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Outbreak-associated *Salmonella enterica* Serotypes and Food Commodities, United States, 1998- 2008

Salmonella enterica is estimated to cause 1.2 million illnesses each year in the United States and to be the leading cause of hospitalizations and deaths from foodborne disease. Overall, salmonellosis incidence has not decreased in the past decade; the incidence has substantially increased for some serotypes and decreased for others.

Salmonella serotypes differ in their natural reservoirs and ability to cause human infections; only a small proportion of more than 2,500 serotypes cause most human infections. In 2009, only 20 serotypes comprised more than 82 percent of the approximately 36,000 serotyped human-derived *Salmonella* isolates in the United States that were reported to the Centers for Disease Control and Prevention.

Outbreak data and case–control studies have linked some serotypes to certain foods or exposures. Information obtained during outbreak investigation is a key tool in understanding which foods are common sources of pathogens contributing to foodborne infections. During outbreak investigations, illnesses can be linked to a particular food by using epidemiologic or laboratory evidence. We analyzed foodborne disease outbreak data to determine associations between food commodities and serotypes to help inform future outbreak investigations, foodborne illness source attribution analyses, and control measures.

State, local, and territorial health departments voluntarily submit reports of foodborne disease outbreak investigations to the Foodborne Disease Outbreak Surveillance System, or the FDOSS, of the Centers for Disease Control and Prevention. A foodborne disease outbreak is defined as more than two cases of a similar illness resulting from ingestion of a common food. Submitted reports include a description of the pathogen, the implicated food or foods, the main ingredients of the food, and the contaminated ingredient, if known. When a *Salmonella* species is the etiologic agent, public health laboratories serotype the isolate. A *Salmonella* species is considered the confirmed etiology of an outbreak when the same serotype is isolated from more than 2 ill persons or when the bacterium is isolated from an epidemiologically implicated food.

To standardize the analysis of foods, we used a modified version of an existing classification scheme to categorize reported foods into 1 of 20 mutually exclusive food commodities. Foods were classified into a single food commodity if a single ingredient was implicated or if all ingredients in a food belonged to a single food commodity. We then combined the individual food commodities into three broad food commodity groups: 1) aquatic animal–derived; 2) land animal–derived; and 3) plant-derived food commodities.

We reviewed all reports of foodborne outbreaks of *Salmonella* infections to FDOSS during 1998–2008 and included in the analysis those outbreaks caused by a single, laboratory-confirmed serotype. We excluded outbreaks in which multiple etiologies were reported, that had an unknown serotype, or that could not be assigned to 1 of the 20 food commodities.

Among all salmonellosis outbreaks and for each *Salmonella* serotype, we calculated the frequency and percentage of outbreaks associated with each food commodity. For each serotype, we also determined the percentage of outbreaks associated with animal-derived food commodities and plant-derived food commodities. We calculated the Gini coefficient as a descriptive measure of the magnitude of food commodity diversity, or inequality among outbreaks caused by a particular serotype. The Gini coefficient was chosen as a measure of diversity because it provides an easily interpretable range of values from 0 to 1. A Gini coefficient of 0 indicates an equal distribution of outbreaks caused by a serotype across all food commodities, and a value of 1 indicates that all outbreaks were attributed to a single food commodity.

We found notable relationships between *Salmonella* serotypes and food commodities that point to major food reservoirs for different serotypes. Certain serotypes, in particular Enteritidis, Heidelberg, Hadar, and Infantis, caused outbreaks predominantly attributed to specific animal-derived food commodities. We also identified serotypes that commonly caused outbreaks associated with plant-derived food commodities, particularly the fruit, vine–stalk vegetable, sprouts, and leafy vegetable food commodities. These serotypes that cause plant-associated outbreaks were found relatively infrequently in *Salmonella* reservoir studies of livestock, which suggests that serotypes with non-livestock reservoirs may be more likely to cause outbreaks by plant-based food vehicles. For example, during an outbreak investigation of serotype Poona infections attributed to cantaloupe consumptions, investigators suspected that melons might have been indirectly contaminated through packing equipment or wash water contaminated by reptiles. Our findings regarding plant-associated serotypes are particularly relevant given recent increases in *Salmonella* outbreaks attributed to fruits or vegetables and a concurrent increase in infection caused by serotype Javiana, a serotype that, compared with other common serotypes in this study, caused a higher percentage of plant-derived food commodity–associated outbreaks.

Our findings of predominant animal-derived food commodities for specific serotypes are supported not only by animal reservoir studies, but also by case–control studies of sporadic illness. Although the percentage of outbreaks attributed to a specific food commodity is not directly comparable to the population–attributable fraction estimated in case–control studies, our results and those of case–control studies show similar dominant food commodity reservoirs for some serotypes.

The high percentages of serotype Heidelberg outbreaks attributed to eggs, chicken, and turkey are also supported by findings from case–control studies and previous reviews. These findings suggest that these products are common vehicles for this serotype. The link we found between serotype Hadar and turkey is consistent with historical data and animal surveillance data showing that serotype Hadar is now the most common serotype isolated from turkey. The link we found between serotype Infantis and pork is also consistent with animal surveillance data showing that this serotype is commonly isolated from swine but not poultry. Three of the four serotypes with the lowest food commodity diversity measured by the Gini coefficient (Enteritidis, Heidelberg, and Hadar) were predominantly associated with eggs and poultry, suggesting that these serotypes are well adapted to poultry reservoirs and are a well-defined target for control measures.

Two of the most common *Salmonella* serotypes, Typhimurium and Newport, had a wider range of implicated food commodities. Serotype Typhimurium has a well-characterized ability to infect various species and can survive for a long time in the environment; these 2 factors enhance the ability of this serotype to be one of the most common causes of salmonellosis in the United States. Although we found serotype Typhimurium was associated with several animal commodities, the most common food commodity was chicken. Among pork-associated outbreaks, Typhimurium was the most common serotype, which corroborates animal data showing that serotype Typhimurium has emerged as the predominant serotype in swine.

For *Salmonella* serotype Newport, diversity of implicated food commodities might be related to intraserotype genetic variation because several distinct clades have been identified.

Antimicrobial drug resistance data might be helpful for differentiating serotype Newport infections transmitted through animal commodities versus those transmitted by plant-derived food commodities. A sporadic case-control study found associations between infections with multidrug-resistant strains of *Salmonella* serotype Newport and beef and egg consumptions, whereas infections with pansusceptible strains was associated with direct or indirect exposure to frogs or lizards. In a similar manner, strains of serotype Newport causing several outbreaks attributed to beef or dairy products have been multidrug resistant, whereas outbreaks attributed to produce have generally been pansusceptible. Therefore, pansusceptibility might be a marker for serotype Newport strains with environmental reservoirs and a greater potential for transmission through produce. Our findings support the hypothesis that *Salmonella* serotypes with environmental, amphibian, or reptile reservoirs might be more likely to be transmitted by fresh produce.

All outbreaks caused by *Salmonella* serotypes Litchfield and Poona were attributed to fruit. These 2 serotypes were responsible for 25 percent of fruit outbreaks despite representing only 2 percent of outbreaks caused by all serotypes in our study. Both serotypes have been established as reptile associated and reptiles might play a role in fruit contamination. In a similar manner, 70 percent of outbreaks caused by serotype Javiana, a serotype associated with reptile and amphibian contact, were linked to plant-derived food commodities.

Among *Salmonella* serotypes causing small numbers of outbreaks, several had particular animal reservoirs.

Salmonella serotype Agona also caused outbreaks attributed to chicken and turkey, consistent with animal surveillance data documenting its frequent isolation in swine, chicken, and turkey since its introduction in animal feed.

Outbreak-associated illnesses represent only a small fraction of all *Salmonella* infections, and food vehicles responsible for outbreaks might differ from those causing sporadic infections. During the 11 years of our study, changes in product contamination frequency or consumption patterns might be associated with changes in the distribution of serotypes causing illness in the general population or the proportion of sporadic illnesses associated with specific food commodities. In a recent analysis of the distribution of serotypes causing foodborne disease outbreaks, the proportion of outbreaks caused by serotype Enteritidis decreased from 44 percent

of *Salmonella* outbreaks during 1998–2000 to 24 percent during 2006–2008, and the percentage of outbreaks caused by *Salmonella enterica* remained relatively constant.

Although outbreak data provide one of the only direct connections between food sources and infections, outbreak investigations are frequently unable to confirm the single contaminated food vehicle, limiting our ability to detect major changes over time. In our study, less than 33 percent of outbreaks had an implicated food that could be assigned a commodity. Investigators may also report suspected food vehicles on the basis of prior knowledge of the most likely foods associated with the serotype; this reporting technique would bias results toward these typical foods. Although genetic heterogeneity and differences in reservoirs exist within serotypes, our results demonstrate that serotyping provides helpful discrimination among certain serotype–food commodity pairs. Further subtyping of *Salmonella* serotypes could help identify major subtype–food commodity relationships, particularly for common serotypes like Enteritidis and Newport.

This systematic examination of foodborne disease outbreaks by *Salmonella* serotype and implicated food commodity provides major evidence linking serotypes to likely reservoirs and pathways of food contamination. Our analysis could have used outbreak-associated illnesses rather than outbreaks; the attributed sources would have been the same, but the percentages would have differed. However, the goal of this study was to describe major commodity sources by serotype, and this goal was not greatly influenced by the number of outbreak-associated illnesses. Using outbreaks or illnesses for analysis would not provide information about the proportion of sporadic illnesses that can be attributed to specific food commodities; more complex models are needed for such analyses. The results of our analysis can provide guidance to investigators when forming hypotheses about contaminated food sources during outbreak investigations, and in suggesting the likely contaminated ingredient in outbreaks associated with foods containing ingredients from multiple commodities. Investigators should also remain alert to uncommon or novel food vehicles, which are regularly being identified. Armed with knowledge of serotype–food commodity associations, public health officials may be able to more quickly form hypotheses, identify likely sources of contamination, and prevent illnesses.

This is an abridged version of an EID article, Outbreak-associated *Salmonella enterica* Serotypes and Food Commodities, United States, 1998- 2008, published in the August 2013 issue of *Emerging Infectious Diseases* at cdc.gov/eid.

If you would like to comment on this presentation, send an email to eideditor@cdc.gov. I'm Dr. Mike Miller for *Emerging Infectious Diseases*.

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