

Trends of foodborne diseases in China: lessons from laboratory-based surveillance since 2011

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Abstract Foodborne disease is one of the most important public health issues worldwide. China faces various and unprecedented challenges in all aspects of the food chain. Data from laboratory-based foodborne disease surveillance systems from 2013 to 2016, as well as different regions and ages, can be found along with differences in the patterns of pathogens detected with diverse characteristics. *Vibrio parahaemolyticus* has been the leading cause of infectious diarrhea in China, especially among adults in coastal regions. *Salmonella* has been a serious and widely distributed pathogen responsible for substantial socioeconomic burden. *Shigella* was mostly identified in Northwest China and the inland province (Henan) with less-developed regions among children under 5 years. Data from foodborne disease outbreak reporting system from 2011 to 2016 showed that poisonous animals and plant factors responsible for most deaths were poisonous mushrooms (54.7%) in remote districts in southwest regions. The biological hazard that caused most cases reported (42.3%) was attributed to *V. parahaemolyticus*, the leading cause of foodborne outbreaks. In this review, we summarize the recent monitoring approach to foodborne diseases in China and compare the results with those in developed countries.

Keywords foodborne diseases; surveillance; TraNet; China

Introduction

Foodborne disease (or foodborne illness) caused by the consumption of food contaminated with microbes, poisonous chemicals, or other harmful substances is a constant threat to public health and a significant impediment to socioeconomic development worldwide [1]. Foodborne disease outbreaks are common and often cause considerable morbidity and mortality. Historically, several catastrophic outbreaks have occurred in China, such as the raw consumption of clams contaminated with hepatitis A virus in 1988 in Shanghai that affected 292 301 people with 11 deaths [2]; the Shiga toxin-producing *Escherichia coli* (STEC) O157:H7 outbreak in 1999, leading to 195 patients being hospitalized with hemolytic uremic syndrome

(HUS) with 177 deaths [3]; and the recent melamine contamination of infant milk formula in 2008 that resulted in 294 000 illness cases, 50 000 hospitalizations, and 6 deaths [4]. The three cases were only at the “tip of the iceberg” of foodborne outbreaks that actually occurred.

Consequently, China faces various and unprecedented challenges in all aspects of the food chain [5–7]. Challenges faced by other countries include globalization of food marketing and distribution along with growing industrialization of food and feed production, as well as intensive farming. These developments catalyzed the appearance and spread of some unique pathogens [8]. Allied to these, the gaps between China and industrialized countries, including social economy, population size, health care system, technical capacity, level of oversight, and food safety compliance, remain significant [5]. Moreover, as economic development is unbalanced across different regions in China, many fragmented, small-scale, family workshop-style firms continue to dominate the local food production, a feature that warrants close attention

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[7,9]. Furthermore, lifestyle changes, such as the increased consumption of fresh and prepared foods, increase the risk from farm to fork [10]. Foodborne diseases appear to be emerging more frequently than ever before, and the capacity of the public health authorities to apply conventional control measures does not seem to be developing at the same speed [8]. Though the government has made efforts to improve surveillance and control of food safety by focusing on inspection, primarily end-product testing, the infrastructure and capacity of the foodborne disease surveillance system remain relatively limited in China [7,11]. The event involving melamine in baby formula that occurred in 2008 highlighted the vulnerability of the surveillance system in China. Consequently, the China National Center for Food Safety Risk Assessment (CFSA) launched a laboratory-based foodborne disease surveillance system along with a foodborne disease outbreak reporting system from 2011. Currently, all provincial centers for disease control and prevention (CDCs) conduct molecular subtyping using pulsed-field gel electrophoresis (PFGE) as a critical part of the TraNet (National Foodborne Disease Molecular Tracing Network) surveillance network on foodborne bacterial strains. Samples are submitted by sentinel hospitals and PFGE profiles are uploaded to a national database for further analysis since 2013. China is currently developing and implementing a foodborne disease surveillance system using a step-by-step approach that addresses existing regional, economic, and traditional differences across the country. This review will describe the current foodborne surveillance systems in China, which uses the collected data both from surveillance and literature.

Top five foodborne pathogens identified through the national surveillance program and comparisons with trends reported by FoodNet

The most important challenge of food safety globally relates to foodborne diseases caused by microorganisms. In 2011, CFSA launched a laboratory-based foodborne disease surveillance system. Between 2011 and 2012, the main task was to build the surveillance infrastructure, and in 2012, this work had been carried out in 111 sentinel

hospitals of 7 provinces to detect *Salmonella* species, *Shigella* species, and *Vibrio parahaemolyticus* from outpatient settings. Later, from 2013 to 2016, more sentinel hospitals ($n = 703$ in 2016) were added to the system and requested to identify foodborne pathogens, including *Salmonella* species, *Shigella* species, *V. parahaemolyticus*, diarrheagenic *Escherichia coli* (DEC), and norovirus, which were all from stools of diarrheal outpatient settings. Strains isolated by clinical laboratories are required to be forwarded to public health laboratories at local CDCs for further subtyping and characterization.

From the database, the average isolation rate of foodborne pathogens detected from diarrheal patients from 2013 to 2016 was 11% and for each pathogen were as follows: norovirus (6.8%), *Salmonella* species (2.9%), *V. parahaemolyticus* (2.1%), DEC (2.2%), and *Shigella* species (0.5%) (Table 1). In the four consecutive years of surveillance, no significant difference has been found among the five pathogens observed (Table 1). A strong seasonal pattern was noted for these organisms, including the prevalence of norovirus in winter and autumn months and those of bacteria in summer months.

Furthermore, most of these isolates were successfully serotyped, and some were subtyped by molecular methods to identify the predominant subtypes. For *Salmonella* species, among the 7240 (56.6%) serotyped, the top serotypes identified were Typhimurium (33.3%), followed by Enteritidis (23.9%). In the case of *V. parahaemolyticus*, among the 2973 (32.9%) serotyped *V. parahaemolyticus* isolates, the most common serotypes were O3:K6 (51.0%) and O4:K8 (13.2%). For *Shigella* species, among the 1722 (79.8%) serotyped *Shigella* isolates, the top serotype was *Shigella flexneri* (49.7%) followed by *Shigella sonnei* (31.0%). For DEC, among the 5683 (67.9%) DEC isolates characterized by the PCR method designed to detect the virulence genes, enteroaggregative *E. coli* (EAEC) (38.3%) was the most common pathotype identified, followed by enterotoxigenic *E. coli* (ETEC) (28.5%) and enteropathogenic *E. coli* (EPEC) (28.2%).

Large gaps exist in the Chinese surveillance system, as well as comparable differences with other systems. (1) Foodborne Disease Active Surveillance Network (FoodNet) is an active surveillance network in the USA since 1996 that tracks the number of foodborne illnesses,

Table 1 Isolation rates of foodborne pathogens from diarrheal patients from 2013 to 2016

Year	<i>Salmonella</i> % (no. positive/samples)	<i>Shigella</i> % (no. positive/samples)	<i>V. parahaemolyticus</i> % (no. positive/samples)	Diarrheagenic <i>E. coli</i> % (no. positive/samples)	Norovirus % (no. positive/samples)
2016	3.39 (4698/138 555)	0.39 (532/138 019)	2.94 (3986/135 530)	3.13 (3347/106 809)	5.37 (3436/63 972)
2015	2.78 (3443/123 819)	0.49 (605/123 055)	1.68 (2020/120 128)	2.79 (2861/102 495)	7.24 (3849/53 198)
2014	2.64 (2790/105 873)	0.52 (515/99 289)	1.87 (1778/95 028)	1.48 (1391/93 807)	10.14 (1961/18 893)
2013	2.83 (2414/85 316)	0.64 (543/85 312)	1.62 (1251/77 330)	0.97 (738/75 952)	/ (/)
Total	2.94 (13 345/453 563)	0.49 (2195/445 675)	2.11 (9035/428 016)	2.20 (8337/379 063)	6.76 (9201/136 063)

/, no detection in that year.

monitors trends in incidence of specific foodborne illnesses over time, attributes illnesses to specific foods and settings, and disseminates information [12]. It is a collaboration between CDC, 10 state health departments, the US Department of Agriculture's Food Safety and Inspection Service (USDA-FSIS), and the Food and Drug Administration (FDA), and monitors the incidence of laboratory-confirmed infections caused by nine bacterial and parasitic pathogens transmitted commonly through food (namely, *Campylobacter*, *Cryptosporidium*, *Cyclospora*, *Listeria*, *Salmonella*, STEC, *Shigella*, *Vibrio*, and *Yersinia* species). In the Chinese system, only five pathogens, including four bacteria and one virus, have been monitored. (2) Since 2012, culture independent diagnostic tests (CIDT), including antigen-based and/or commercial DNA-based panel tests, that are often ordered based on a clinical syndrome rather than a specific suspected pathogen represent a major shift in clinical microbiology practices and have important implications for physicians, patients, and public health [13]. Of note, the incidence of *Cryptosporidium* and STEC non-O157 infections in 2015 was significantly higher than the average for the previous 3 years using this method; moreover, it is the main current method used in China to identify bacterial pathogens by culture, along with the PCR method for DEC and Virus. (3) Another notable difference between both surveillance systems is that FoodNet can monitor trends in the incidence of specific foodborne illnesses over time but TraNet cannot, because only a minority of patients with food poisoning will seek medical care; hence, epidemiological investigation is not well developed and foodborne diseases often go undetected. (4) Some of the prevailing serotypes are different: FoodNet reported among 6827 (88%) *Salmonella* isolates that were serotyped, the top serotypes detected were Enteritidis, 1358 (20%); Newport, 816 (12%); and Typhimurium, 739 (11%) [14], a trend that is different compared with the top serotypes reported in China.

Major pathogens and their geographic regions locations

In China, differences in demographic, socioeconomic, environmental hygiene, and geographic factors across different regions are notable. In different regions, the patterns of pathogens have diverse characteristics. Based on the data obtained from the laboratory-based foodborne disease surveillance system from 2013 to 2016, the following features can be noted.

V. parahaemolyticus as the leading pathogen in coastal regions and big cities

V. parahaemolyticus is the leading cause of foodborne outbreaks and cases of infectious diarrhea in China

especially in coastal regions [15,16]. From the surveillance database, this bacterium can be detected in all but three provinces, with positive rates ranging 0.1%–7.3%. The top 10 positive rates (1.1%–7.3%) are mostly in coastal and big cities where the consumption of seafood is popular. However, the isolate rates in two coastal provinces, Guangdong and Guangxi, are relatively lower than those of other coastal provinces. The main reason is the selection of sentinel hospitals with different clinical laboratory practices, and this has also been found in FoodNet [17].

Two surveys in Shanghai, a coastal city located in the eastern part of China, showed that the prevalence of *V. parahaemolyticus* was the predominant bacterial pathogen isolated from outpatients, with a prevalence of 8.3% from 2006 to 2011 [15] and 5.0% from 2013 to 2014 [18], possibly because of favorable environmental factors, because *V. parahaemolyticus* is widely distributed in temperate, oceanic, and coastal environments. Consumption of contaminated seafood, which is a leading cause of acute diarrhea in adults, is largely responsible for the high isolation rate of *V. parahaemolyticus* in this region. Another surveillance program from 2007 to 2012 showed that *V. parahaemolyticus* (6.0%) was also a major cause of diarrhea in Shenzhen in the southern coastal region of China [16]. Unlike the patients in Shanghai, most patients were transient residents who lived in rural areas and seldom ate seafood. However, epidemiologic data showed that *V. parahaemolyticus* infections were associated with eating outside the home and consumption of salad vegetables. Cross contamination in food preparation might be the source of infection [19].

Widely disseminated *Salmonella* species in China

Salmonella enterica, the etiologic agent of salmonellosis, is an endemic foodborne pathogen that causes heavy global socioeconomic burden. From the surveillance database, *S. enterica* has been detected in all provinces except for Tibet (for which no surveillance data exists), with positive rates ranging from 0.3% to approximately 9.7%. The top 10 positive rates were reported mostly in inland regions and big cities. Of these, the two most common serotypes are Typhimurium (33.3%) and Enteritidis (23.9%).

Recent years, non-typhoidal *Salmonella* (NTS) has been recognized as the dominant pathogen in foodborne diseases in China [20–23]; moreover, in some regions, its prevalence has increased to 12.1% [24]. From a national surveillance of *Salmonella* in 2008, *Salmonella* (3.0%) were commonly detected between April and October, during which *S. enterica* serovar Enteritidis (31.4%) and *S. enterica* serovar Typhimurium (27.3%) were the most common serotypes [25]. In Shanghai *S. enterica* serovar Enteritidis and *S. enterica* serovar Typhimurium were also the most commonly detected serotypes, which account for

27.6% and 25.5%, respectively [23]. However, the distribution of other *S. enterica* serotype varied among regions, many of them having notable distribution patterns. The most common serotype from Henan were *S. enterica* serovar Typhimurium (26.9%), *S. enterica* serovar Enteritidis (16.8%), and *S. enterica* serovar Derby (9.6%) [26]. Similarly, in Guangdong Province, *S. enterica* serovar Typhimurium (30%), followed by *S. enterica* serovar 4,5,12:i:- (14%) and *S. enterica* serovar Enteritidis (13%) were common [27]. *Salmonella* serotype 4,5,12:i:- is a monophasic variant of serotype Typhimurium with similar antigenic and genotypic characteristics, and this serotype is becoming one of the most common to be reported in Guangdong. In Europe, the monophasic *S.* serotype 4,5,12:i:- has exhibited a marked increase and is being linked to foodborne infections in particular pig meat [28]. This serotype has also been recognized as an emerging cause of infection in other countries [28].

***Shigella* in the Northwest and Central China**

Currently, shigellosis remains a major health problem in many parts of world, especially in children under 5 years old and living in developing countries [29]. From the TraNet database, *Shigella* has been detected in all provinces except for Tibet (no surveillance data) with positive rates ranging approximately 0.04%–3.6%. The top four positive rates were mostly reported in Northwest China (Ningxia, Xinjiang, and Qinghai) and the inland province (Henan). In this case, the top species reported was *Shigella flexneri* (49.7%) along with *Shigella sonnei* (31.0%).

The same trend was also presented by another surveillance of bacillary dysentery [30]. Northwest China (Tibet, Xinjiang, Gansu, and Ningxia), Beijing, and Tianjin consistently had higher incidence rates of bacillary dysentery from 2004 to 2014 than other regions, and *S. flexneri* (63.9%) was the most prevalent species followed by *S. sonnei* (34.9%) [30]. The high incidence rates of northwest regions were consistent with their relatively low gross domestic production, and high rates in Beijing and Tianjin could be explained by the high-population density, having numerous transient people living in the suburban areas without proper sanitation and access to clean water. Similar to the reports in developed countries, *S. sonnei* was the dominant species observed in Beijing and Shanghai, but in some less developed regions, such as Anhui, Henan, and Shanxi, *S. flexneri* remains the predominant species [30].

Public health risks associated with EAEC

DEC infection is a major health problem in developing countries [31]. Prevalence and characteristics of DEC have not been thoroughly investigated in China. From surveil-

lance database, DEC has been detected in all provinces (except Tibet) with the positive isolate rate ranging 0.04%–16.2%. The top prevalent rates were mostly detected in big cities (Beijing and Shanghai) and inland provinces. Main subtypes were EAEC followed by ETEC and EPEC, and this is the same in a surveillance of 29 provinces in China during 2012–2015 [32].

More recently, EAEC has been identified as an important cause of acute diarrhea in children and adults in many countries. Literature showed the high public health risks associated with EAEC as a foodborne pathogen [33]. Of particular note is the major outbreak of Stx-producing EAEC serotype O104:H4, which was first identified in northern Germany in May 2011 and epidemiologically associated with the consumption of fenugreek sprouts [34]. These outbreaks indicated that the horizontal gene transfer of such elements powers *E. coli* genomic plasticity and is the driver for the continuous emergence of new pathotypes [34].

Leading pathogens in children under 5 years of age

Diarrhea is one of the leading causes of morbidity and mortality among children aged under 5 years and has an estimated rate of 1.73 billion episodes and 711 800 deaths each year [35]. The diverse patterns of pathogens have existed in different ages. From the surveillance database, the proportion of diarrhea cases by age groups of four bacterial pathogens showed that cases in children (under 5 years of age) accounted for 48.6% (*Salmonella*), 38.1% (*Shigella*), and 24.9% (DEC) of each total number (Fig. 1).

A survey on the prevalence of bacterial pathogens isolated from childhood diarrhea in Beijing showed that DEC ranked first with the most prevalent category EPEC (4.6%) followed by *Salmonella* (4.3%) and *V. parahemolyticus* (0.4%) [22]. This finding was consistent with the microbiological results from PubMed's 5 years (2009–2013) of surveillance data of diarrheal illness among children aged < 5 years who were presented to a hospital outpatient setting in China, showing that the most commonly detected pathogens were rotavirus (29.7% of cases), norovirus (11.8%), DEC, with the most prevalent category, EPEC (5.0%), adenovirus (4.8%), non-typhoidal *Salmonella* (NTS; 4.3%), and *Shigella* (3.6%) [36]. In case of *Shigella*, cases in children < 5 years accounted for 31.47% of the total number [37]. With children aged < 5 years, DEC, especially for EPEC, *Salmonella*, *Shigella*, and rotavirus were the burden and etiology of diarrheal diseases in infants and young children in China and this has also been proved in developing countries by the Global Enteric Multicenter Study [38]. In Guangdong Province, *S. enterica* serovar Typhimurium and *S. enterica* serovar 4,5,12:i:- affected infants, whereas *S. enterica* serovar Enteritidis affected adults [20].

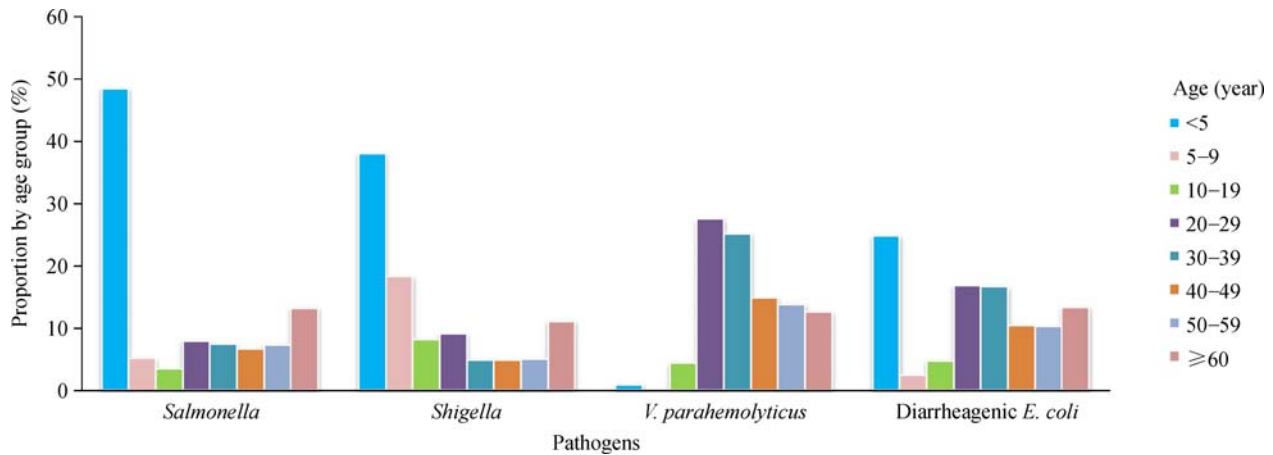


Fig. 1 Proportion of diarrhea cases by age groups of four different pathogens.

V. parahaemolyticus in young working people

From the surveillance database, more than half of *V. parahaemolyticus* infections (52.8%) occurred often in patients aged 20–40 years, which was consistent with a 5-year surveillance in Shanghai [39]. Another survey showed that 92.9% of patients infected with *V. parahaemolyticus* were 15–39 years of age and in a transient population living in Shenzhen [16]. *V. parahaemolyticus* infection was highly common in two adult groups, namely, 20–39 years (7.2%) and 40–59 years (5.4%) [40]. Moreover, *V. parahaemolyticus* infection mainly occurred in adults, which cost millions in lost productivity and medical and legal expenses. These results indicated that the frequency of each bacterium differed significantly among different age groups.

Pathogens of travelers

With globalization, food and people traveled more frequently; hence, pathogens disseminated more easily [41]. These pathogens vary, of which 13% of persons infected with a pathogen monitored by FoodNet had recently traveled internationally [17]. FoodNet showed that 3% of people infected with *Salmonella*, which is an important cause of travel-associated diarrhea associated with *Salmonella* serotype Typhimurium, had traveled from China [42]. The occurrence is not only in the people who travel, but may also be caused by the food, which originates or makes a stop in another part of the country and therefore may be contaminated with pathogens that are not typically encountered in China [43]. Unfortunately, we found limited information about the globalization of pathogens. This finding suggests that an efficient international cooperation is required in the near future.

Reported outbreaks caused by pathogens or poisons

During 2011–2016, the timeliness of outbreak investigation and reporting has been greatly improved, and the rate of misreporting has been decreased. The number of reported foodborne outbreaks increased from 554 per year during 1992–2010 to 1777 per year during 2011–2016 (Table 2). Data from the system have identified the role of high-risk foods and risk factors in outbreaks caused by pathogens, chemical factors, and poisonous animals and plants. During 2011–2016, 10 664 outbreaks (1777 per year), 113 986 cases (18 998 per year), and 803 deaths (134 per year) were reported. The causes in the most cases were microorganisms (48 250 cases, accounting for 42.3%) of bacteria (46 829 cases) and virus (1421 cases), followed by poisonous animals and plants (15 101 cases, 13.2%), poisonous mushroom (11 835 cases, 10.4%), and chemicals (6791 cases, 6.0%). At the same time, the major cause of deaths was consumption of poisonous mushrooms (440 deaths, 54.7%), followed by chemical exposures (133, 16.6%), poisonous animals and plants (109, 16.6%), and microorganisms (52, 6.5%).

Many differences were observed compared with the data from the Surveillance for Foodborne Disease Outbreaks in the USA from 2011 to 2015 [44–47]. (1) The cause of most deaths was poisonous mushrooms: among the 803 deaths reported in China from 2011 to 2016, 440 (54.7%) were attributed to poisonous mushrooms, whereas in the USA, 104 deaths (86.7%) were attributed to bacterial etiologies from 2011 to 2015 (*Listeria monocytogenes* [61 deaths], *Salmonella* [21 deaths]) [44–47]. Many cities in China commercially sold cultivated mushrooms, which are consumed by most citizens every day. Nonetheless, the Chinese generally believe that wild-harvested products, including mushrooms, have high nutritional and medicinal

Table 2 Reported outbreaks caused by etiologies: Foodborne Disease Outbreak Surveillance System, China, from 2011 to 2016

Year	Poisonous mushroom			Microorganism			Poisonous animals and plants			Chemicals			Others		
	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths
2016	991	4230	146	778	12 910	4	469	3179	34	193	1438	13	1625	11055	16
2015	794	3199	79	444	7861	12	320	3084	23	157	1070	17	686	6160	8
2014	354	1783	61	437	8181	12	252	3089	17	108	1040	18	329	3558	3
2013	226	1309	47	320	7162	2	183	2038	22	81	687	15	191	3217	4
2012	201	831	76	255	6844	11	96	1185	13	107	1305	25	258	3514	12
2011	104	483	31	212	5292	11	108	2526	0	112	1251	45	273	4505	26
Total	2670	11 835	440	2446	48 250	52	1428	15 101	109	758	6791	133	3362	32 009	69

values. The risky behavior of collecting and consuming wild mushrooms happens mostly in remote districts in household clusters, such as Yunnan, Guizhou, and Hunan provinces, which are located in the southwest and less-developed regions. (2) For the bacterial etiologies of most outbreaks and illnesses, in the USA, bacteria caused most outbreaks (1124 outbreaks, 25 327 illnesses), followed by viruses (808 outbreaks, 20 536 illnesses) from 2011 to 2015 [44–47], whereas bacteria caused 2382 outbreaks (46 829 illnesses), with only 64 virus outbreaks (1421 illnesses) in China. The reason for this phenomenon is that virus outbreak is reported by another surveillance system in China, that is, “Public Health Emergency: the National Infectious Disease Information Reporting System” which is responsible for collecting the data of infectious diseases. Most norovirus outbreaks by person-to-person transmission vehicles were reported to this system. (3) Private home is the most common location of food preparations associated with the outbreaks: among the 10 664 outbreaks and 113 986 illnesses with a reported single location where food was prepared, 4615 outbreaks (43.3%), 23 629 associated illnesses (20.7%), and 669 deaths (83.3%) were attributed to foods prepared in private homes. Among these outbreaks, most were associated with family clusters of poisonous mushrooms. Except for poisonous mushrooms, most deaths during outbreaks occurred at home and are often caused by *Pseudomonas cocovenenans* subsp. *farinofermentans*, *Botulinum* toxin, and tetrodotoxin, suggesting the lack of food safety knowledge among the public. Therefore, increasing public awareness about food safety and hand hygiene are important elements of preventing and controlling future infections and foodborne disease outbreak. Moreover, 3127 outbreaks (29.3%), 41 499 associated illnesses (36.4%), and 46 deaths (5.7%) were attributed to foods prepared in a sit-down dining-style restaurant, which is the type of restaurant most commonly reported as the location, whereas in the USA from 2011 to 2015, the reported outbreaks were 3488 (49.2%) with 49 664 illnesses (43.9%) [44–47].

Top 5 bacterial etiologies of outbreaks

Data from 2011 to 2016 supported the relatively high burden of foodborne diseases caused by microorganisms and highlighted the importance of food safety in China. The top five bacterial pathogens responsible for foodborne outbreaks in China are *V. parahaemolyticus*, *Salmonella*, *Staphylococcus aureus* (enterotoxin), *Bacillus cereus*, and DEC and have been reported to cause 1987 outbreaks (331 per year) and 38 687 cases (6448 per year). The cause that resulted in the most cases was *Salmonella* (13 219 cases, accounting for 34.2%), followed by *V. parahaemolyticus* (13 013 cases, 33.6%), *Staphylococcus aureus* (enterotoxin) (5196 cases, 13.4%), and *Bacillus cereus* (4342 cases, 11.2%) (Table 3). Compared with the data of foodborne outbreaks in the USA from 2011 to 2015 [44–47], except *Salmonella* (652 outbreaks, 16 224 cases), the relatively likely causes are human pathogenic bacteria, such as Shiga toxin-producing *E. coli* (131 outbreaks, 1668 cases), *Campylobacter* (118 outbreaks, 1477 cases), and *Clostridium perfringens* (72 outbreaks, 3106 cases).

Most common confirmed pathogen–food category pairs

Pathogen–food category pairs are important in analyzing foodborne outbreaks. Etiologic agents and food category pairs were analyzed from the 2016 data. The most common confirmed pathogen–food category pairs resulting in outbreaks, outbreak-associated illnesses, hospitalizations, and deaths from Outbreak Surveillance System are analyzed in detail in Table 4. The pathogen–food category pairs responsible for most outbreaks with a single confirmed etiologic agent were *Salmonella* in eggs (39 outbreaks), *V. parahaemolyticus* in crustacea (31), and *Salmonella* in pork (25). The pathogen–food category pairs responsible for most illnesses in outbreaks with a single confirmed etiologic agent were *Salmonella* in pork (463

Table 3 Foodborne disease outbreaks, outbreak-associated illnesses, and deaths, by bacterial etiologies: Foodborne Disease Outbreak Surveillance System, China, from 2011 to 2016

Year	<i>V. parahaemolyticus</i>			<i>Salmonella</i>			<i>Staphylococcus aureus</i> (enterotoxin)			DEC			<i>Bacillus cereus</i>		
	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths	Outbreaks	Illness	Deaths
2016	275	4567	1	186	2984	0	94	1122	0	54	903	0	61	677	2
2015	147	2315	1	101	2494	1	56	805	0	31	315	0	38	700	2
2014	134	1812	0	73	2122	1	52	825	0	20	457	0	27	617	1
2013	89	1636	2	74	1898	0	40	859	0	14	557	0	31	809	0
2012	73	1280	0	60	2089	1	45	979	1	12	583	0	28	949	0
2011	72	1403	0	45	1632	1	27	606	0	7	102	1	21	590	0
Total	790	13 013	4	539	13 219	4	314	5196	1	138	2917	1	206	4342	5

Table 4 Most common confirmed pathogen–food category pairs resulting in outbreaks, outbreak-associated illnesses, hospitalizations, and deaths: Foodborne Disease Outbreak Surveillance System, China, 2016

Etiology	Food category	No. of outbreaks	No. of illnesses	No. of hospitalizations	No. of deaths
Top five pathogen–food category pairs resulting in outbreaks					
<i>Salmonella</i>	Egg	39	237	96	0
<i>V. parahaemolyticus</i>	Crustacea	31	407	64	0
<i>Salmonella</i>	Pork	25	463	302	0
<i>V. parahaemolyticus</i>	Shellfish	18	304	16	0
<i>Staphylococcus aureus</i>	Pork	18	239	61	0
Top five pathogen–food category pairs resulting in outbreak-associated illnesses					
<i>Salmonella</i>	Pork	25	463	302	0
<i>V. parahaemolyticus</i>	Crustacea	31	407	64	0
<i>V. parahaemolyticus</i>	Pork	12	325	31	0
<i>V. parahaemolyticus</i>	Shellfish	18	304	16	0
<i>Staphylococcus aureus</i>	Pork	18	239	61	0
<i>Salmonella</i>	Egg	39	237	96	0
Top five pathogen–food category pairs resulting in outbreak-associated hospitalizations					
<i>Salmonella</i>	Pork	25	463	302	0
<i>Bacillus cereus</i>	Rice	18	227	107	0
<i>V. parahaemolyticus</i>	Chicken	6	180	105	0
<i>Salmonella</i>	Egg	39	237	96	0
<i>Salmonella</i>	Chicken	13	205	68	0

illnesses), *V. parahaemolyticus* in crustacea (407), and *V. parahaemolyticus* in pork (325). The pathogen–food category pairs responsible for most hospitalizations in outbreaks with a single confirmed etiologic agent were *Salmonella* in pork (302 hospitalizations), *Bacillus cereus* in rice (107), and *V. parahaemolyticus* in chicken (105).

Comparisons of Chinese data with those from Surveillance for Foodborne Disease Outbreaks in the USA in 2015 revealed several significant differences [44]. The pathogen–food category pairs responsible for most outbreaks with a single confirmed etiologic agent is ciguatoxin in fish (20 outbreaks), which is seldom reported in China [44]. The pathogen–food category pair responsible for most illnesses in outbreaks with a single

confirmed etiologic agent was *Salmonella* in seeded vegetables (1048 illnesses), which is not in the top 10 confirmed pathogen–food category pairs in China [44].

The main reason for these differences is the eating habit. In China, (1) eating out (including hotels, restaurants, fast food restaurants, and enterprise canteens) is the most common location for bacterial foodborne outbreaks. (2) Cross contamination of microorganisms during food handling indicates the poor compliance with hand and food hygiene practices for ready-to-eat food, such as fruits, vegetables, and meat. Moreover, aquatic products are also associated with a high-outbreak risk in China. (3) The staple food of rice and bean products is the main vehicle of *Bacillus cereus*. Otherwise, in the USA, dairy foods, which

accounted less in China, are the main vehicles for *Campylobacter*; and raw vegetables are the main sources of Shiga toxin-producing *E. coli* [44].

Lessons from laboratory-based surveillance since 2011

Surveillance systems and surveys provide vital information about the burden of foodborne illnesses in China, but they do not capture every illness. Given that only a fraction of illnesses is diagnosed and reported, we need periodic assessments of the total burden of illness to set public health goals, allocate resources, and measure the economic effects of diseases.

With the globalization of food marketing and distribution, the spread of pathogens has been a great challenge to humans. The foodborne disease surveillance system in China remains in the early stage of development in a step-wise fashion, and the system has various limitations. In comparison with some industrialized countries, foodborne disease surveillance and control are relatively new for public health officials in China. USA is one of the few countries in the world that generate good estimates of disease burden caused by foodborne infections: each year, 31 major pathogens acquired in the USA caused 9.4 million episodes of foodborne illness [48]. Approximately 90% of these foodborne infections were caused by seven pathogens: *Salmonella*, norovirus, *Campylobacter*, *Toxoplasma gondii*, *Escherichia coli* O157, *Listeria*, and *Clostridium perfringens* [48]. The health burden of foodborne diseases from UK showed 511 000–566 000 cases of foodborne illnesses each year, and *Campylobacter*, *Salmonella*, *C. perfringens*, and norovirus were the main pathogens [49]. These data reflect many years of work by experts in surveillance, laboratory detection, epidemiological investigation, and statistical analysis.

We need to strengthen the following areas: (1) Public awareness about food safety of poisonous mushrooms in remote districts should be increased. (2) Hand hygiene is an important element of preventing and controlling future infections and foodborne disease outbreak. (3) Policies on the development of interventions to reduce the burden of foodborne illness should be dependent on different regions and age groups. (4) The range of pathogens under surveillance should be spent in the future with increased data quality and exposure data. (5) TraNet should be more “real time” in identifying the etiologic causes and tracking contaminated foods in several foodborne outbreaks.

For the past decades, China has been striving to enhance its foodborne disease surveillance approaches and methodologies so that they will be more suitable for the country, and it has been striving to improve the collection and use of surveillance data to provide a foundation for food safety policies and illness prevention guidelines. Such a system

will more accurately describe the human health burden of foodborne illness and help to improve the food safety in China.

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Compliance with ethics guidelines

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References

1. Havelaar AH, Kirk MD, Torgerson PR, Gibb HJ, Hald T, Lake RJ, Praet N, Bellinger DC, de Silva NR, Gargouri N, Speybroeck N, Cawthorne A, Mathers C, Stein C, Angulo FJ, Devleesschauwer B; World Health Organization Foodborne Disease Burden Epidemiology Reference Group. World Health Organization global estimates and regional comparisons of the burden of foodborne disease in 2010. *PLoS Med* 2015; 12(12): e1001923
2. Halliday ML, Kang LY, Zhou TK, Hu MD, Pan QC, Fu TY, Huang YS, Hu SL. An epidemic of hepatitis A attributable to the ingestion of raw clams in Shanghai, China. *J Infect Dis* 1991; 164(5): 852–859
3. Xiong Y, Wang P, Lan R, Ye C, Wang H, Ren J, Jing H, Wang Y, Zhou Z, Bai X, Cui Z, Luo X, Zhao A, Wang Y, Zhang S, Sun H, Wang L, Xu J. A novel *Escherichia coli* O157:H7 clone causing a major hemolytic uremic syndrome outbreak in China. *PLoS One* 2012; 7(4): e36144
4. Chen JS. A worldwide food safety concern in 2008 — melamine-contaminated infant formula in China caused urinary tract stone in 290,000 children in China. *Chin Med J (Engl)* 2009; 122(3): 243–244
5. Chen JS. Food safety : an important public health problem in China. *Chin J Epidemiol (Zhonghua Liu Xing Bing Xue Za Zhi)* 2003; 24(8): 649–650 (in Chinese)
6. Liu X. International perspectives on food safety and regulations — a need for harmonized regulations: perspectives in China. *J Sci Food Agric* 2014; 94(10): 1928–1931
7. [No authors listed]. Food safety in China: a long way to go. *Lancet* 2012; 380(9837): 75
8. Buchholz U, Bernard H, Werber D, Böhmer MM, Remschmidt C, Wilking H, Deléré Y, an der Heiden M, Adlhoch C, Dreesman J, Ehlers J, Ethelberg S, Faber M, Frank C, Fricke G, Greiner M, Höhle M, Ivarsson S, Jark U, Kirchner M, Koch J, Krause G, Lubert

- P, Rosner B, Stark K, Kühne M. German outbreak of *Escherichia coli* O104:H4 associated with sprouts. *N Engl J Med* 2011; 365(19): 1763–1770
9. Li D, Yap KS. Climate change and its impact on food and nutrition security and food safety in China. *World Rev Nutr Diet* 2011; 102: 175–182
 10. Pei X, Li N, Guo Y, Liu X, Yan L, Li Y, Yang S, Hu J, Zhu J, Yang D. Microbiological food safety surveillance in China. *Int J Environ Res Public Health* 2015; 12(9): 10662–10670
 11. Wu Y, Chen Y. Food safety in China. *J Epidemiol Community Health* 2013; 67(6): 478–479
 12. [No authors listed]. Foodborne Diseases Active Surveillance Network, 1996. *JAMA* 1997; 277(17): 1344–1345
 13. Marder EP, Cieslak PR, Cronquist AB, Dunn J, Lathrop S, Rabatsky-Ehr T, Ryan P, Smith K, Tobin-D'Angelo M, Vugia DJ, Zansky S, Holt KG, Wolpert BJ, Lynch M, Tauxe R, Geissler AL. Incidence and trends of infections with pathogens transmitted commonly through food and the effect of increasing use of culture-independent diagnostic tests on surveillance — Foodborne Diseases Active Surveillance Network, 10 U.S. Sites, 2013–2016. *MMWR Morb Mortal Wkly Rep* 2017; 66(15): 397–403
 14. Huang JY, Henao OL, Griffin PM, Vugia DJ, Cronquist AB, Hurd S, Tobin-D'Angelo M, Ryan P, Smith K, Lathrop S, Zansky S, Cieslak PR, Dunn J, Holt KG, Wolpert BJ, Patrick ME. Infection with pathogens transmitted commonly through food and the effect of increasing use of culture-independent diagnostic tests on surveillance—Foodborne Diseases Active Surveillance Network, 10 U.S. Sites, 2012–2015. *MMWR Morb Mortal Wkly Rep* 2016; 65(14): 368–371
 15. Zhang Y, Zhao Y, Ding K, Wang X, Chen X, Liu Y, Chen Y. Analysis of bacterial pathogens causing acute diarrhea on the basis of sentinel surveillance in Shanghai, China, 2006–2011. *Jpn J Infect Dis* 2014; 67(4): 264–268
 16. Li Y, Xie X, Shi X, Lin Y, Qiu Y, Mou J, Chen Q, Lu Y, Zhou L, Jiang M, Sun H, Ma H, Cheng J, Hu Q. *Vibrio parahaemolyticus*, Southern Coastal Region of China, 2007–2012. *Emerg Infect Dis* 2014; 20(4): 685–688
 17. Henao OL, Jones TF, Vugia DJ, Griffin PM; Foodborne Diseases Active Surveillance Network (FoodNet) Workgroup. Foodborne Diseases Active Surveillance Network-2 Decades of Achievements, 1996–2015. *Emerg Infect Dis* 2015; 21(9): 1529–1536
 18. Li J, Hu J, Wu H, Pan H, Zhang X, Xue Y, Wu F. Etiological surveillance for diarrhea in Shanghai from August 2013 to July 2014. *Chin J Epidemiol (Zhonghua Liu Xing Bing Xue Za Zhi)* 2015; 36(10): 1099 (in Chinese)
 19. Liao Y, Li Y, Wu S, Mou J, Xu Z, Cui R, Klena JD, Shi X, Lu Y, Qiu Y, Lin Y, Xie X, Ma H, Li Z, Yu H, Varma JK, Ran L, Hu Q, Cheng J. Risk factors for *Vibrio parahaemolyticus* infection in a southern coastal region of China. *Foodborne Pathog Dis* 2015; 12(11): 881–886
 20. Ke B, Sun J, He D, Li X, Liang Z, Ke CW. Serovar distribution, antimicrobial resistance profiles, and PFGE typing of *Salmonella enterica* strains isolated from 2007–2012 in Guangdong, China. *BMC Infect Dis* 2014; 14(1): 338
 21. Dong B, Liang D, Lin M, Wang M, Zeng J, Liao H, Zhou L, Huang J, Wei X, Zou G, Jing H. Bacterial etiologies of five core syndromes: laboratory-based syndromic surveillance conducted in Guangxi, China. *PLoS One* 2014; 9(10): e110876
 22. Qu M, Lv B, Zhang X, Yan H, Huang Y, Qian H, Pang B, Jia L, Kan B, Wang Q. Prevalence and antibiotic resistance of bacterial pathogens isolated from childhood diarrhea in Beijing, China (2010–2014). *Gut Pathog* 2016; 8(1): 31
 23. Zhang J, Jin H, Hu J, Yuan Z, Shi W, Ran L, Zhao S, Yang X, Meng J, Xu X. Serovars and antimicrobial resistance of non-typhoidal *Salmonella* from human patients in Shanghai, China, 2006–2010. *Epidemiol Infect* 2014; 142(4): 826–832
 24. Shen H, Zhang J, Li Y, Xie S, Jiang Y, Wu Y, Ye Y, Yang H, Mo H, Situ C, Hu Q. The 12 gastrointestinal pathogens spectrum of acute infectious diarrhea in a sentinel hospital, Shenzhen, China. *Front Microbiol* 2016; 7: 1926
 25. Ran L, Wu S, Gao Y, Zhang X, Feng Z, Wang Z, Kan B, Klena JD, Lo Fo Wong DM, Angulo FJ, Varma JK. Laboratory-based surveillance of nontyphoidal *Salmonella* infections in China. *Foodborne Pathog Dis* 2011; 8(8): 921–927
 26. Xia S, Hendriksen RS, Xie Z, Huang L, Zhang J, Guo W, Xu B, Ran L, Aarestrup FM. Molecular characterization and antimicrobial susceptibility of *Salmonella* isolates from infections in humans in Henan Province, China. *J Clin Microbiol* 2009; 47(2): 401–409
 27. Liang Z, Ke B, Deng X, Liang J, Ran L, Lu L, He D, Huang Q, Ke C, Li Z, Yu H, Klena JD, Wu S. Serotypes, seasonal trends, and antibiotic resistance of non-typhoidal *Salmonella* from human patients in Guangdong Province, China, 2009–2012. *BMC Infect Dis* 2015; 15(1): 53
 28. Soyer Y, Moreno Switt A, Davis MA, Maurer J, McDonough PL, Schoonmaker-Bopp DJ, Dumas NB, Root T, Warnick LD, Gröhn YT, Wiedmann M. *Salmonella enterica* serotype 4,5,12:i:-, an emerging *Salmonella* serotype that represents multiple distinct clones. *J Clin Microbiol* 2009; 47(11): 3546–3556
 29. Jin Q, Yuan Z, Xu J, Wang Y, Shen Y, Lu W, Wang J, Liu H, Yang J, Yang F, Zhang X, Zhang J, Yang G, Wu H, Qu D, Dong J, Sun L, Xue Y, Zhao A, Gao Y, Zhu J, Kan B, Ding K, Chen S, Cheng H, Yao Z, He B, Chen R, Ma D, Qiang B, Wen Y, Hou Y, Yu J. Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity through comparison with genomes of *Escherichia coli* K12 and O157. *Nucleic Acids Res* 2002; 30(20): 4432–4441
 30. Chang Z, Zhang J, Ran L, Sun J, Liu F, Luo L, Zeng L, Wang L, Li Z, Yu H, Liao Q. The changing epidemiology of bacillary dysentery and characteristics of antimicrobial resistance of *Shigella* isolated in China from 2004–2014. *BMC Infect Dis* 2016; 16(1): 685
 31. Kotloff KL, Nataro JP, Blackwelder WC, Nasrin D, Farag TH, Panchalingam S, Wu Y, Sow SO, Sur D, Breiman RF, Faruque AS, Zaidi AK, Saha D, Alonso PL, Tamboura B, Sanogo D, Onwuchekwa U, Manna B, Ramamurthy T, Kanungo S, Ochieng JB, Omoro R, Oundo JO, Hossain A, Das SK, Ahmed S, Qureshi S, Quadri F, Adegbola RA, Antonio M, Hossain MJ, Akinsola A, Mandomando I, Nhampossa T, Acácio S, Biswas K, O'Reilly CE, Mintz ED, Berkeley LY, Muhsen K, Sommerfelt H, Robins-Browne RM, Levine MM. Burden and aetiology of diarrhoeal disease in infants and young children in developing countries (the Global Enteric Multicenter Study, GEMS): a prospective, case-control study. *Lancet* 2013; 382(9888): 209–222
 32. Zhang ZK, Lai SJ, Yu JX, Yang WQ, Wang X, Jing HQ, Li ZJ, Yang WZ. Epidemiological characteristics of diarrheagenic *Escherichia*

- coli* among diarrhea outpatients in China, 2012–2015. *Chin J Epidemiol (Zhonghua Liu Xing Bing Xue Za Zhi)* 2017; 38(4): 419 (in Chinese)
33. Panel on Biological Hazards. Public health risks associated with enteroaggregative *Escherichia coli* (EAEC) as a food-borne pathogen. *Efsa J* 2015; 13(12): 112–212
 34. King LA, Nogareda F, Weill FX, Mariani-Kurkdjian P, Loukiadis E, Gault G, Jourdan-DaSilva N, Bingen E, Macë M, Thevenot D, Ong N, Castor C, Noël H, Van Cauteren D, Charron M, Vaillant V, Aldabe B, Goulet V, Delmas G, Couturier E, Le Strat Y, Combe C, Delmas Y, Terrier F, Vendrely B, Rolland P, de Valk H. Outbreak of Shiga toxin-producing *Escherichia coli* O104:H4 associated with organic fenugreek sprouts, France, June 2011. *Clin Infect Dis* 2012; 54(11): 1588–1594
 35. Walker CL, Rudan I, Liu L, Nair H, Theodoratou E, Bhutta ZA, O'Brien KL, Campbell H, Black RE. Global burden of childhood pneumonia and diarrhoea. *Lancet* 2013; 381(9875): 1405–1416
 36. Yu J, Jing H, Lai S, Xu W, Li M, Wu J, Liu W, Yuan Z, Chen Y, Zhao S, Wang X, Zhao Z, Ran L, Wu S, Klens JD, Feng L, Li F, Ye X, Qiu Y, Wang X, Yu H, Li Z, Yang W. Etiology of diarrhea among children under the age five in China: results from a five-year surveillance. *J Infect* 2015; 71(1): 19–27
 37. Chang Z, Zhang J, Ran L, Sun J, Liu F, Luo L, Zeng L, Wang L, Li Z, Yu H, Liao Q. The changing epidemiology of bacillary dysentery and characteristics of antimicrobial resistance of *Shigella* isolated in China from 2004–2014. *BMC Infect Dis* 2016; 16(1): 685
 38. Kotloff KL, Nataro JP, Blackwelder WC, Nasrin D, Farag TH, Panchalingam S, Wu Y, Sow SO, Sur D, Breiman RF, Faruque AS, Zaidi AK, Saha D, Alonso PL, Tamboura B, Sanogo D, Onwuchekwa U, Manna B, Ramamurthy T, Kanungo S, Ochieng JB, Omere R, Oundo JO, Hossain A, Das SK, Ahmed S, Qureshi S, Quadri F, Adegbola RA, Antonio M, Hossain MJ, Akinsola A, Mandomando I, Nhampossa T, Acácio S, Biswas K, O'Reilly CE, Mintz ED, Berkeley LY, Muhsen K, Sommerfelt H, Robins-Browne RM, Levine MM. Burden and aetiology of diarrhoeal disease in infants and young children in developing countries (the Global Enteric Multicenter Study, GEMS): a prospective, case-control study. *Lancet* 2013; 382(9888): 209–222
 39. Zhang SX, Yang CL, Gu WP, Ai L, Serrano E, Yang P, Zhou X, Li SZ, Lv S, Dang ZS, Chen JH, Hu W, Tian LG, Chen JX, Zhou XN. Case-control study of diarrheal disease etiology in individuals over 5 years in southwest China. *Gut Pathog* 2016; 8(1): 58
 40. Qu M, Deng Y, Zhang X, Liu G, Huang Y, Lin C, Li J, Yan H, Li X, Jia L, Kan B, Huang F, Wang Q. Etiology of acute diarrhea due to enteropathogenic bacteria in Beijing, China. *J Infect* 2012; 65(3): 214–222
 41. McEntire J. Foodborne disease: the global movement of food and people. *Infect Dis Clin North Am* 2013; 27(3): 687–693
 42. Johnson LR, Gould LH, Dunn JR, Berkelman R, Mahon BE; Foodnet Travel Working Group. *Salmonella* infections associated with international travel: a Foodborne Diseases Active Surveillance Network (FoodNet) study. *Foodborne Pathog Dis* 2011; 8(9): 1031–1037
 43. McEntire J. Foodborne disease: the global movement of food and people. *Infect Dis Clin North Am* 2013; 27(3): 687–693
 44. Centers for Disease Control and Prevention (CDC). Surveillance for Foodborne Disease Outbreaks, United States, 2015, Annual Report. Atlanta, Georgia: US Department of Health and Human Services, CDC, 2017
 45. Centers for Disease Control and Prevention (CDC). Surveillance for Foodborne Disease Outbreaks, United States, 2014, Annual Report. Atlanta, Georgia: US Department of Health and Human Services, CDC, 2016.
 46. Centers for Disease Control and Prevention (CDC). Surveillance for Foodborne Disease Outbreaks, United States, 2013, Annual Report. Atlanta, Georgia: US Department of Health and Human Services, CDC, 2015.
 47. Centers for Disease Control and Prevention (CDC). Surveillance for Foodborne Disease Outbreaks, United States, 2011, Annual Report. Atlanta, Georgia: US Department of Health and Human Services, CDC, 2013.
 48. Scallan E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, Jones JL, Griffin PM. Foodborne illness acquired in the United States — major pathogens. *Emerg Infect Dis* 2011; 17(1): 7–15
 49. O'Brien SJ, Larose TL, Adak GK, Evans MR, Tam CC; Foodborne Disease Attribution Study Group. Modelling study to estimate the health burden of foodborne diseases: cases, general practice consultations and hospitalisations in the UK, 2009. *BMJ Open* 2016; 6(9): e011119