

**Foodborne illness source attribution
estimates for 2020 for *Salmonella*,
Escherichia coli O157, and
Listeria monocytogenes using multi-year
outbreak surveillance data,
United States**

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

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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 percentages of foodborne illness attributed to certain sources using outbreak data from 1998 through the most recent year for IFSAC's priority pathogens: *Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*, and *Campylobacter*. IFSAC described this method and the estimates for 2012 in a [report](#), in a [peer-reviewed journal article](#), and at a [public meeting](#).

Unlike in prior [IFSAC Annual Reports](#), attribution estimates for *Campylobacter* are not presented in this year's report. Evidence suggests the sources of *Campylobacter* outbreaks likely differ considerably from the sources of non-outbreak-associated illnesses caused by this pathogen. IFSAC is exploring alternative approaches for estimating the sources of *Campylobacter* illnesses.

IFSAC derived the estimates for 2020 using the same method used for the previous estimates, with some modifications. The data came from 1,287 foodborne disease outbreaks that occurred from 1998 through 2020 and for which each confirmed or suspected implicated food was assigned to a single food category. The method relies most heavily on the most recent five years of outbreak data (2016 – 2020). 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.**

More than 75% of *Salmonella* illnesses were attributed to seven food categories: Chicken, Fruits, Pork, Seeded Vegetables (such as tomatoes), Other Produce (such as fungi, herbs, nuts, and root vegetables), Beef, and Turkey.

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

More than 80% of illnesses were linked to these two categories.

***Listeria monocytogenes* illnesses were most often linked to Dairy products, Fruits, and Vegetable Row Crops.**

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

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 the four priority foodborne pathogens: *Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*, and *Campylobacter*. Unlike in prior [IFSAC Annual Reports](#), attribution estimates for *Campylobacter* are not presented in this year’s report due to continued concerns about the limitations of using outbreak data to attribute *Campylobacter* illnesses to food sources. In this report, we use the term *Listeria* to refer to *Listeria monocytogenes*, and *E. coli* to refer to *Escherichia coli*. IFSAC considers these four 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 report, in a peer-reviewed article,³ and at a public meeting.⁴ IFSAC derived the estimates for 2020 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.

The 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 2020 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 (defined as two or more illnesses with a common exposure)⁷ that were confirmed or suspected to be caused by three priority pathogens — *Salmonella*, *E. coli* O157, and *Listeria* — from 1998 through 2020. We excluded outbreaks that met one or more of the following conditions: occurred in a U.S. territory; had no identified food vehicle or contaminated ingredient; were caused by more than one pathogen (including pathogens not included in this report). Given our method³ of running two separate models for Enteritidis and non-Enteritidis *Salmonella* outbreaks and the fact that this analysis does not include non-O157 STEC, we excluded outbreaks that were caused by both *Salmonella* serotype Enteritidis and another *Salmonella* serotype and those that were caused by both *E. coli* O157 and another *E. coli* serogroup, as these were difficult to classify for modeling purposes. We included outbreaks caused by multiple serotypes of *Salmonella* if none were Enteritidis.

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 (2016 – 2020), based on the year of each outbreak's first illness because we considered foods more recently implicated to be the 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, 70% of overall information came from the most recent five years, 25% from the next most recent five years (2011 – 2015), and 5% from the oldest data (1998 – 2010).

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.

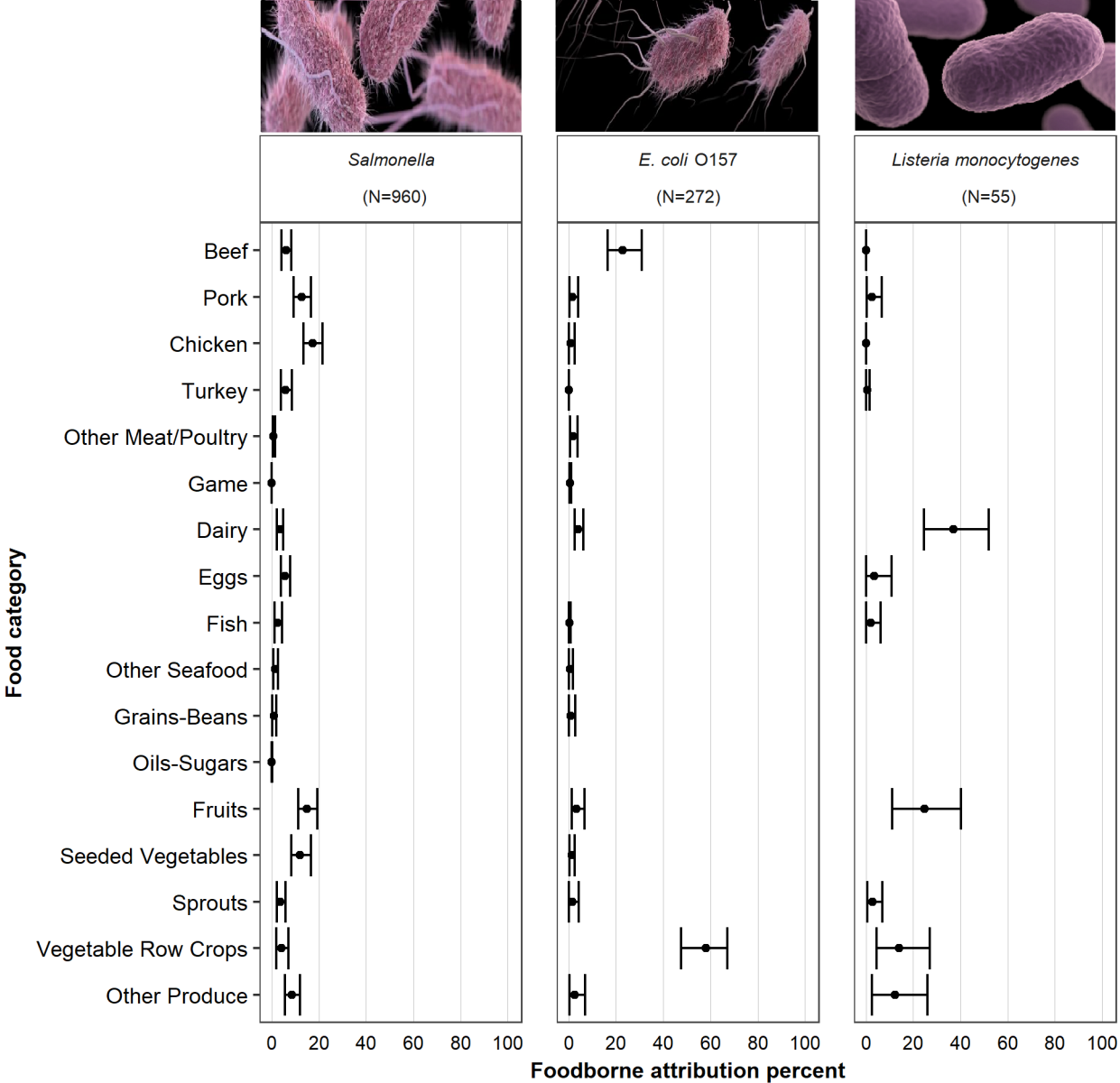
Results

We identified 3,749 outbreaks that occurred from 1998 through 2020 and that were confirmed or suspected to be caused by *Salmonella*, *E. coli* O157, or *Listeria*, including 192 outbreaks that were confirmed or suspected to be caused by multiple pathogens or serotypes. Of these, we excluded 96 outbreaks according to our pathogen-exclusion criteria, leaving 3,653 outbreaks. We further excluded 1,524 outbreaks without a confirmed or suspected implicated food, 836 outbreaks for which the food vehicle could not be assigned to one of the 17 food categories, and six that occurred in a U.S. territory.

The resulting dataset included 1,287 outbreaks in which the confirmed or suspected implicated food or foods could be assigned to a single food category: 960 caused or suspected to be caused by *Salmonella*, 272 by *E. coli* O157, and 55 by *Listeria*. These include 43 outbreaks caused by multiple serotypes of *Salmonella*. Due to down-weighting, the last five years of outbreaks provide the majority of information for the estimates; outbreaks from 2016 through 2020 provide 71% of model-estimated illnesses used to calculate attribution for *Salmonella*, 67% for *E. coli* O157, and 62% for *Listeria*.

The overall results and those for each pathogen are shown in Figures 1 through 4.

Figure 1: Estimated percentage (with 90% credibility intervals) for 2020 of foodborne *Salmonella*, *Escherichia coli* O157, and *Listeria monocytogenes* illnesses attributed to 17 food categories, based on multi-year outbreak data,* United States. Click here to download data.

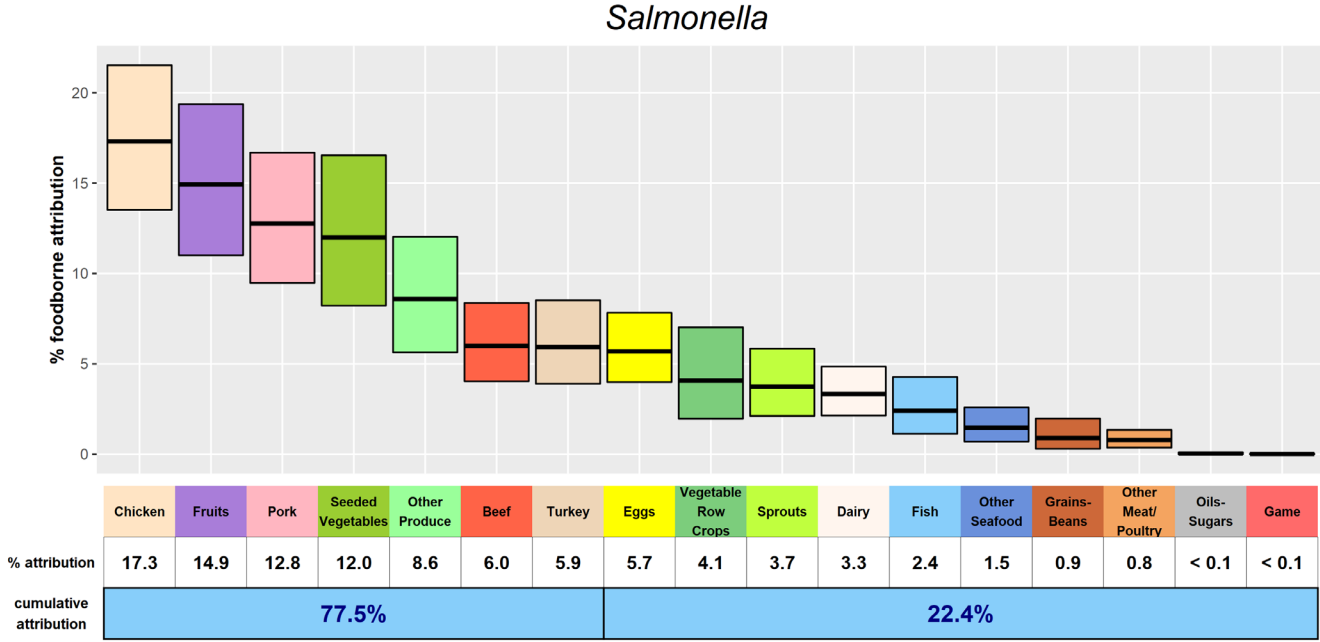


*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2016 – 2020), and exponentially less weight to each earlier year (1998 – 2015).

Overall Key Results

- The results are based on 960 outbreaks caused or suspected to be caused by *Salmonella*, 272 by *E. coli* O157, and 55 by *Listeria*.
- Estimated *Salmonella* illnesses were more evenly distributed across food categories than illnesses caused by *E. coli* O157 and *Listeria*; most of the illnesses for those pathogens were attributed to one or two food categories.
- The credibility intervals overlap for the *Salmonella* and *Listeria* 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 2020, in descending order, attributed to each of 17 food categories, based on multi-year outbreak data,* United States. [Click here to download data.](#)

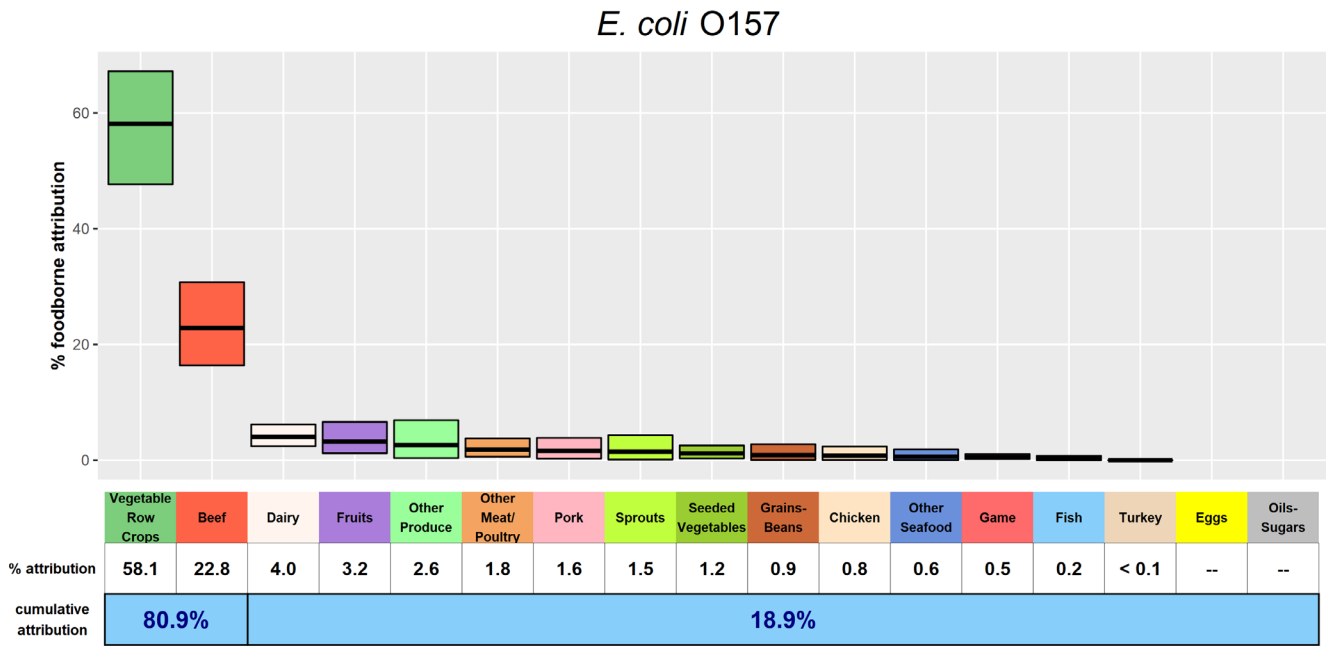


*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2016 – 2020) and exponentially less weight to each earlier year (1998 – 2015).

Salmonella Key Results

- More than 75% of illnesses were attributed to seven food categories: Chicken, Fruits, Pork, Seeded Vegetables (such as tomatoes), Other Produce (such as fungi, herbs, nuts, and root vegetables), Beef, and Turkey.
- The credibility intervals for each of the seven food categories that account for 77.5% of all illnesses overlap with some of the others.

Figure 3: Estimated percentage of foodborne *Escherichia coli* O157 illnesses (with 90% credibility intervals) for 2020, in descending order, attributed to each of 17 food categories, based on multi-year outbreak data,* United States. Click here to download data.

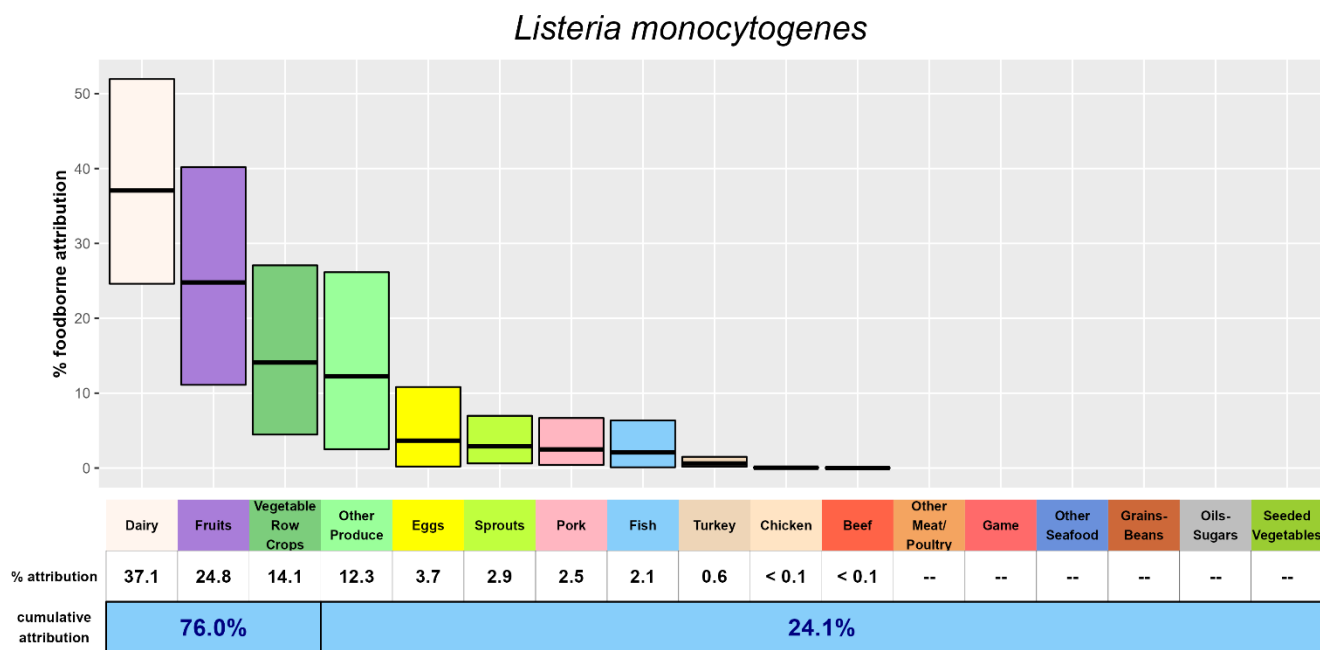


*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2016 – 2020) and exponentially less weight to each earlier year (1998 – 2015).

***E. coli* O157 Key Results**

- More than 80% of *E. coli* O157 illnesses were attributed to Vegetable Row Crops (such as leafy greens) and Beef.
- Vegetable Row Crops had a significantly higher estimated attribution percentage than all other categories.
- Beef had a significantly higher estimated attribution percentage than all categories other than Vegetable Row Crops.
- No illnesses were attributed to Eggs or Oils-Sugars.

Figure 4: Estimated percentage of foodborne *Listeria monocytogenes* illnesses (with 90% credibility intervals) for 2020, in descending order, attributed to each of 17 food categories, based on multi-year outbreak data,* United States. Click here to download data.



*Based on a model using outbreak data that gives equal weight to each of the most recent five years of data (2016– 2020) and exponentially less weight to each earlier year (1998 – 2015).

***Listeria monocytogenes* Key Results**

- More than 75% of illnesses were attributed to Dairy, Fruits, and Vegetable Row Crops.
- More than 90% of illnesses were attributed to non-meat food categories.
- The credibility intervals for the Dairy, Fruits, Vegetable Row Crops, and Other Produce categories were quite wide, partly due to the small total number of outbreaks (55 total). The credibility intervals overlapped each other, and the intervals for the Fruits, Vegetable Row Crops, and Other Produce categories overlapped those for some food categories with much smaller estimated attribution percentages, such as Eggs, Sprouts, Pork, and Fish.
- No illnesses were attributed to Other Meat/Poultry, Game, Other Seafood, Grains-Beans, Oils-Sugars, or Seeded Vegetables.

Discussion

This report uses data from 1998 through 2020 to provide outbreak-based attribution estimates for 2020 of the percentages of illnesses caused by three (*Salmonella*, *E. coli* O157, and *Listeria*) of the four priority pathogens, attributing illnesses to each of the 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 using data from the years 2004 to 2011 found that outbreak and sporadic infections caused by the four priority pathogens (*Salmonella*, *E. coli* O157, *Listeria*, and *Campylobacter*) were generally demographically similar; this finding supports the use of foodborne outbreaks for source attribution.⁸ These estimates can inform food safety decision-making and provide pathogen-specific direction for reducing foodborne illness.

In 2020, only 24 outbreaks caused by the three pathogens this report covers met inclusion criteria for the model, a lower number for these pathogens than in previous years (e.g., 59 in 2016, 66 in 2017, 65 in 2018, 59 in 2019). There are several possible reasons for these differences.⁹ First, changes in healthcare-seeking behaviors due to the COVID-19 pandemic may have decreased the detection of illnesses and reduced the number of reported outbreaks. Second, public health interventions implemented to prevent the spread of SARS-CoV-2, such as restaurant and school closures, may have reduced exposures to contaminated food and, thus, the number of illnesses and outbreaks. Third, fewer events and gatherings typically associated with outbreaks may have occurred in 2020, reducing the opportunities for outbreaks to occur. Finally, the pandemic consumed public health resources, which likely resulted in a reduced capacity for investigating clusters of illnesses and may have reduced the number of recognized and reported outbreaks.

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. Similar to prior reports, Vegetable Row Crops had a significantly higher estimated attribution percentage than all other food categories.

As with *E. coli* O157, most *Listeria* illnesses were also 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,¹⁰ and outbreaks from fruits contaminated by *Listeria* have been observed in recent years.

Unlike in prior IFSAC Annual Reports, attribution estimates for *Campylobacter* are not presented in this year's report due to continued concerns about the limitations of using outbreak data to attribute *Campylobacter* illnesses to sources. As described in prior reports, these concerns are largely due to the outsized influence of outbreaks in certain foods, as described below, that pose a high individual risk for *Campylobacter* infection but do not represent the risk to the general population. Most of the reported *Campylobacter* outbreaks related to dairy were associated with unpasteurized milk (145/160, 91%), which is not widely consumed. The most recent FoodNet Population Survey estimates[†] indicate that only 2% of respondents reported consuming raw milk in the previous seven days. Similarly, the majority of *Campylobacter* outbreaks related to chicken were due to chicken liver products (38/67, 57%), which are not widely consumed. An analysis of National Health and Nutrition Examination Survey (NHANES) data found that only about 0.1% of all chicken products consumed are

[†]<https://www.cdc.gov/FoodNetFast/PopSurvey>

liver or liver-derived.[‡] Other studies have found that consumption of raw milk and chicken liver each confers a higher individual risk of infection than most other foods, but that consumption of poultry, beef, and pork confers the highest population risk.¹¹⁻¹⁷ A lack of representativeness heightens the likelihood that the sources of reported *Campylobacter* outbreaks differ considerably from the sources of non-outbreak-associated illnesses. In response to these limitations, IFSAC analysts are developing other methods to estimate the sources of *Campylobacter* infection. IFSAC's priorities and activities are described in the 2022 – 2023 [strategic plan](#).¹⁸

This analysis includes two *Listeria* outbreaks that spanned multiple years and were not included in prior reports because the investigations had not been completed. Each of the outbreaks had a first illness onset date before 2020 and a last illness onset date during or after 2020. These outbreaks were solved in large part because whole-genome sequencing (WGS) was used to link human and food isolates from multiple years.

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 illnesses in 34% (1,287 of 3,749) of reported outbreaks caused by the three pathogens because we excluded outbreaks that occurred in a U.S. territory, those in which the implicated food could not be assigned to a single food category, and those that did not meet our pathogen inclusion criteria. The ones we included might not be representative of all outbreaks caused by 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

IFSAC'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.

IFSAC continues to enhance attribution efforts through projects that address the limitations identified in this report. For more information on IFSAC's completed and ongoing projects, visit <http://www.cdc.gov/foodsafety/ifsac/index.html>.

[‡] FSIS analyzed nine two-year cycles (1996–2016) of National Health and Nutrition Examination Survey (NHANES) data constituting 18 years of food consumption data. They estimated the U.S. population average daily consumption of chicken livers and all chicken products using population weights provided.

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