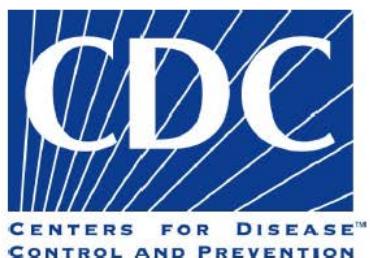


**Foodborne illness source attribution
estimates for 2017 for *Salmonella*,
Escherichia coli O157,
Listeria monocytogenes, and
Campylobacter using multi-year outbreak
surveillance data,
United States**

**The Interagency Food Safety Analytics Collaboration
(IFSAC)**

September 2019



Acknowledgments

The methods used for this report were developed by members of the Interagency Food Safety Analytics Collaboration (IFSAC), which includes the Centers for Disease Control and Prevention (CDC), the U.S. Food and Drug Administration (FDA), and the U.S. Department of Agriculture's Food Safety and Inspection Service (USDA-FSIS).

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Suggested Citation

Interagency Food Safety Analytics Collaboration. Foodborne illness source attribution estimates for 2017 for *Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*, and *Campylobacter* using multi-year outbreak surveillance data, United States. GA and D.C.: U.S. Department of Health and Human Services, CDC, FDA, USDA-FSIS. 2019.

Executive Summary

Each year in the United States an estimated 9 million people get sick, 56,000 are hospitalized, and 1,300 die of foodborne disease caused by known pathogens. These estimates help us understand the scope of this public health problem. However, to develop effective prevention measures, we need to understand the types of foods contributing to the problem.

The Interagency Food Safety Analytics Collaboration (IFSAC) is a tri-agency group created by the Centers for Disease Control and Prevention (CDC), the U.S. Food and Drug Administration (FDA), and the U.S. Department of Agriculture's Food Safety and Inspection Service (USDA-FSIS). IFSAC developed a method to estimate the sources of foodborne illness using outbreak data from 1998 through the most recent year for four priority pathogens: *Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*, and *Campylobacter*. IFSAC described this method and the estimates for 2012 in a [report](#) and at a [public meeting](#).

IFSAC derived the estimates for 2017 using the same method used for the 2012 estimates, with some modifications. The data came from 1,329 foodborne disease outbreaks that occurred from 1998 through 2017 and for which each confirmed or suspected implicated food fell into a single food category. The method relies most heavily on the most recent five years of outbreak data (2013 – 2017). Foods are categorized using a [scheme IFSAC created](#) to classify foods into 17 categories that closely align with the U.S. food regulatory agencies' classification needs.

***Salmonella* illnesses came from a wide variety of foods.**

Salmonella illnesses were broadly attributed across multiple food categories. More than 75% of *Salmonella* illnesses were attributed to seven food categories: Seeded Vegetables (such as tomatoes), Chicken, Fruits, Pork, Eggs, Other Produce (such as nuts), and Beef.

***E. coli* O157 illnesses were most often linked to Vegetable Row Crops (such as leafy greens) and Beef.**

Nearly 75% of illnesses were linked to these two categories.

***Listeria monocytogenes* illnesses were most often linked to Dairy products and Fruits.**

More than 75% of illnesses were attributed to these two categories, but the rarity of *Listeria monocytogenes* outbreaks makes these estimates less reliable than those for other pathogens.

Non-Dairy *Campylobacter* illnesses were most often linked to Chicken.

Nearly 80% of non-Dairy foodborne illnesses were attributed to Chicken, Other Seafood (such as shellfish), Turkey, and Other Meat/Poultry (such as lamb or duck), with *Campylobacter* illnesses most often linked to Chicken. An attribution percentage for Dairy is not included because, among other reasons, most foodborne *Campylobacter* outbreaks were associated with unpasteurized milk, which is not widely consumed, and we think these over-represent Dairy as a source of illness caused by *Campylobacter*. Removing Dairy illnesses from the calculations highlights important sources of illness from widely consumed foods, such as Chicken.

This collaborative effort to provide annual attribution estimates continues IFSAC's work to improve foodborne illness source attribution, which can help inform efforts to prioritize food safety initiatives, interventions, and policies for reducing foodborne illnesses. These consensus estimates allow all three agencies to take a consistent approach to identifying food safety priorities to protect public health. For more information on IFSAC projects visit <https://www.cdc.gov/foodsafety/ifsac/projects/index.html>.

Introduction

Each year in the United States, an estimated 9 million people get sick, 56,000 are hospitalized, and 1,300 die of foodborne disease caused by known pathogens—these estimates help us understand the scope of this public health problem.¹ However, to develop effective prevention-oriented measures, we need to understand the percentage of foodborne illnesses associated with specific foods; we call this work foodborne illness source attribution.

With the creation of the Interagency Food Safety Analytics Collaboration (IFSAC) in 2011, the Centers for Disease Control and Prevention (CDC), the U.S. Food and Drug Administration (FDA), and the U.S. Department of Agriculture's Food Safety and Inspection Service (USDA-FSIS) agreed to improve data and methods used to estimate foodborne illness source attribution and provide timely estimates of the food sources of four priority foodborne pathogens: *Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*, and *Campylobacter*. In this report, we use the term *Listeria* to refer to *Listeria monocytogenes*. IFSAC considers these priority pathogens because of the frequency (estimated 1.9 million illnesses each year combined) and severity of illness they cause, and because targeted interventions can significantly reduce these illnesses.

IFSAC developed a method for analyzing outbreak data to estimate which foods are responsible for illnesses related to the four priority pathogens, using a scheme IFSAC created to classify foods into 17 categories that closely align with the U.S. food regulatory agencies' classification needs.² IFSAC described this method and the resulting estimates for the year 2012 in a report³ and at a public meeting.⁴ IFSAC derived the estimates for 2017 using the same method, with some modifications. IFSAC publishes annual estimates of the sources of foodborne illness for the priority pathogens while continuing to work on methods to further improve these estimates.

Consensus among the three agencies on methods and attribution estimates can help inform efforts to prioritize food safety initiatives, interventions, and policies for reducing foodborne illnesses. The 2017 estimates achieve IFSAC's goals of using improved methods to develop estimates of foodborne illness source attribution for priority pathogens and of achieving consensus that these are the best current estimates for the agencies to use in their food safety activities. These estimates can also help scientists; federal, state, and local policy-makers; the food industry; consumer advocacy groups; and the public to assess whether prevention-oriented measures are working.

Methods

We analyzed data extracted from CDC's Foodborne Disease Outbreak Surveillance System (FDOSS)^{5,6} (www.cdc.gov/foodsafety/fdoss) on outbreaks that were confirmed or suspected to be caused by the four priority pathogens from 1998 through 2017. We excluded outbreaks that occurred in a U.S. territory, were caused by multiple etiologies, or had no identified food vehicle or contaminated ingredient.

Each outbreak was assigned to a single food category using the IFSAC food categorization scheme² based on confirmed or suspected implicated foods and ingredients (i.e., a single ingredient was confirmed or suspected to be implicated or all ingredients in the food were assigned to the same food category). We excluded outbreaks that could not be assigned to a single food category, usually because the food was complex (i.e., composed of ingredients belonging to more than one category) and the contaminated ingredient in the complex food could not be identified.

We developed pathogen-specific analysis of variance (ANOVA) models using our previously described method³ to mitigate the impact of large outbreaks and control for epidemiological factors. We estimated the number of log-transformed illnesses associated with each outbreak based on three factors deemed to be important based on our exploratory analyses: food category, type of preparation location (e.g., restaurant, home), and whether the outbreak occurred in one or more states.

These model estimates were then back-transformed and down-weighted with a function that declines exponentially for outbreaks older than the most recent five years (2013 – 2017) because we considered foods more recently implicated to be most relevant for estimating current attribution.

We used the resulting down-weighted model-estimated illnesses to calculate each estimated attribution percentage: the sum of illnesses associated with a pathogen-food category pair was divided by the sum of illnesses associated with that pathogen across all food categories. We calculated 90% credibility intervals and considered non-overlapping credibility intervals an indication of statistical significance at the $p<0.10$ level. After down-weighting, 69% of overall information came from the most recent five years, 26% from the next most recent five years (2008 – 2012), and 5% from the oldest data (1998 – 2007). Among the 236 *Campylobacter* outbreaks that occurred during the study period, the 147 assigned to Dairy were excluded from the final calculation of the attribution percentage. Thus, the *Campylobacter* attribution point estimates primarily reflect data from 89 outbreaks.

In the graphs and tables, food categories appear in descending order of their estimated attribution percentage, and those that contributed to a cumulative attribution of approximately 75% of illnesses are indicated.

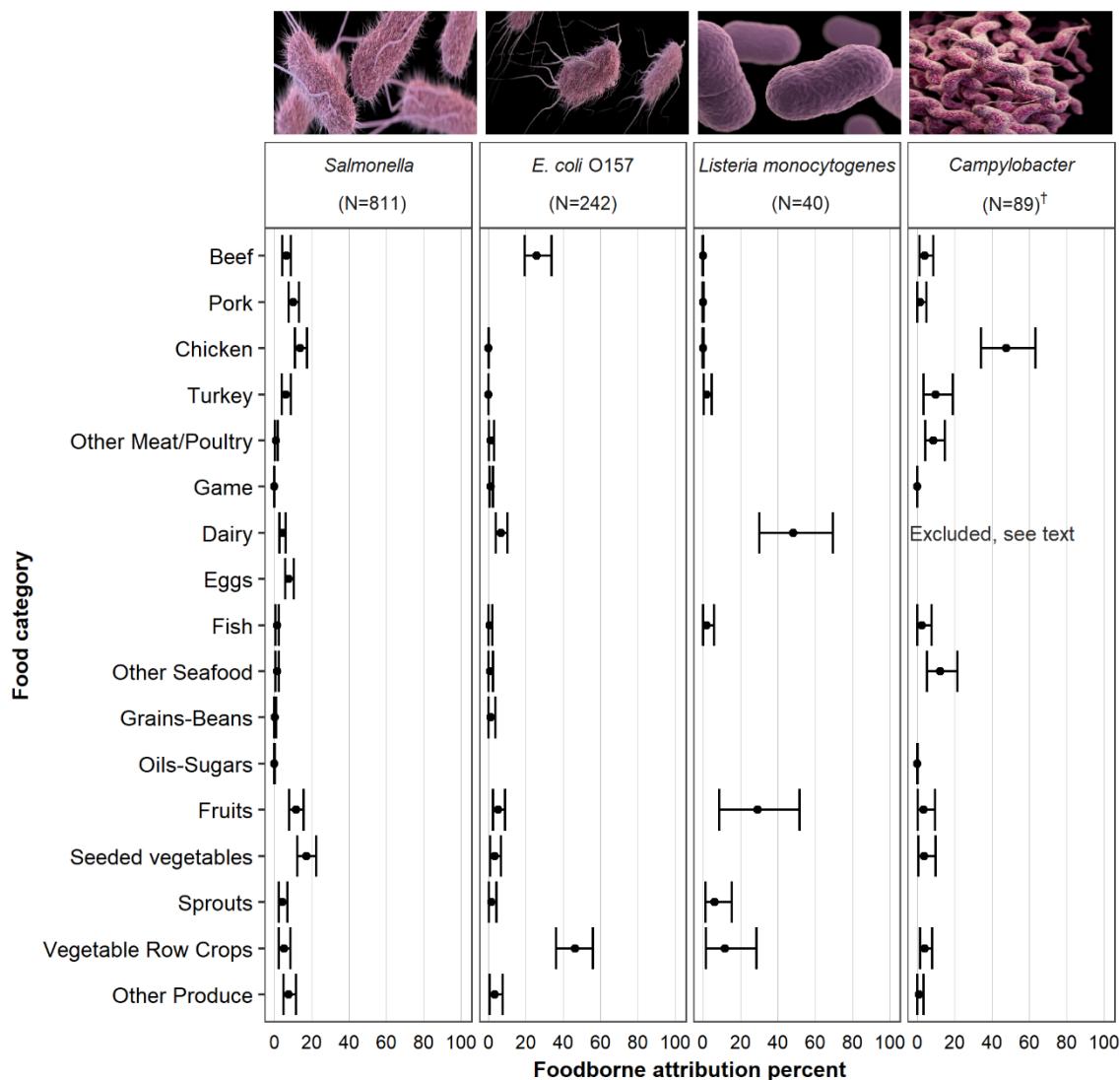
Results

We identified 3,728 outbreaks that occurred from 1998 through 2017 and that were confirmed or suspected to be caused by *Salmonella*, *E. coli* O157, *Listeria*, or *Campylobacter*. Of these, we excluded 152 outbreaks with multiple confirmed or suspected etiologies. We further excluded 1,420 outbreaks without a confirmed or suspected implicated food, 824 outbreaks for which the food vehicle could not be assigned to one of the 17 food categories, and three that occurred in a U.S. territory.

The resulting dataset included 1,329 outbreaks in which the confirmed or suspected implicated food or foods could be assigned to a single food category: 811 caused or suspected to be caused by *Salmonella*, 242 by *E. coli* O157, 40 by *Listeria*, and 236 by *Campylobacter*. Due to down-weighting, the last five years of outbreaks provide the majority of information for the estimates; outbreaks from 2013 through 2017 provide 72% of model-estimated illnesses used to calculate attribution for *Salmonella*, 62% for *E. coli* O157, 79% for *Listeria*, and 58% for *Campylobacter*.

The overall results and those for each pathogen are shown in Figures 1 through 5.

Figure 1: Estimated percentage (with 90% credibility intervals) for 2017 of foodborne *Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*, and *Campylobacter* illnesses attributed to 17 food categories, based on multi-year outbreak data,*† United States. Click here to download relevant data.



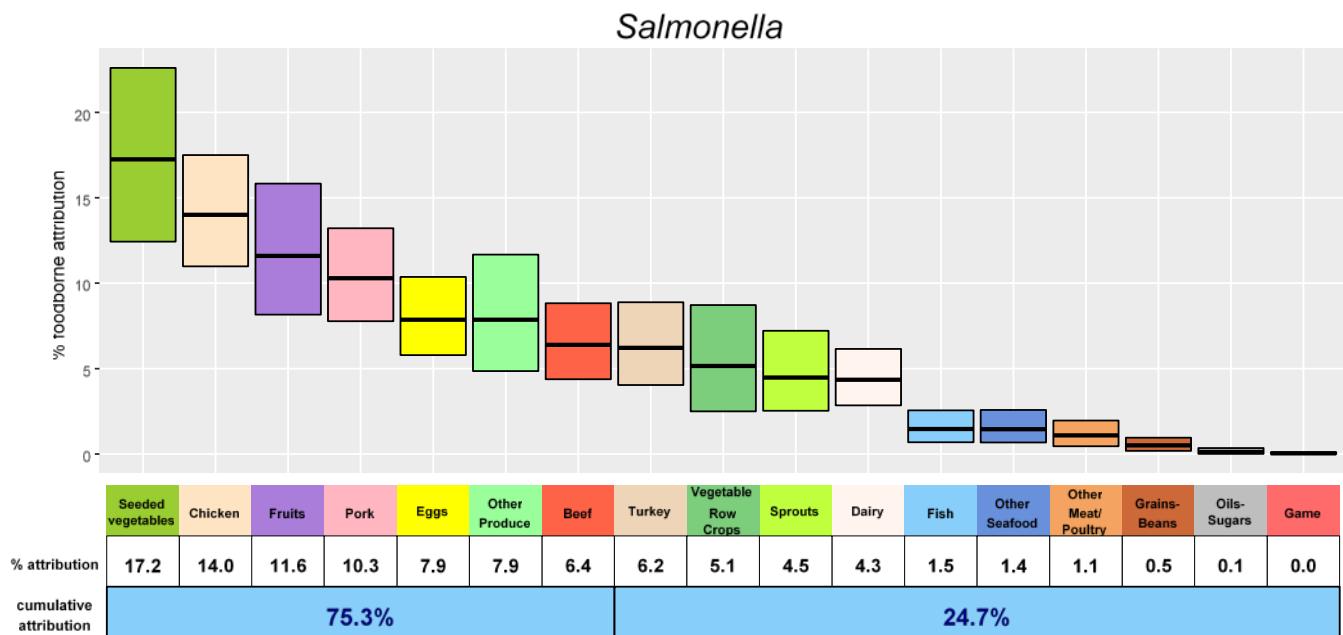
*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2013 – 2017), and exponentially less weight to each earlier year (1998 – 2012).

† *Campylobacter* estimates exclude results derived from Dairy outbreak data.

Overall Key Results

- The results are based on 811 outbreaks caused or suspected to be caused by *Salmonella*, 242 by *E. coli* O157, 40 by *Listeria*, and 89 by *Campylobacter* (after 147 outbreaks due to Dairy were excluded).
- Estimated *Salmonella* and *Campylobacter* illnesses were more widely distributed across food categories than illnesses from *E. coli* O157 and *Listeria*; most of the illnesses for the latter two pathogens were attributed to two food categories.
- For most pathogens, the credibility intervals overlap for categories with the highest attribution percentages, indicating no statistically significant difference among them.

Figure 2: Estimated percentage of foodborne *Salmonella* illnesses (with 90% credibility intervals) for 2017, in descending order, attributed to each of 17 food categories, based on multi-year outbreak data,* United States. Click here to download relevant data.

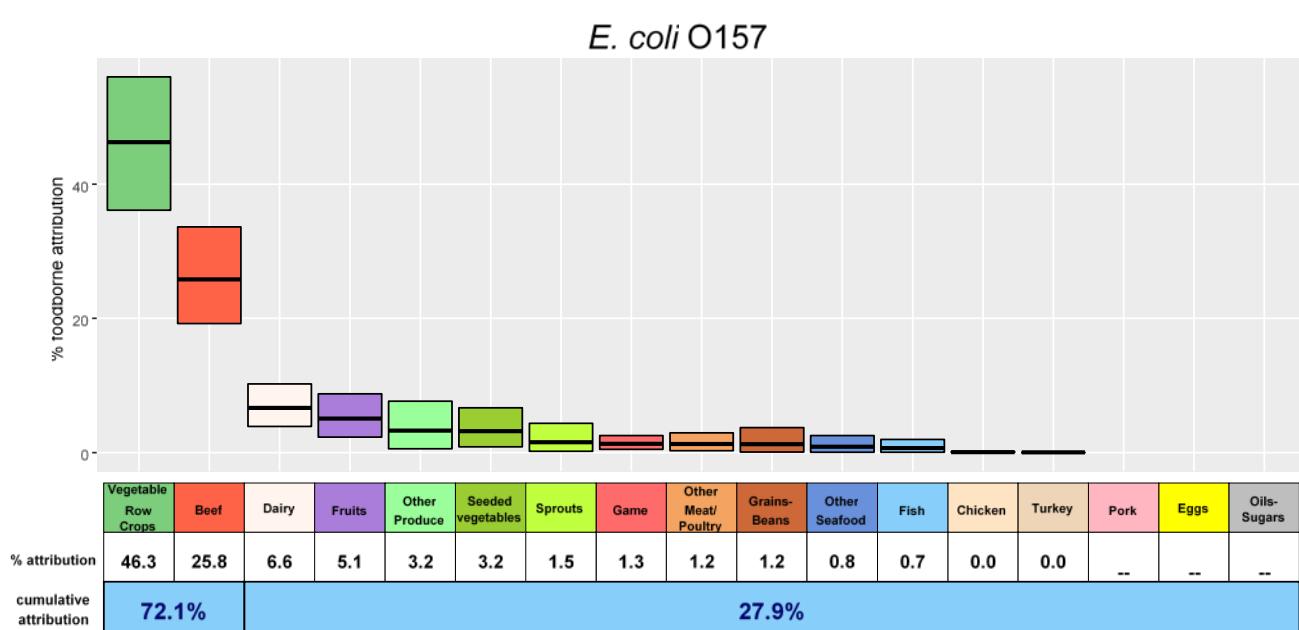


*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2013 – 2017) and exponentially less weight to each earlier year (1998 – 2012).

Salmonella Key Results

- Over 75% of illnesses were attributed to seven food categories: Seeded Vegetables (such as tomatoes), Chicken, Fruits, Pork, Eggs, Other Produce, and Beef.
- The credibility intervals for the categories with an estimated attribution percentage of more than 10% (Seeded Vegetables, Chicken, Fruits, and Pork) do not overlap with those with an estimated attribution of less than 2% (Fish, Other Seafood, Other Meat/Poultry, Grains-Beans, Oils-Sugars, and Game), indicating statistically significant differences in the estimated attribution percentages between these two groups of categories.

Figure 3: Estimated percentage of foodborne *Escherichia coli* O157 illnesses (with 90% credibility intervals) for 2017, in descending order, attributed to each of 17 food categories, based on multi-year outbreak data,* United States. Click here to download relevant data.

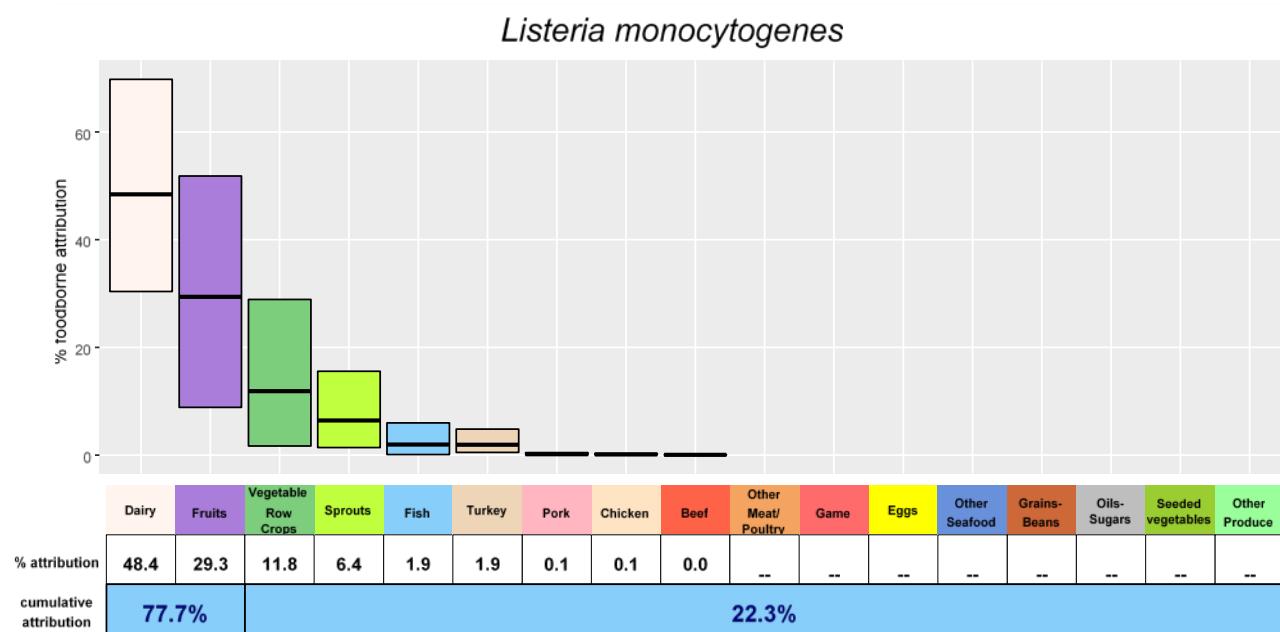


*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2013 – 2017) and exponentially less weight to each earlier year (1998– 2012).

E. coli O157 Key Results

- Nearly 75% of *E. coli* O157 illnesses were attributed to Vegetable Row Crops (such as leafy vegetables) and Beef.
- Vegetable Row Crops had a statistically significant higher estimated attribution percentage than all other categories.
- Beef had a statistically significant higher estimated attribution percentage than all categories other than Vegetable Row Crops.
- No illnesses were attributed to Pork, Eggs, or Oils-Sugars.

Figure 4: Estimated percentage of foodborne *Listeria monocytogenes* illnesses (with 90% credibility intervals) for 2017, in descending order, attributed to each of 17 food categories, based on multi-year outbreak data,* United States. Click here to download relevant data.

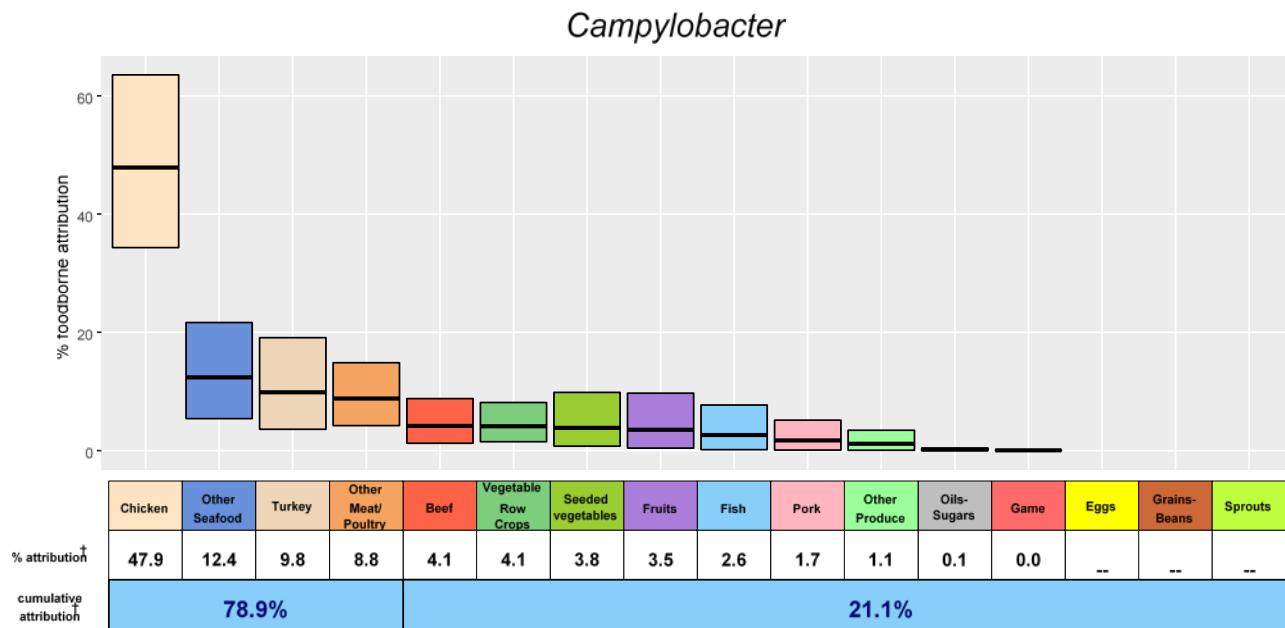


*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2013–2017) and exponentially less weight to each earlier year (1998–2012).

***Listeria monocytogenes* Key Results**

- Over 75% of illnesses were attributed to Dairy and Fruits.
- The credibility intervals for the Dairy and Fruits categories were quite wide, partly due to the small total number of outbreaks (40). The credibility intervals overlapped each other, and the intervals for the Fruits category overlapped those for some food categories with much smaller estimated attribution percentages, such as Vegetable Row Crops.
- No illnesses were attributed to Other Meat/Poultry, Game, Eggs, Other Seafood, Grains-Beans, Oils-Sugars, Seeded Vegetables or Other Produce.

Figure 5: Estimated percentage of foodborne *Campylobacter* illnesses (with 90% credibility intervals) for 2017, in descending order, attributed to each of 16 food categories, based on multi-year outbreak data, *† United States. Click here to download relevant data.



*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2013 – 2017) and exponentially less weight to each earlier year (1998 – 2012).

[†] *Campylobacter* estimates exclude results derived from Dairy outbreak data

***Campylobacter* Key Results**

- Nearly 80% of non-Dairy illnesses were attributed to Chicken, Other Seafood, Turkey, and Other Meat/Poultry.
- The credibility interval for Chicken did not overlap with the credibility intervals for the other categories, indicating a statistically significant higher estimated attribution percentage for Chicken than for any other food category.
- No statistically significant differences in the estimated attribution percentages were found among most other food categories.
- No illnesses were attributable to Eggs, Grains-Beans, or Sprouts.
- An attribution percentage for Dairy is not presented partly because most foodborne *Campylobacter* outbreaks were associated with unpasteurized milk, which is not widely consumed. The attribution percentages before removing Dairy were Dairy 62.6%, Chicken 17.9%, Other Seafood 4.6%, Turkey 3.7%, and Other Meat/Poultry 3.3%, and were less than 2% for each of the other categories. The Chicken attribution percentage increased to 47.9% after removing Dairy.

Discussion

This report uses data from 1998 through 2017 to provide outbreak-based attribution estimates for 2017 of the percentage of illnesses caused by four priority pathogens, assigning illnesses to each of 17 food categories. Data from foodborne disease outbreaks are the foundation of many foodborne illness source attribution analyses, in part because outbreak investigations often link illnesses to a specific food and the data are captured nationally. An IFSAC study found that outbreak and sporadic infections caused by the four priority pathogens were generally demographically similar; this supports the use of foodborne outbreaks for source attribution.⁷ These estimates can inform food safety decision-making and provide pathogen-specific direction for reducing foodborne illness.

The attribution of *Salmonella* illnesses to multiple food categories suggests that interventions designed to reduce illnesses from these pathogens need to target a variety of food categories. In contrast, the majority of *E. coli* O157 illnesses were attributed to two food categories: Vegetable Row Crops and Beef. The data suggest that interventions for *E. coli* O157 focusing on these two food categories may be most effective in reducing illnesses. In contrast to previous reports, the credibility interval for Vegetable Row Crops did not overlap with the credibility intervals for any other category, indicating a statistically significant higher estimated attribution percentage than all other categories.

As with *E. coli* O157, the majority of *Listeria* illnesses were attributed to two food categories: Dairy and Fruits. Although the limited number of outbreaks and wide credibility intervals dictate caution in interpreting the attribution percentage for Dairy, the risk to pregnant women and persons with weakened immune systems of consuming soft cheese made from unpasteurized milk or in unsanitary conditions is well-recognized,⁹ and outbreaks from Fruits contaminated by *Listeria* have been observed in recent years.

Like *Salmonella*, *Campylobacter* illnesses were broadly attributed across multiple food categories. The attribution percentages for Dairy are not presented in the figures for *Campylobacter* for several reasons. Most *Campylobacter* outbreaks included in the database were associated with unpasteurized milk, which is not widely consumed by the general population. Moreover, an analysis of 38 case-control studies of sporadic campylobacteriosis found a much smaller percentage of illnesses attributable to consumption of raw milk than chicken.¹⁰ For example, a U.S. FoodNet case-control study attributed 1.5% of campylobacteriosis cases to consumption of unpasteurized milk, compared with 24% to consumption of chicken prepared in a restaurant.¹¹ Structured expert judgment studies estimate about 8–10% of foodborne campylobacteriosis to be attributable to dairy products (principally raw milk), compared with 33–72% to chicken.^{12–14} Thus, *Campylobacter* outbreaks in the Dairy food category appear to over-represent Dairy as a source of *Campylobacter* illness. After removing the Dairy outbreaks, the Chicken attribution increased to 47.9%, which is consistent with published literature.^{10, 16} The credibility interval for Chicken did not overlap with the credibility intervals for the other food categories, indicating a statistically significant higher estimated attribution percentage for Chicken than for any other food category.

Our approach addresses several issues with outbreak-based foodborne illness source attribution, yet limitations associated with generalizing outbreak data to sporadic illnesses remain and are well-documented.^{5, 6} Our analysis is also subject to other uncertainties and biases. For pathogens with a small number of outbreaks, outbreaks with a very large illness count can have substantial influence on the attribution point estimate. Further, this analysis only included 36% of reported outbreaks caused by the four priority pathogens (1,329 of 3,728 outbreaks in which the confirmed or suspected implicated food could be assigned to a single food category), which may not be representative of all outbreaks from these pathogens. Finally, our analysis includes illnesses that occurred among institutionalized populations, such as those in

prisons, hospitals, and schools; these populations are easier to identify and collect complete data from, have fewer food options, and are not representative of the general population.

These estimates should not be interpreted as suggesting that all foods in a category are equally likely to transmit pathogens. Caution should also be exercised when comparing estimates across years, as a decrease in a percentage may result, not from a decrease in the number of illnesses attributed to that food, but from an increase in illnesses attributed to another food. This is especially true for *Listeria*, as the attribution percentages might vary widely from year to year due to the limited number of outbreaks and the zero-sum nature of the attribution percentages. The analyses show relative changes in percentage, not absolute changes in attribution to a specific food. Therefore, we advise using these results with other scientific data for decision-making.

Conclusions

IF SAC's work to provide a harmonized analytic approach for estimating foodborne illness source attribution from outbreak data can provide consistency in the use and interpretation of estimates across public health and regulatory agencies. As more data become available and methods evolve, attribution estimates may improve. Annual updates to these estimates will enhance IFSAC's efforts to inform and engage stakeholders, and further their ability to assess whether prevention-oriented measures are working.

IF SAC continues to enhance attribution efforts through projects that address limitations identified in this report. For more information on IFSAC's completed and ongoing projects, visit

<http://www.cdc.gov/foodsafety/ifsac/index.html>.

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