Increased antimicrobial resistance (AMR), or antibiotic resistance, has resulted in initiatives to reduce the use of antibiotics in food production animals (1,2), but quantification of the public health effects of decreasing antibiotic use in livestock remains limited (3,4). Reduction of antibiotic use in livestock can lower resistance prevalence (i.e., proportion of pathogens with resistance) in animals (4), but some studies show that pathogen prevalence may be higher in livestock raised without antibiotics (5). Because transmission of foodborne pathogens is proportional to the prevalence of pathogens in the food source (6), quantifying the change in human antibiotic-resistant foodborne illnesses resulting from reduced antibiotic use in livestock is vital.

In the United States, the most common bacterial cause of foodborne illness is nontyphoidal Salmonella (NTS), which leads to >1 million foodborne illnesses and 20,000 hospitalizations per year (7). Antibiotic-resistant NTS is among the top 18 AMR threats in the United States (8), causing 100,000 infections annually. The Centers for Disease Control and Prevention National Antimicrobial Resistance Monitoring System (NARMS) tracks resistance to 25 antibiotics in patient samples positive for isolates such as NTS (9), including the clinically relevant antibiotics ciprofloxacin and ceftriaxone.

Multiple assessments of human AMR risk from meats have been performed (10–14). However, most focused on only 1 class of antibiotic (10,11), had limited or no longitudinal data (14), or were not based on nationwide surveillance at the animal source (11). Quantitative assessments of AMR risk with a more comprehensive resistance definition (15), such as resistance to any class, or to ≥3 classes, that use representative, longitudinal data, are critical to defining the risks and benefits from policy with regard to antibiotic use in livestock (3). Surveillance studies of antibiotic use and AMR in humans and livestock can be used to generate estimates of risk based on empirical data and can show the results of long-term conditions or systematic changes over time.

Our objective with this study was to use beef as a model to quantify trends in the longitudinal relationship between human NTS infections and antibiotic-resistant NTS in meats. We also used the estimates to predict change in antibiotic-resistant salmonellosis resulting from hypothetical scenarios of antibiotic restriction in beef cattle.

Methods
We developed a stochastic model to quantify the risk for antibiotic-resistant nontyphoidal salmonellosis
per meal made with beef during 2002–2010. Our model follows the method of previously published AMR risk assessments (6,16) but uniquely addresses temporal changes and relies solely on nationwide surveillance data (Appendix Table 1, https://wwwnc.cdc.gov/EID/article/26/9/19-0922-App1.pdf). We used this model for 3 objectives: 1) estimate the risk for antibiotic-resistant nontyphoidal salmonellosis per meal made with beef, using the yearly cases of illnesses (ill_res) and the number of meals made with beef that year (Meal_res) (Figure 1); 2) evaluate change over time in all model outcomes; and 3) assess the effect that potential future restrictions on antibiotic use in beef cattle would have on antibiotic-resistant nontyphoidal salmonellosis disease burden (Appendix).

Risk for Antibiotic-Resistant Nontyphoidal Salmonellosis Attributable to Beef

Annual Incidence of Beef-Attributable Antibiotic-Resistant Nontyphoidal Salmonellosis (ill_res Incidence) per 100,000 Persons

We obtained the annual total nontyphoidal salmonellosis cases in the United States for 1998–2015 from FoodNet (https://www.cdc.gov/foodnet), an active foodborne disease surveillance system, after adjusting for the proportion of the US population included in FoodNet surveillance sites. To correct for under-diagnosis and restrict case estimates to domestically acquired foodborne cases, we also included adjustment factors constant for the study period. By using annual food attribution estimates derived from the National Outbreak Reporting System (NORS; https://www.cdc.gov/nors/index.html), cases of nontyphoidal salmonellosis were further restricted to foodborne cases attributed to ground beef and intact beef. To ensure that the resistance fraction is specific to nontyphoidal salmonellosis attributed to consumption of beef, we estimated the fraction of beef-attributed nontyphoidal salmonellosis cases with AMR by matching cases in the Centers for Disease Control and Prevention data collected from clinical patient samples as part of NARMS (17) with beef-attributable outbreak data from NORS by using sample metadata, (Appendix Table 1). We calculated incidence of ill_res by using the population of the United States in the relevant year.

Annual Meals Prepared with Beef Initially Contaminated with Antibiotic-Resistant NTS (Meals_res)

We calculated the number of beef meals consumed annually in the United States by using beef disappearance data from the US Department of Agriculture (USDA) (18) and the mean grams of beef consumed per beef meal from the National Health and Nutrition Examination Survey (19). We estimated the prevalence of NTS in beef by using USDA Food Safety and Inspection Service surveillance data, and we derived the fraction of isolates with AMR from USDA NARMS and US Food and Drug Administration NARMS data (9). Meals_res were stratified by beef cut (ground beef data for 2002–2015 vs. intact beef for 1998–2010). By using Meals_res, we assumed that the beef used to prepare a meal was initially contaminated (as measured at the slaughter plant or retail) with the pathogen. This assumption does not necessarily mean that the actual meal consumed was contaminated because safe cooking and handling practices would reduce or completely inactivate the bacterial load.

Risk for Antibiotic-Resistant Nontyphoidal Salmonellosis per Beef Meal

Dividing ill_res by Meals_res resulted in the probability of antibiotic-resistant nontyphoidal salmonellosis per meal made with beef initially contaminated with antibiotic-resistant NTS (P_meal). Also, by using all meals in the denominator, we calculated the probability of antibiotic-resistant nontyphoidal salmonellosis per meal made with beef, regardless of contamination status (P_meal) (Figure 1). We report both risk outcomes per 1 million meals, on a per-year basis (P_meal and P_meal) and as the mean of each for all years combined (P_meal,overall and P_meal,overall). We repeated the analyses for NTS with multidrug resistance (NTS_MDR) (i.e., resistance to ≥3 antimicrobial classes) and for clinically relevant resistance (NTS_CRR), also known as resistance of concern (i.e., resistance to ≥5 drugs or quinolones [ciprofloxacin] or third-generation cephalosporins [ceftriaxone]) (8).

Testing for Temporal Changes

To identify the confidence of a consistent increase (or decrease) in each outcome over the study period, we used Mann-Kendall trend test bootstrapping (20). In addition, we used numerical integration to compute the confidence in pairwise year-to-year Bayesian posterior differences (21) and the difference between the mean of each outcome in the last years of the study period versus the remaining previous years. Unlike the Mann-Kendall tests, the year-to-year test identified short-term changes, and the comparison of the first versus the last 5 years of the study period provided an assessment of nonlinear changes during the study period.
Scenario Analysis: Effects of Hypothetical Antibiotic Restriction in Beef Production

Relationship between Antibiotic Use and Antibiotic-Resistant NTS in Beef
To model the relationship between antibiotic use and antibiotic-resistant NTS, we used nationwide data (C.P. Fossler, USDA, pers. comm., 2018 Jul 16) from the National Animal Health Monitoring System feedlot survey (22). The feedlot survey is based on a nationwide representative sample of farms and thus captures the effect of long-term and current antibiotic practices on AMR. In the survey, individual fecal pats from raised-without-antibiotics cattle and conventionally raised cattle were collected to estimate the prevalence of NTS isolates and the fraction of these with AMR. These 2 parameters were combined to measure the overall prevalence of antibiotic-resistant NTS in raised-without-antibiotics cattle and conventionally raised cattle and to derive the relative risk (RR) of antibiotic-resistant NTS prevalence in raised-without-antibiotics versus conventionally raised cattle.

Prediction of Changes in Beef-Attributable Antibiotic-Resistant Nontyphoidal Salmonellosis
We constructed 2 scenarios to evaluate \( Ill_{rots} \) changes from hypothetical antibiotic restriction in beef production. We assumed no changes in slaughtering, processing, consumer habits, and food preparation.

For scenario 1, we estimated the change in antibiotic-resistant nontyphoidal salmonellosis if all beef production were switched to raised-without-antibiotics by using the annual estimated \( Ill_{rots} \) for 2002–2010 and the RR of antibiotic-resistant NTS prevalence in raised-without-antibiotics versus conventionally raised cattle. By doing so, we assumed that the animal-level prevalence of antibiotic-resistant NTS is proportional (but not equal to) its prevalence in meals prepared with beef and that RR has a direct linear effect on the change in \( Ill_{rots} \). This relationship is documented for food pathogens (6,23), including NTS (24), so here we assumed that it extends to antibiotic-resistant isolates.

To relax this assumption, for scenario 2, we empirically estimated the relationship between antibiotic-resistant NTS prevalence in beef and \( Ill_{rots} \) via Poisson

---

**Figure 1.** Conceptual model and data sources for calculation of risk for beef-attributable antibiotic-resistant nontyphoidal salmonellosis per 1 million beef meals (\( P_{rot} \)) for study of risk for antimicrobial-resistant salmonellosis from beef, United States, 2002–2010. NTS, nontyphoidal *Salmonella*; NTS\(_{rots}\), antibiotic-resistant NTS.
regression and used the Poisson regression to create an adjustment factor to the calculations done for scenario 1. For each scenario, we reported the posterior confidence in the change in being <0 (i.e., reduction of antibiotic-resistant nontyphoidal salmonellosis) for each year of the study and for all years combined.

**Model Implementation**

We used R version 3.4.1 (https://www.R-project.org) to perform all analyses. We used Monte Carlo simulation to calculate the posterior uncertainty in all outcomes. Statistical significance was assessed at the 95% confidence level. We performed a sensitivity analysis of the key drivers of and by calculating the effect that extreme values of each input had on the output means (Appendix).

**Results**

**Descriptive Statistics of Main Parameters and Risk Measures**

During 2002–2010, approximately 554 billion beef meals were consumed, 59% as ground beef. Of these meals, 4% came from beef at slaughter or retail with NTS, half of which were antibiotic-resistant (11.23 billion, 95% CrI 9.08–13.54 billion). Approximately 93% of meals with beef initially contaminated with antibiotic-resistant NTS were made with ground beef (10.4 billion meals, 95% CrI 8.3–12.73 billion) (Figure 2), resulting from higher prevalence of both NTS and antibiotic-resistant NTS in ground than intact beef (Table 1). Yet, the attribution of nontyphoidal salmonellosis, regardless of antibiotic resistance, was relatively even between ground and intact beef (Figure 2). The total incidence of was 0.64 (0.0036–2.75)/100,000 persons.

During 2002–2010, the mean risk for antibiotic-resistant nontyphoidal salmonellosis was 0.031 cases (95% CrI 0.0018–0.14)/1 million beef meals; intact and ground beef contributed equally to the rate (Table 1; Figure 2). The risk per million beef meals initially contaminated with NTS was 1.8 (95% CrI 0.007–8.5) overall, 1.16 (95% CrI 0.0015–5.2) for ground beef and 9.5 (95% CrI 0.03–50) for intact beef (Figure 2). The higher for intact beef possibly indicates a higher risk from consumption of intact beef carrying antibiotic-resistant NTS.

**Tests for Temporal Changes in Main Parameters and Risk Measures**

None of the tested parameters or outcomes based on a resistance definition of >1 antibiotic (i.e., or or per 100,000 population [Figure 2], or or [Figure 3]) showed a sustained change (Table 2). We also observed no change when we used multidrug resistance (MDR) and clinically relevant resistance (CRR) as the definition of resistance (Table 2; Appendix Figures 5–8), except that meals made with ground beef contaminated with NTS CRR declined during 2002–2015. More differences based on the last 5 years of the study period were found. The risk for NTS MDR per 1 million meals made with ground beef initially contaminated with NTS MDR increased during 2010–2015, while the number of these meals made with NTS MDR-contaminated ground
Table 1. Calculations of beef consumption, NTS, and risk for antimicrobial-resistant salmonellosis from beef, United States*

<table>
<thead>
<tr>
<th>Input</th>
<th>2002–2010†</th>
<th>Any years with data</th>
</tr>
</thead>
<tbody>
<tr>
<td>Meals prepared with beef</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>554B (527B–581B)</td>
<td>554B (527B–581B)</td>
</tr>
<tr>
<td>Ground</td>
<td>326B (306B–345B)</td>
<td>497B (473B–521B)</td>
</tr>
<tr>
<td>Intact</td>
<td>228B (219B–238B)</td>
<td>329B (319B–339B)</td>
</tr>
<tr>
<td>Meals prepared with beef carrying NTS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>24.9B (22.5B–27.0B)</td>
<td>24.9B (22.5B–27.0B)</td>
</tr>
<tr>
<td>Ground</td>
<td>22.5B (20.3B–24.9B)</td>
<td>36.3B (31.1B–42.7B)</td>
</tr>
<tr>
<td>Intact</td>
<td>2.4B (2.1B–2.7B)</td>
<td>4.2B (3.7B–4.6B)</td>
</tr>
<tr>
<td>Meals prepared with beef carrying NTS&lt;sub&gt;r&lt;/sub&gt; (Meal&lt;sub&gt;raw&lt;/sub&gt;)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>11.2B (9.08B–13.54B)</td>
<td>11.2B (9.08B–13.54B)</td>
</tr>
<tr>
<td>Ground</td>
<td>10.4B (8.3B–12.71B)</td>
<td>16.22B (12.69B–20.90B)</td>
</tr>
<tr>
<td>Intact</td>
<td>811M (708M–925M)</td>
<td>1.30B (1.16B–1.46B)</td>
</tr>
<tr>
<td>Nontyphoidal salmonellosis attributable to beef, no. cases/100,000 US population</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>15.10 (0.096–44.44)</td>
<td>15.10 (0.096–44.44)</td>
</tr>
<tr>
<td>Ground</td>
<td>8.27 (0.028–25.99)</td>
<td>8.99 (0.028–26.94)</td>
</tr>
<tr>
<td>Intact</td>
<td>6.83 (0.028–20.07)</td>
<td>6.75 (0.043–19.72)</td>
</tr>
<tr>
<td>ll&lt;sub&gt;raw&lt;/sub&gt;100,000 US population</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>0.64 (0.0036–2.75)</td>
<td>0.64 (0.0036–2.75)</td>
</tr>
<tr>
<td>Ground</td>
<td>0.39 (0.0007–1.54)</td>
<td>0.36 (0.0008–1.46)</td>
</tr>
<tr>
<td>Intact</td>
<td>0.25 (0.001–1.25)</td>
<td>0.31 (0.00084–1.54)</td>
</tr>
<tr>
<td>Nontyphoidal salmonellosis attributable to beef/1 million beef meals</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>0.74 (0.0046–2.20)</td>
<td>0.74 (0.0046–2.20)</td>
</tr>
<tr>
<td>Ground</td>
<td>0.70 (0.0022–2.25)</td>
<td>0.78 (0.0024–2.35)</td>
</tr>
<tr>
<td>Intact</td>
<td>0.81 (0.0034–2.38)</td>
<td>0.78 (0.0051–2.29)</td>
</tr>
<tr>
<td>Nontyphoidal salmonellosis attributable to beef/1 million NTS beef meals</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>17.1 (11.4–24.0)</td>
<td>17.1 (11.4–24.0)</td>
</tr>
<tr>
<td>Ground</td>
<td>10.2 (6.73–14.4)</td>
<td>12.9 (8.6–18.2)</td>
</tr>
<tr>
<td>Intact</td>
<td>82.1 (53.8–118.1)</td>
<td>70.4 (46.7–100)</td>
</tr>
<tr>
<td>P&lt;sub&gt;meal&lt;/sub&gt;</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>0.031 (0.00018–0.14)</td>
<td>0.031 (0.00018–0.14)</td>
</tr>
<tr>
<td>Ground</td>
<td>0.031(0.000056–0.13)</td>
<td>0.031 (0.000067–0.13)</td>
</tr>
<tr>
<td>Intact</td>
<td>0.032 (0.0001–0.15)</td>
<td>0.036 (0.00013–0.18)</td>
</tr>
<tr>
<td>P&lt;sub&gt;s&lt;/sub&gt;</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>1.78 (0.007–8.56)</td>
<td>1.78 (0.007–8.56)</td>
</tr>
<tr>
<td>Ground</td>
<td>1.15 (0.001–5.38)</td>
<td>1.25 (0.001–5.21)</td>
</tr>
<tr>
<td>Intact</td>
<td>9.10 (0.039–47.21)</td>
<td>9.48 (0.032–50.19)</td>
</tr>
</tbody>
</table>

*Years included are 2002–2015 for ground beef, 1998–2010 for intact beef, and 2002–2010 for total beef. Calculations include measures of exposure (meals prepared from beef with various states of microbiological contamination), disease incidence (no. illness cases/100,000 US population), and different measures of disease risk per meals consumed. B, billion; ll<sub>raw</sub>, antibiotic-resistant nontyphoidal salmonellosis attributable to beef; M, million; NTS, nontyphoidal Salmonella; NTS<sub>r</sub>, antibiotic-resistant NTS; P<sub>meal</sub>, antibiotic-resistant nontyphoidal salmonellosis/1 million beef meals; P<sub>s</sub>, antibiotic-resistant nontyphoidal salmonellosis/1 million NTS<sub>r</sub> beef meals.

†Years 2002–2010 summary statistics reflect the data used to create the combined totals.

beef decreased (Table 2). In contrast, for CRR, the beef-attributable risk for CRR nontyphoidal salmonellosis was significantly lower for all beef meals initially contaminated—and ground beef specifically—in the last 5 years of data, as were both the incidence of CRR nontyphoidal salmonellosis and its risk per 1 million beef meals, overall and for intact beef (Table 2).

We found some year-to-year variations in ll<sub>ref</sub>, P<sub>ref</sub>, and P<sub>meal</sub> but generally no yearly changes in meals made with beef initially contaminated with antibiotic-resistant NTS (Meal<sub>raw</sub>). For all beef and for ground beef and intact beef individually, defining resistance as resistance to ≥1 antibiotic, ll<sub>ref</sub>, P<sub>ref</sub>, and P<sub>meal</sub> were higher in 2003 and 2009 and a peak for ground beef also occurred in 2014. Meals<sub>raw</sub> showed no significant year-to-year changes for all beef cuts combined. Intact beef Meals<sub>raw</sub> had 1 peak in 2001 (100% confidence). When MDR and CRR were used as the resistance definition, only the peaks in 2003 and in 2014 remained significant. A peak in some intact beef risks and illnesses was also observed in 2000 (Table 2).

Scenario Analysis of Changes in Antibiotic-Resistant Nontyphoidal Salmonellosis Resulting from Antibiotic Restriction in Beef Production

In the first scenario analysis, we found no significant changes (≤94.3% confidence) in antibiotic-resistant salmonellosis for any year when switching from current antibiotic practices to hypothetical 100% raised-without-antibiotics production. The mean change in the number of antibiotic-resistant nontyphoidal salmonellosis cases across the study period was −5,218 (Figure 4), ranging from an additional 1,441 resistant...
nontyphoidal salmonellosis cases to a reduction of 14,350 cases.

The second scenario (Figure 4), in which the direct linear assumption was relaxed, predicted significant decreases (>98% confidence) in cases for 2003 (–5,152) and 2009 (–4,763) and a significant increase of 1,098 cases (99.9% confidence) in 2010. However, switching to 100% raised-without-antibiotics production did not significantly change the number of antibiotic-resistant nontyphoidal salmonellosis cases over the full study period combining all 9 years (–8,588, 95% CrI –27,842 to 16,317, 60% confidence).

Discussion

Our risk analysis uses nationwide surveillance data on animal production and human illnesses to longitudinally estimate antibiotic-resistant nontyphoidal salmonellosis in the United States and assess how it might be affected by antibiotic restriction in livestock. Our approach is grounded in empirical data and minimizes assumptions while modeling parameter uncertainty and its effect on the results. Although farm-to-fork AMR risk analyses have been published (10), recent work has followed more parsimonious approaches like ours (11–14). However, direct comparison with other published risk analyses is difficult because most focus on the association between antibiotic use and AMR for a single drug and rarely include longitudinal data.

In our 2002–2010 analysis, the risks were stable over time; on average, a case of antibiotic-resistant salmonellosis occurred <1 time per 32 million meals made with beef or <1 time per 500,000 meals made with beef initially contaminated with antibiotic-resistant nontyphoidal 

\[ \text{Salmonella} \] 

NTS. Likewise, prevalence of the antibiotic-resistant pathogen in beef available at retail in the United States and in the food production chain remained stable. Exceptions were 2 years in which more beef-attributable illnesses occurred than was typical for other years: 5 average-sized outbreaks (8% of attributable outbreaks) in 2003 and 2 Salmonella Montevideo outbreaks with high total case numbers in 2009.

The proportion of MDR and CRR was higher in NTS isolates from NARMS matched to outbreaks in 2003 and 2009 than in other years: 80% of matched samples in 2003 had CRR, and all 2009 Salmonella Montevideo matched samples to (71% of all matched 2009 cases) had MDR. This increase remained after we adjusted for exposure to infection in the form of meals prepared with beef with NTS and the fraction of these with AMR, which were stable. The association between MDR and CRR and larger/more frequent outbreaks may suggest a link between MDR/CRR and pathogenicity or infectivity, as described by Guillard et al. (25). Yet, in vitro phenotypic resistance does not fully capture actual clinical outcomes. Current foodborne surveillance programs do not record outcomes of AMR illnesses such as treatment failures and their consequences (e.g., extra hospitalizations). Estimating treatment failures resulting from resistant infections and the relative contribution of different sources of AMR—including antibiotic use in livestock—would better quantify the...
societal cost benefit of curtailing resistant illnesses from livestock.

In our analysis, we had to estimate AMR specific to beef-attributable cases because the NARMS database contains salmonellosis cases of any source and yet resistance of salmonella varies by source (9). Lacking direct links between the NORS outbreak data used in source attribution and the outbreaks in NARMS, we used timing of the infection, state, and serotype to match cases. Although this method enabled us to approximate resistance in beef-attributable cases (5% vs. 22% AMR across human NARMS samples for NTS over the study period), use of this method probably resulted in some misclassification of the NARMS samples. This issue would be easily alleviated if a unique outbreak identifier were available in both datasets.

Of note, the per-portion risk for susceptible or resistant salmonellosis from beef initially contaminated was ≈8 times higher for intact cuts of beef than for ground beef. Because the prevalence of susceptible and resistant pathogens is greater for ground beef, the total illnesses are evenly split between types of beef, as are attributed illnesses, a result also noted by Laufer et al. (26). Intact cuts include some high-risk foods such as delicatessen

Table 2. Confidence in a significant monotonic trend in the data (bootstrapped Mann-Kendall test) and in the difference between posteriors estimates of the last 5 years versus the previous years for measures of beef consumption, NTS illnesses, and risk for antimicrobial resistant salmonellosis from beef, United States*

<table>
<thead>
<tr>
<th>Variable</th>
<th>Monotonic (confidence trend exists), %</th>
<th>Last 5 vs. previous years (confidence difference exists), %</th>
<th>Years found significantly higher based on all pairwise comparisons†</th>
</tr>
</thead>
<tbody>
<tr>
<td>Meals_{CRR}</td>
<td>38.2</td>
<td>68.7</td>
<td>None</td>
</tr>
<tr>
<td>Ground</td>
<td>66.6</td>
<td>44.7</td>
<td>None</td>
</tr>
<tr>
<td>Intact</td>
<td>88.0</td>
<td>93.8</td>
<td>None</td>
</tr>
<tr>
<td>Meals_{CRR,MDR}</td>
<td>87.0</td>
<td>86.3</td>
<td>None</td>
</tr>
<tr>
<td>Ground</td>
<td>94.5 (D)</td>
<td>85.8</td>
<td>2001</td>
</tr>
<tr>
<td>Intact</td>
<td>53.0</td>
<td>98.4 (D)</td>
<td>None</td>
</tr>
<tr>
<td>Meals_{CRR,MDR}</td>
<td>82.0</td>
<td>85.7</td>
<td>None</td>
</tr>
<tr>
<td>Ground</td>
<td>96.7 (D)</td>
<td>94.5</td>
<td>None</td>
</tr>
<tr>
<td>Intact</td>
<td>34.2</td>
<td>91.4</td>
<td>None</td>
</tr>
<tr>
<td>Ill_{CRR}</td>
<td>82.0</td>
<td>67.2</td>
<td>2003, 2009</td>
</tr>
<tr>
<td>Ground</td>
<td>66.8</td>
<td>55.3</td>
<td>2003, 2009, 2014</td>
</tr>
<tr>
<td>Intact</td>
<td>57.3</td>
<td>69.0</td>
<td>2003, 2009</td>
</tr>
<tr>
<td>Ill_{CRR,MDR}</td>
<td>86.6</td>
<td>87.2</td>
<td>2003</td>
</tr>
<tr>
<td>Ground</td>
<td>67.0</td>
<td>57.6</td>
<td>2003, 2014</td>
</tr>
<tr>
<td>Intact</td>
<td>61.9</td>
<td>84.5</td>
<td>2000, 2003</td>
</tr>
<tr>
<td>Ill_{CRR,MDR}</td>
<td>90.6</td>
<td>100 (D)</td>
<td>2003</td>
</tr>
<tr>
<td>Ground</td>
<td>70.1</td>
<td>54.7</td>
<td>2003</td>
</tr>
<tr>
<td>Intact</td>
<td>66.2</td>
<td>98.6 (D)</td>
<td>2000, 2003</td>
</tr>
<tr>
<td>P_{meal}</td>
<td>82.1</td>
<td>84.7</td>
<td>2003, 2009</td>
</tr>
<tr>
<td>Ground</td>
<td>62.9</td>
<td>54.7</td>
<td>2003, 2009, 2014</td>
</tr>
<tr>
<td>Intact</td>
<td>56.8</td>
<td>70.5</td>
<td>2003, 2009</td>
</tr>
<tr>
<td>P_{meal,MDR}</td>
<td>86.7</td>
<td>97.7 (D)</td>
<td>2003</td>
</tr>
<tr>
<td>Ground</td>
<td>66.9</td>
<td>50.8</td>
<td>2003, 2014</td>
</tr>
<tr>
<td>Intact</td>
<td>61.9</td>
<td>85.0</td>
<td>2000, 2003</td>
</tr>
<tr>
<td>P_{meal,CRR}</td>
<td>91.0</td>
<td>99.9 (D)</td>
<td>2003</td>
</tr>
<tr>
<td>Ground</td>
<td>67.2</td>
<td>49.9</td>
<td>2003</td>
</tr>
<tr>
<td>Intact</td>
<td>70.4</td>
<td>98.7(D)</td>
<td>2003</td>
</tr>
<tr>
<td>P_{A}</td>
<td>87.3</td>
<td>84.1</td>
<td>2003, 2009</td>
</tr>
<tr>
<td>Ground</td>
<td>54.4</td>
<td>75.2</td>
<td>2003, 2009, 2014</td>
</tr>
<tr>
<td>Intact</td>
<td>42.6</td>
<td>49.9</td>
<td>2003, 2009</td>
</tr>
<tr>
<td>P_{A,MDR}</td>
<td>82.2</td>
<td>86.0</td>
<td>2003</td>
</tr>
<tr>
<td>Ground</td>
<td>46.5</td>
<td>97.6 (I)</td>
<td>2003, 2014</td>
</tr>
<tr>
<td>Intact</td>
<td>53.2</td>
<td>66.1</td>
<td>2003, 2014</td>
</tr>
<tr>
<td>P_{A,CRR}</td>
<td>87.0</td>
<td>99.6 (D)</td>
<td>2003</td>
</tr>
<tr>
<td>Ground</td>
<td>36.8</td>
<td>99.9 (D)</td>
<td>2003, 2014</td>
</tr>
<tr>
<td>Intact</td>
<td>70.5</td>
<td>91.7</td>
<td>2000, 2003</td>
</tr>
</tbody>
</table>

* D indicates that a significant decrease was found; I indicates that a significant increase was found, based on a 95% limit. CRR, clinically relevant resistance; Ill_{CRR}, human cases of beef-attributable antibiotic-resistant NTS; Ill_{CRR,MDR}, human cases of beef-attributable MDR NTS; Ill_{CRR,MDR}, human cases of beef-attributable CRR NTS; Meals, meals prepared with beef initially contaminated with antibiotic-resistant NTS resistant to ≥1 antibiotic; Meals_{CRR,MDR}, meals prepared with beef initially contaminated with NTS resistant to ≥2 antibiotics; Meals_{CRR,MDR}, meals prepared with beef initially contaminated with NTS with CRR; MDR, multidrug-resistant; NTS, nontyphoidal Salmonella; P_{A}, probability of antibiotic-resistant NTS per meal made with beef of any kind; P_{A,MDR}, probability of MDR NTS per meal made with beef of any kind; P_{A,CRR}, probability of CRR NTS per meal made with beef initially contaminated with CRR NTS.

†Based on pairwise posterior comparisons between all years.
roast beef and ready-to-eat products (27). Done-
ess might also partly explain this finding. A sur-
vey found that 61% of US consumers preferred
their steak medium or rarer (28), and another study
found that 21% of restaurant customers requested
medium or rarer hamburgers (29).

Using NTS in beef, beef-attributable salmo-
nellosis cases, and resistance to ≥1 antibiotic pro-
vided a case definition that maximizes the chances
of finding a statistical signal in this dataset, should
a trend exist in the outcomes. Consequently, the
lack of sustained change suggests that the mod-
eled risks were indeed stable nationwide. Assum-
ing that, as often described, antibiotic use in beef
production is a key driver of AMR illnesses in hu-
mans, we consider 2 alternative explanations for
this stability: either antibiotic use was stable during
the study period or sustained use in beef resulted
in a plateau in AMR salmonellosis so that changes
in use can no longer affect the outcome. Although
nationwide data on antibiotic use is unavailable for
the study period, antibiotic use in beef is unlikely
to have remained stable. For example, the fraction
of beef cattle treated with tylosin in feed or water
increased from 42.3% in 1999 to 71.2% in 2010 (30,31),
whereas in Canada, where beef production practices
are equivalent to those in the United States, overall
use in beef decreased during 2008–2012 (32). A hy-
pothetical resistance plateau cannot be empirically an-
swered without detailed use data, but its implication
is that changes such as the recent US Food and Drug
Administration feed directive should eventually
reduce beef-attributable antibiotic-resistant nonty-
phoidal salmonellosis. This hypothesis warrants a
re-estimation of our model in the future.

An alternative hypothesis for the lack of change is
that antibiotic use in beef does not significantly affect
incidence of human AMR salmonellosis. This hypoth-
esis does not necessarily imply a lack of risk but a risk
that is too small or confounded to be measured. Em-
pirical data for this effect are scarce because field stud-
ies typically link antibiotic use to AMR in animals or
animal products, not in human illnesses. Benedict et
al. (33) described how exposure to antibiotics in feed-
lot cattle did not affect AMR presence in non-type-
specific Escherichia coli. Others have described a lower
prevalence of resistance resulting from decreased use
(4), although pathogen prevalence among raised-
without-antibiotics livestock may be higher than that
among conventionally raised animals (5). Although
our study cannot confirm or refute this hypothesis,
it provides new empirical evidence based on nation-
wide estimates and can be further updated as antibi-
otic practices in livestock are documented.

The scenarios with all raised-without-antibiotics
beef cattle enabled us to model a hypothetical upper
limit of the human health effect of antibiotic reduc-
ion and resulted in nonsignificant changes in resis-
tant illnesses overall. This finding held true even un-
der an unrealistic assumption of a direct decrease in
resistant illnesses resulting from decreased pathogen
prevalence and resistance after complete withdrawal
of antibiotics. Being based solely on nationwide esti-
mates—resistant illnesses based on surveillance data
and the effect of antibiotic use on antibiotic-resistant
NTS based on a nationwide survey (22)—these find-
ings suggest that, according to collected surveillance
data, reducing antibiotic use in cattle may not signifi-
cantly reduce antibiotic-resistant nontyphoidal sal-
monellosis by a measurable level. Although external
validation is not feasible because no other study, to
our knowledge, has directly tested human and ani-
mal resistance at a national level, these results are
consistent with those of recent studies of cecal con-
tenls of fed cattle (5) and ground beef (34) that found
few AMR differences between raised-without-anti-
biotics and conventionally raised cattle production.
Our findings also demonstrate that a direct relation-
ship between prevalence of antibiotic-resistant NTS
in beef and resulting AMR salmonellosis is not sup-
ported by current surveillance data.

This analysis suggests that the risk of contracting
antibiotic-resistant nontyphoidal salmonellosis from
beef consumption is <1 time/32 million beef meals
assessing salmonellosis only, our work highlights improvements needed to better quantify the effect that antibiotic use in livestock has on human health: monitoring of clinical outcomes in foodborne surveillance programs, better connection between surveillance for foodborne pathogen resistance and outbreak sourcing, and detailed studies exploring the effect of raised-without-antibiotics production practices on pathogen prevalence and resistance throughout the farm-to-fork production chain. Elucidating not only consumers’ exposure to resistant pathogens but also how exposure translates into resistant illnesses and, ultimately, treatment failures, is required for the development of optimal AMR reduction strategies.

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References

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Supplemental Description of Methods

We developed a stochastic model to 1) estimate the risk of human antibiotic-resistant non-typhoidal salmonellosis per meal made with beef using the yearly incidence of antibiotic-resistant non-typhoidal salmonellosis illness and number of meals made with beef that year, 2) evaluate temporal trends in all model outcomes over the period 2002-2010, and 3) assess the effect that potential future antibiotic use (AMU) restrictions in beef cattle would have on this antibiotic-resistant non-typhoidal salmonella disease burden, using national surveillance data.

The Appendix Table provides a detailed summary of the variables and sources of data used to estimate each of the outcomes described below.

1. Risk of human antibiotic-resistant non-typhoidal salmonellosis illness attributable to beef

   a. Annual incidence of beef-attributable antibiotic-resistant non-typhoidal salmonellosis illness per 100,000 people ($Ill_{res}$)

   We estimated the number of nontyphoidal salmonellosis illnesses attributable to beef consumption per year ($Ill$), and the number of these with AMR ($Ill_{res}$):

   $Ill = NTSc \times FB \times UD \times (GBA + IBA) \times DA \div USFN$ [Equation 1]

   $Ill_{res} = Ill \times AMR_{perc}$ [Equation 2]

   The annual total $NTSc$ illnesses in the USA from years 1998-2015 were obtained from the FoodNet active surveillance system, and adjusted for the FoodNet catchment area ($USFN$), domestically-acquired fraction ($DA$), underdiagnosis ($UD$), attribution to food ($FB$), and attribution of foodborne cases to ground beef (GBA) or Intact beef (IBA). The adjustment factors $UD$, $FB$ and $DA$ were constant for the study period.
To derive the AMR fraction specific to beef-attributable cases of human illness, $AMR_{perc}$, we used metadata available in both datasets (serotype, date, and location) to match cases in the NARMS data collected by the CDC from clinical patient samples (1) with outbreaks from NORS attributed to beef consumption (2). The NORS data includes information on identified food source, and these variables were used to identify ground vs intact beef-attributable outbreaks among all salmonella outbreaks.

b. Annual meals prepared with beef initially contaminated with antibiotic-resistant non-typhoidal salmonellosis ($Meals_{res}$)

$Meals_{res}$ quantifies the meals initially contaminated (as measured at the slaughter plant or retail) with the pathogen. This doesn’t necessarily mean that the actual meal consumed was contaminated, as safe cooking and handling practices would reduce or completely inactivate the bacterial load. $Meals_{res}$ was calculated as the sum of meals prepared with either ground or intact beef initially contaminated with antibiotic-resistant non-typhoidal salmonellosis and consumed annually in the US:

$$Meals_{res} = \frac{(1-GBF) \times Beef_{dtot}}{MS_{GB}} \times Pp_{IB} \times AMR_{IB} + \frac{GBF \times Beef_{dtot}}{MS_{GB}} \times Pp_{GB} \times AMR_{GB} \quad [Equation \ 3]$$

To estimate the annual number of meals, we combined beef disappearance data from USDA Economic Research Service to estimate total beef available for consumption ($Beef_{dtot}$) with the mean amount of beef consumed per meal containing beef stratified by beef cut ($MS_{GB}$ and $MS_{IB}$) estimated using NHANES data (GB, years 2002-2015 vs IB, years 1998-2010) using the proportion of beef sold as ground beef (National Cattlemen’s Beef Association, pers. com., 2018).

We estimated the prevalence $Pp$ of nontyphoidal salmonella in beef using samples collected by USDA Food Safety and Inspection Service (FSIS). We then calculated the prevalence of the pathogen with AMR in IB ($AMR_{IB}$ and $AMR_{GB}$) nontyphoidal salmonella using a combination of USDA-NARMS data from meat samples collected during IB and GB production for the years available and FDA-NARMS retail studies from GB (3) for years 2002-2010. Although these datasets are based on a national catchment area and are the most comprehensive sampling efforts to date, the evolution of the FSIS program targets over time and the small sample size of the FDA-NARMS study in particular may limit the ability to calculate true prevalence from these data.
c. Risk of antibiotic-resistant non-typhoidal salmonellosis per meal with beef

We estimated the probability of human antibiotic-resistant non-typhoidal salmonellosis illness per meal made with beef initially contaminated with antibiotic-resistant non-typhoidal salmonellosis \((P_{ill})\) by dividing the estimated number of antibiotic-resistant non-typhoidal salmonellosis illnesses for a given year \((Ill_{res})\) by the number of meals made with beef with antibiotic-resistant non-typhoidal salmonellosis that year \((Meals_{res})\).

\[
P_{ill} = \frac{Ill_{res}}{Meals_{res}} \quad \text{[Equation 4]}
\]

As explained earlier, we derive \(Meals_{res}\) considering the initial contamination of the intact beef carcass (IB) and through the production of ground beef (GB), not the contamination of the meal as consumed. Food preparation will likely modify pathogen prevalence and load, but such practices are unlikely to change as result of AMU changes, so by using \(Meals_{res}\) to calculate \(P_{ill}\) we avoid the issue of modeling the risk per prepared meal since surveillance data focuses on production and slaughter.

To provide context, we also calculated \(P_{meal}\), the \(Ill_{res}\) per consumption of any meal of beef \(Beef_{dot}\), irrespective of contamination:

\[
P_{meal} = \frac{Ill_{res}}{Beef_{dot}} \quad \text{[Equation 5]}
\]

See Appendix Figure 1.

2. Testing for temporal changes

We tested for monotonic yearly change for all outcomes via Mann-Kendall test for the overall study period, and bootstrapped the test statistic to calculate a of a consistent increase \((4)\).

Using numerical integration \((5)\), we computed the posterior confidence in pairwise year-to-year differences and in the difference between the mean of the parameter in the last five years versus the remaining years.

3. Scenario analysis: Effect of hypothetical restriction on AMU in beef production

a. Relationship between AMU and antibiotic-resistant non-typhoidal salmonellosis in beef

We used unpublished nationwide data (C.P. Fossler, pers. comm., 2018). from the NAHMS feedlot survey \((6)\) to model nontyphoidal salmonella prevalence in cattle RWA vs raised under conventional (CONV) AMU practices: we estimated the sample-positive prevalence
of nontyphoidal salmonella (PrevNTS,CONV and PrevNTS,RWA), and the fraction of nontyphoidal salmonella isolates with AMR (PrevAMR,CONV and PrevAMR,RWA).

The relative risk (ΔRR) of antibiotic-resistant non-typhoidal salmonellosis prevalence in cattle RWA versus CONV was estimated as:

$$\Delta RR = \left(\frac{\text{PrevNTS},\text{RWA}}{\text{PrevNTS},\text{CONV}}\right) \times \left(\frac{\text{PrevAMR},\text{RWA}}{\text{PrevAMR},\text{CONV}}\right)$$ [Equation 6]

b. Prediction of changes in Illres

We constructed two scenarios to evaluate Illres changes from a hypothetical AMU restriction in beef production, assuming no changes in consumer habits and food preparation.

We modified the methods described by Williams et al. (7) to model the change in Illres if switching all production to RWA, as follows:

$$\Delta\text{Ill}_{res} = \text{Ill}_{res} \times (1 - \Delta RR)$$ [Equation 7]

where ΔRR is estimated in Equation 6.

In scenario 1, by using ΔRRs rather than prevalence of antibiotic-resistant non-typhoidal salmonellosis, we assumed that animal-level prevalence is proportional (but not equal to) prevalence in meals and ΔRR has a direct linear (i.e. 1:1) effect on ΔIll_{res}.

To relax this assumption, in a second scenario we empirically estimated the relationship between antibiotic-resistant non-typhoidal salmonellosis prevalence in beef and Illres via Poisson regression, and used it to create an adjustment factor to the calculations done for scenario 1.

In scenario 2, we empirically estimated the relationship between antibiotic-resistant non-typhoidal salmonellosis prevalence in beef and Illres via Poisson regression (see section i. below). Then, to relax the assumption of scenario 1, we used the slope of this Poisson regression to create an adjustment factor to Equation 7 (Appendix Figures 2-5).

We tested the confidence in ΔIll_{res} being less than zero (i.e. reduction of human antibiotic-resistant non-typhoidal salmonellosis illnesses) using numerical integration.
i. Regression between Beef nontyphoidal *Salmonella* and -resistant non-typhoidal salmonellosis human illnesses

To adjust the estimated AMR illnesses associated with antibiotic-resistant non-typhoidal salmonellosis prevalence in beef under a 100% raised-without-antibiotic production system, the relationship between prevalence in beef and illnesses may either be assumed to be 1:1 or may be adjusted by an empirically estimated adjustment factor. The adjustment factor was calculated using a Poisson regression of illnesses with beef-attributed antibiotic-resistant non-typhoidal salmonellosis predicted by the centered and transformed product of the prevalence of salmonella and percentage of resistance in beef salmonella as the predictor of case count in one year.

$$\text{Pred}_{\text{trans}} = \sin^{-1}\sqrt{\text{Prevalence} \times \text{Resistant \%}} - \text{mean}(\sin^{-1}\sqrt{\text{Prevalence} \times \text{Resistant \%}})$$

This regression was carried out omitting the years 2003 and 2009, as these years with abnormally large case counts (Appendix Figure 2) impact prevalence (Appendix Figure 3) rather than resistance (Appendix Figure 4). This is because the relationship between human resistant cases and % resistance is improved by the inclusion of these years, but the regression of prevalence vs human resistant cases is worsened (Appendix Figure 5). The coefficient of the transformed predictor was estimated to be 59.36 (SE 42.3, p=0.233), and the intercept was 6.68 (SE 0.34).

**Appendix Table.** Variable distributions and parameters used in the computation of the probability of beef-attributable resistant illness per meal made with beef contaminated with resistant nontyphoidal Salmonella

<table>
<thead>
<tr>
<th>Variable</th>
<th>Definition</th>
<th>Distribution type</th>
<th>2010 Distribution Parameters</th>
<th>2010 Distribution Summary Statistics</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>NTS</em>&lt;sub&gt;c&lt;/sub&gt;</td>
<td>Cases per state per year in FoodNet States of Non-Typhoidal Salmonella by Serotype</td>
<td>Discrete</td>
<td>580, 686, 479, 2785, 468, 451, 343, 295, 989, 1063</td>
<td>total cases=8483 national est = 53404</td>
<td>CDC FoodNet</td>
</tr>
<tr>
<td><em>USFN</em></td>
<td>Multiplier per state per year to scale the catchment area of FoodNet states to the US population</td>
<td>Discrete</td>
<td>0.017, 0.011, 0.031, 0.014, 0.012, 0.007, 0.009, 0.019, 0.021</td>
<td>total % of US population = 14.1%</td>
<td>CDC FoodNet</td>
</tr>
<tr>
<td><em>FB</em></td>
<td>Fraction of cases of nontyphoidal salmonellosis which are attributed to food</td>
<td>Pert</td>
<td>min=0.91, mode=0.94, max=0.96</td>
<td>mean=0.94, sd=0.01</td>
<td>Scallan et.al 2011.</td>
</tr>
<tr>
<td><em>UD</em></td>
<td>Underdiagnosis multiplier</td>
<td>Gamma</td>
<td>shape=32.83, scale=0.74</td>
<td>mean=24.3, sd=4.2</td>
<td>Ebel et al., 2016</td>
</tr>
<tr>
<td><em>GBA</em></td>
<td>Proportion of Foodborne cases attributed to ground beef</td>
<td>Beta</td>
<td>α=1, β=3260</td>
<td>mean=0.0003, sd=0.0003</td>
<td>CDC NORS</td>
</tr>
<tr>
<td><em>WBA</em></td>
<td>Proportion of Foodborne cases attributed to intact beef</td>
<td>Beta</td>
<td>α=1, β=3260</td>
<td>mean=0.0003, sd=0.0003</td>
<td>CDC NORS</td>
</tr>
<tr>
<td><em>DA</em></td>
<td>Proportion of cases acquired in the United States</td>
<td>Pert</td>
<td>min=0.07, mode=0.11, max=0.15</td>
<td>mean=0.89, sd=0.015</td>
<td>Scallan et.al 2011.</td>
</tr>
<tr>
<td>Variable</td>
<td>Definition</td>
<td>Distribution type</td>
<td>2010 Distribution Parameters</td>
<td>2010 Distribution Summary Statistics</td>
<td>Source</td>
</tr>
<tr>
<td>------------</td>
<td>----------------------------------------------------------------------------</td>
<td>-------------------</td>
<td>------------------------------</td>
<td>-------------------------------------</td>
<td>--------------</td>
</tr>
<tr>
<td>AMRperc</td>
<td>Fraction of nontyphoidal Salmonella samples in the NARMS CDC data (matched to NORS outbreaks attributable to beef) with resistance to 1 or more AMD</td>
<td>Beta</td>
<td>$\alpha=2, \beta=1, \alpha=1, \beta=5; \alpha=0, \beta=13; \alpha=2, \beta=1$</td>
<td>mean=0.046, sd=0.014</td>
<td>CDC NARMS</td>
</tr>
<tr>
<td>GBF</td>
<td>Proportion of beef production sold as ground beef</td>
<td>Discrete</td>
<td>0.58</td>
<td>0.58</td>
<td>NCBA</td>
</tr>
<tr>
<td>Beefdtot</td>
<td>Total beef disappearance annually, adjusted for food waste in lbs</td>
<td>Discrete</td>
<td>$3.91 \times 10^{12}$</td>
<td>$3.91 \times 10^{12}$</td>
<td>USDA ERS</td>
</tr>
<tr>
<td>MSbe</td>
<td>Meal Size of beef consumed, not ground, in lbs</td>
<td>Normal</td>
<td>mean = 67.2 grams, sd=3.9</td>
<td>mean = 67.2 grams, sd=3.9</td>
<td>NHANES</td>
</tr>
<tr>
<td>Ppa</td>
<td>Percent Positive for nontyphoidal Salmonella from carcass sampling per establishment per year</td>
<td>Beta</td>
<td>for establishment 187, $\alpha=5, \beta=82$</td>
<td>mean=0.057, sd=0.025</td>
<td>USDA FSIS</td>
</tr>
<tr>
<td>AMRsb</td>
<td>Proportion of nontyphoidal Salmonella resistant to AMR from NARMS USDA carcass samples</td>
<td>Beta</td>
<td>$\alpha=97, \beta=152$</td>
<td>mean=0.39, sd=0.031</td>
<td>USDA NARMS</td>
</tr>
<tr>
<td>MSgb</td>
<td>Meal Size of beef consumed, ground, in lbs</td>
<td>Normal</td>
<td>mean = 61.0 grams, sd=4.8</td>
<td>mean = 61.0 grams, sd=4.8</td>
<td>NHANES</td>
</tr>
<tr>
<td>Ppgb</td>
<td>Proportion Positive for nontyphoidal Salmonella from ground beef sampling, per establishment per year</td>
<td>Beta</td>
<td>$\alpha=34, \beta=54$</td>
<td>mean=0.61, sd=0.05</td>
<td>USDA FSIS</td>
</tr>
<tr>
<td>AMRggb</td>
<td>Proportion of nontyphoidal Salmonella resistant to AMR from NARMS FDA retail ground beef samples, and by establishment for USDA FSIS samples</td>
<td>Beta</td>
<td>for establishment 795, $\alpha=4, \beta=2$</td>
<td>mean=0.67, sd=0.18</td>
<td>FDA NARMS, USDA FSIS</td>
</tr>
<tr>
<td>PrevNTS,CONV</td>
<td>Prevalence of nontyphoidal Salmonella in the NAHMS study among conventionally-raised cattle.</td>
<td>Beta</td>
<td>$\alpha=678, \beta=4940$</td>
<td>mean=0.12, sd=0.005</td>
<td>Unpublished data</td>
</tr>
<tr>
<td>PrevNTS,RWA</td>
<td>Prevalence of nontyphoidal Salmonella in the NAHMS study among raised-without-antibiotic cattle.</td>
<td>Beta</td>
<td>$\alpha=54, \beta=679$</td>
<td>mean=0.09, sd=0.01</td>
<td>Unpublished data</td>
</tr>
<tr>
<td>PrevAMR,CONV</td>
<td>Proportion of nontyphoidal Salmonella with AMR in the NAHMS study among conventionally-raised cattle.</td>
<td>Beta</td>
<td>$\alpha=134, \beta=650$</td>
<td>mean=0.26, sd=0.02</td>
<td>Unpublished data</td>
</tr>
<tr>
<td>PrevAMR,RWA</td>
<td>Proportion of nontyphoidal Salmonella with AMR in the NAHMS study among raised-without-antibiotic cattle.</td>
<td>Beta</td>
<td>$\alpha=11, \beta=66$</td>
<td>mean=0.23, sd=0.06</td>
<td>Unpublished data</td>
</tr>
</tbody>
</table>
Appendix Figure 1. Probability of non-typhoidal salmonellosis with resistance to one or more antibiotic (antibiotic-resistant non-typhoidal salmonellosis) per million meals made with beef ($P_{\text{meal,overall}}$), and per million meals made with beef initially contaminated with antibiotic-resistant non-typhoidal salmonellosis ($P_{\text{i,overall}}$) in 2002-2010. The sunburst diagrams represent the data used for parameterization, stratified by beef type – ground and intact: meals prepared with beef (approximately 554 billion), and human cases of non-typhoidal salmonellosis attributed to beef (over 400,000). The diagrams indicate, from center to periphery: the relative proportions of ground (grey) and intact (white) beef, the proportion of meals contaminated with nontyphoidal Salmonella (stripes), and the proportion of antibiotic-resistant nontyphoidal Salmonella (grid). The symbols in the equations for $P_{\text{meal,overall}}$ and $P_{\text{i,overall}}$ refer to the data used for parameterization and represented in the sunburst diagrams, and the bar sizes represent the relative magnitude of these probability means.
Appendix Figure 2. Poisson regression estimated cases (line) plotted over the human resistant cases and transformed resistance-prevalence in beef.

Appendix Figure 3. The centered, transformed prevalence of salmonella in beef as a predictor for human cases with resistance, omitting years 2003 and 2009.
Appendix Figure 4. The centered, transformed percent of beef with resistance as a predictor for human cases with resistance, including all years 2002-2010.

Appendix Figure 5. The centered, transformed prevalence of salmonella in beef as a predictor for human cases with resistance, including all years 2002-2010.
Supplemental Text on Multidrug (MDR) and Clinically relevant resistances (CRR)

The mean $P_{\text{ill,overall}}$ for nontyphoidal *Salmonella* MDR was 0.023 per million meals made with beef with nontyphoidal *Salmonella* MDR (95% CrI: 0.011 - 0.1), and beef-attributable nontyphoidal *Salmonella* MDR did not increase over time. The mean $P_{\text{ill,overall}}$ for nontyphoidal *Salmonella* CRR was 2.66 per million (95% CrI: 0.006 - 18 per million), and $P_{\text{meal,overall}}$ was 0.0268 (0.00011 - 0.12 per million). The mean population incidence of these beef-attributed CRR cases across all years was 0.54 per 100,000 (0.002 - 2.45).

Of the 24 beef-attributable outbreaks in the NORS dataset that were matched to NARMS samples with resistance to any drug, only 6 of those were resistant to just one class. Eleven of the 24 were resistant to 5 or more classes, and most CRR outbreaks fit that part of the definition rather than resistance to fluoroquinolones or third generation cephalosporins specifically. Interestingly, the NARMS samples with Fluoroquinolone resistance which were matched to two beef outbreaks were not resistant to any other antibiotics in the panel. In contrast, the third-generation cephalosporin-resistant outbreaks were also resistant to more than five other antibiotic classes in all but one case – which was resistant to four classes.

The trends in MDR and CRR $P_{\text{ill, Mealsres, Illres}}$, and $P_{\text{meal}}$ for all cuts of beef combined are shown in Appendix figures 5-8.
Appendix Figure 6. Mean and 95% Credible Interval of the incidence of salmonellosis cases with resistance to three or more AMD classes, or to more than 4 classes or 3rd Generation Cephalosporins or Fluoroquinolones, attributable to beef (intact, ground, or any) per 100,000 of the US population.

Appendix Figure 7. Mean average estimated consumed beef meals in the millions (ground, intact cuts, or both) with resistance to 3 or more classes (MDR), or to 4 or more classes or 3rd Generation Cephalosporins or Fluoroquinolones (CRR), for all years with available data, with 95% confidence limit.
Appendix Figure 8. Mean and 95% Credible Interval of the MDR and CRR $P_{ill}$, or the Probability of resistant salmonellosis per million meals consumed made with beef containing non-typhoidal salmonella resistant to more than 2 class of antibiotic (MDR) or to more than 4 classes, or specifically to 3rd Generation Cephalosporins and Fluoroquinolones (CRR).
Appendix Figure 9. Mean and 95% Credible Interval of the MDR and CRR $P_{\text{meal}}$, or the Probability of (combined, ground, or intact) beef-attributable salmonellosis resistant to more than 2 class of antibiotic (MDR) or to more than 4 classes, or specifically to 3rd Generation Cephalosporins and Fluoroquinolones (CRR) per consumed meal made with beef per year (irrespective of nontyphoidal *Salmonella* contamination status).

**Supplemental Text on Sensitivity Analysis**

The most influential drivers of Pill uncertainty were illness attributions for both IB and GB. The fraction of human nontyphoidal *Salmonella* cases which had AMR was third highest (Figure 9). Resistance prevalence in GB was the fourth most influential factor, followed by underdiagnosis and nontyphoidal *Salmonella* prevalence in GB. nontyphoidal *Salmonella* prevalence and resistance prevalence in IB, in contrast, were among the least influential of variables. When considering the change in influence over time, however, nontyphoidal *Salmonella* prevalence in IB steadily increased in importance over the period of the study to become the highest in 2010, (Figure 10). The fraction of nontyphoidal *Salmonella* attributable to IB was the most important factor for every year in the study except 2010, and attribution to GB had the greatest year-to-year change in rank of influence. Uncertainty of AMR prevalence among
human cases and uncertainty in GB nontyphoidal *Salmonella* prevalence remained relatively stable by comparison.

**Appendix Figure 10.** Tornado plot of conditional means analysis for the average $P_{III,overall}$ across all 9 years of estimates for all types of beef. The broader the band, the more impact the input variable had in $P_{III,overall}$.

**Appendix Figure 11.** Yearly rankings of the impact of uncertainty in predictors on the uncertainty of the outcome $P_{III}$, where a rank of 1 shows the most impact on uncertainty.

**References**


