**1.49E+01**	**1.50E+00**	1.51E−01	1.42E−02	7.73E−04	2.73E−05	9.34E−06	2.24E−06	2.19E−07
90	**1.01E+06**	**1.92E+05**	**7.82E+04**	**2.32E+04**	**5.51E+03**	**8.36E+02**	**9.59E+00**	4.10E−02	9.35E−04	3.12E−04	7.50E−05	7.32E−06
95	**1.00E+09**	**1.06E+08**	**1.06E+07**	**1.06E+06**	**1.06E+05**	**1.05E+04**	**9.88E+02**	**5.64E+01**	3.88E−03	1.22E−03	2.90E−04	2.82E−05
99	**1.00E+09**	**1.60E+08**	**1.60E+07**	**1.60E+06**	**1.67E+05**	**1.74E+04**	**1.71E+03**	**1.32E+02**	**4.21E+00**	4.23E−02	4.12E−03	2.54E−04
99.5	**1.00E+09**	**7.63E+08**	**7.63E+07**	**7.63E+06**	**8.06E+05**	**9.57E+04**	**1.12E+04**	**1.11E+03**	**6.49E+01**	**1.44E+01**	3.12E−01	5.07E−03
99.9	**1.00E+09**	**1.00E+09**	**1.00E+09**	**1.00E+09**	**2.55E+08**	**2.55E+07**	**2.55E+06**	**3.30E+05**	**4.37E+04**	**1.79E+04**	**4.54E+03**	**4.54E+02**
Mean	9.74E+07	1.61E+07	4.24E+06	1.80E+06	9.51E+05	5.29E+05	2.89E+05	1.55E+05	9.01E+04	6.71E+04	4.39E+04	3.14E+04

[a] Values are given as CFU per 100 g. Bold values indicate numbers of *Salmonella* cells consumed with increased probability to cause illness.

TABLE 7. *Mean value of the different outputs of the model for the different fixed inputs of contamination level*[a]

Salmonella contamination level	N_{rCMP}	N_r	N_t	N_c	N_{cc}	P_{cc}	N_{cu}	P_{cu}	N_{cons}	P_{cons}	P_{ill}
10^7 CFU/g	1.00E+09	1.00E+09	1.00E+09	1.00E+09	2.98E+04	4.75E−01	9.74E+07	1.00E−01	9.74E+07	5.27E−01	1.30E−01
10^6 CFU/g	1.00E+08	1.00E+08	1.09E+08	1.66E+08	4.98E+03	4.75E−01	1.61E+07	1.00E−01	1.61E+07	5.27E−01	1.03E−01
10^5 CFU/g	1.00E+07	1.00E+07	1.09E+07	4.42E+07	1.35E+03	4.75E−01	4.24E+06	1.00E−01	4.24E+06	5.27E−01	7.52E−02
10^4 CFU/g	1.00E+06	1.00E+06	1.09E+06	1.85E+07	6.13E+02	4.75E−01	1.80E+06	1.00E−01	1.80E+06	5.27E−01	5.33E−02
10^3 CFU/g	1.00E+05	1.00E+05	1.09E+05	9.28E+06	3.18E+02	4.75E−01	9.51E+05	1.00E−01	9.51E+05	5.27E−01	3.88E−02
10^2 CFU/g	1.00E+04	1.00E+04	1.09E+04	5.01E+06	1.80E+02	4.75E−01	5.28E+05	1.00E−01	5.29E+05	5.27E−01	2.89E−02
10 CFU/g	1.00E+03	1.00E+03	1.09E+03	2.65E+06	9.21E+01	4.75E−01	2.89E+05	1.00E−01	2.89E+05	5.27E−01	1.80E−02
1 CFU/g	1.00E+02	1.00E+02	1.09E+02	1.52E+06	4.96E+01	4.75E−01	1.55E+05	1.00E−01	1.55E+05	5.27E−01	5.21E−03
1 CFU/10 g	1.00E+01	1.00E+01	1.09E+01	9.05E+05	3.26E+01	4.75E−01	9.01E+04	1.00E−01	9.01E+04	5.27E−01	1.14E−03
1 CFU/25 g	4.00E+00	4.00E+00	4.38E+00	7.42E+05	2.88E+01	4.75E−01	6.70E+04	1.00E−01	6.71E+04	5.27E−01	8.59E−04
1 CFU/100 g	1.00E+00	1.00E+00	1.09E+00	5.49E+05	1.68E+01	4.75E−01	4.39E+04	1.00E−01	4.39E+04	5.27E−01	5.89E−04
1 CFU/1,000 g	1.00E−01	1.00E−01	1.09E−01	3.88E+05	5.64E+00	4.75E−01	3.14E+04	1.00E−01	3.14E+04	5.27E−01	3.28E−04

[a] Each parameter is explained in Table 1.

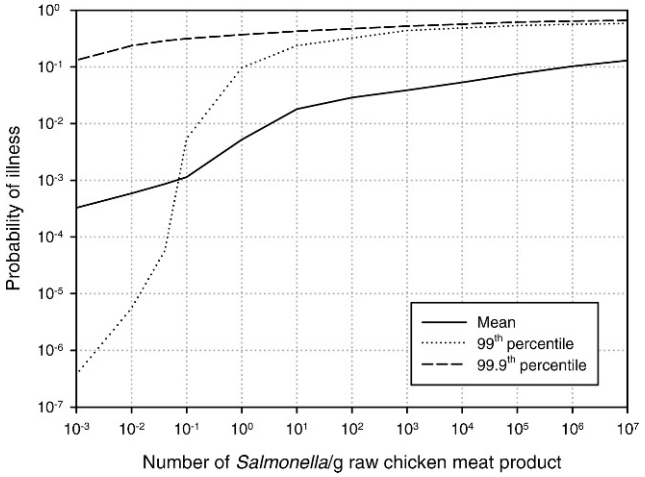

FIGURE 4. *Probability of illness for different fixed levels of* Salmonella *in chicken meat preparations.*

tion of *Salmonella,* for example by imposing strict criteria, will not eliminate all cases of salmonellosis. A zero risk for salmonellosis will not be obtained.

This QMRA of *Salmonella* in CMPs indicated, both by narrowing the standard deviation of the current distribution and using the fixed input, that especially the higher levels of contamination (>1 CFU/g) contribute to the increased risk for salmonellosis. The setting of a microbiological criterion, however, must take into account more than a maximum acceptable (or tolerable) level at a specified step in the food chain (performance objective) that may be derived from a QMRA *(20, 42).* A microbiological criterion includes the definition of a sampling plan with a confidence level for lot rejection and the selection of a detection method with appropriate sensitivity. Risk analysis sets the appropriate framework to communicate in a professional and open way about decisions made by the national authorities on food safety measures (including setting of criteria), and this scientific approach should lead to better understanding by the stakeholders and greater dedication to efforts to meet the criteria.

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