

Estimates of the Burden of Foodborne Illness in Canada for 30 Specified Pathogens and Unspecified Agents, Circa 2006

M. Kate Thomas,¹ Regan Murray,¹ Logan Flockhart,¹ Katarina Pintar,² Frank Pollari,¹
Aamir Fazil,² Andrea Nesbitt,¹ and Barbara Marshall¹

Abstract

Estimates of foodborne illness are important for setting food safety priorities and making public health policies. The objective of this analysis is to estimate domestically acquired, foodborne illness in Canada, while identifying data gaps and areas for further research. Estimates of illness due to 30 pathogens and unspecified agents were based on data from the 2000–2010 time period from Canadian surveillance systems, relevant international literature, and the Canadian census population for 2006. The modeling approach required accounting for under-reporting and underdiagnosis and to estimate the proportion of illness domestically acquired and through foodborne transmission. To account for uncertainty, Monte Carlo simulations were performed to generate a mean estimate and 90% credible interval. It is estimated that each year there are 1.6 million (1.2–2.0 million) and 2.4 million (1.8–3.0 million) episodes of domestically acquired foodborne illness related to 30 known pathogens and unspecified agents, respectively, for a total estimate of 4.0 million (3.1–5.0 million) episodes of domestically acquired foodborne illness in Canada. Norovirus, *Clostridium perfringens*, *Campylobacter* spp., and nontyphoidal *Salmonella* spp. are the leading pathogens and account for approximately 90% of the pathogen-specific total. Approximately one in eight Canadians experience an episode of domestically acquired foodborne illness each year in Canada. These estimates cannot be compared with prior crude estimates in Canada to assess illness trends as different methodologies were used.

Introduction

FOODBORNE ILLNESS REMAINS a global public health concern (Flint *et al.*, 2005; Newell *et al.*, 2010). Causes of foodborne illness include bacteria, parasites, viruses, toxins, metals, and prions. Symptoms can range from mild and self-limiting vomiting and diarrhea to severe and life-threatening neurological conditions. Estimates of foodborne illness are important for public health decision-makers. Determining these estimates can be challenging, given the large variability within foodborne illness in terms of pathogen, host, and environmental factors. Several attempts by different countries have been made to estimate foodborne illness at a national level (Mead *et al.*, 1999; Adak *et al.*, 2002; Adak *et al.*, 2005; Hall *et al.*, 2005; Vaillant *et al.*, 2005; Cressey *et al.*, 2011; Gkogka *et al.*, 2011; Scallan *et al.*, 2011a; Scallan *et al.*, 2011b; Havelaar *et al.*, 2012).

Cases of foodborne illness are underascertained by public health surveillance systems because of underdiagnosis (i.e., cases that do not seek medical care, are not tested or the lab-

oratory test does not identify a causative agent) and under-reporting (i.e., positive laboratory test results are not reported to surveillance systems) (MacDougall *et al.*, 2008). In order to be captured in a laboratory-based surveillance system in Canada, a sick individual must (1) seek care; (2) have a sample (stool, urine, or blood) requested; (3) submit a sample for testing; (4) the sample must be tested with a test capable of identifying the causative agent; and finally (5) this positive test result must be reported to the surveillance system (Thomas *et al.*, 2008). In order to more accurately estimate the burden of foodborne illness, it is necessary to account for underascertainment and to estimate what proportion of cases result from foodborne transmission, as pathogens rarely are exclusive to one transmission route.

The Public Health Agency of Canada (the Agency) previously used values derived in part from earlier United States (U.S.) estimates (Mead *et al.*, 1999) to generate a crude estimate of 11 million episodes of foodborne illness each year in Canada (Thomas *et al.*, 2008). A more refined methodology and the most current available data have been used to

¹Centre for Food-borne, Environmental, and Zoonotic Infectious Diseases, Public Health Agency of Canada, and ²Laboratory for Food-borne Zoonoses, Guelph, Ontario, Canada.

generate updated estimates of foodborne illness domestically acquired in Canada from both known pathogens and unspecified agents. Similar methodology to that which was recently used by the U.S. Centers for Disease Control and Prevention (U.S.-CDC) was employed (Scallan *et al.*, 2011a; Scallan *et al.*, 2011b). The objective of this analysis is to provide a more accurate estimate of domestically acquired foodborne illness in Canada, while identifying data gaps and areas for further research.

Materials and Methods

The recent U.S.-CDC published list of 31 pathogens was used for the development of the Canadian estimates (Scallan *et al.*, 2011b). Based on expert consultation, *Mycobacterium bovis* and *Streptococcus* Group A were excluded as they were not deemed to be foodborne pathogens for Canada; adenovirus was added to this list based on expert consultation and its potential to be foodborne (FAO/WHO, 2008; Hall *et al.*, 2005), for a total of 30 pathogens included in the Canadian estimates of foodborne illness.

Analytical approach

Estimates were developed from stochastic models to consider uncertainty of the input values. Two main modeling approaches were utilized: (1) laboratory-confirmed cases of pathogens scaled up to account for underascertainment due to underdiagnosis and under-reporting (Fig. 1) and (2) models that started with the total Canadian population and used incidence data to scale down the estimated number of illnesses (Fig. 2). Model outputs are described as mean values with 90% credible intervals (90%CrI).

Data sources focused on the 2000–2010 time period, and all estimates were based on the approximate Canadian population in 2006 (32,500,000 people) as a midpoint of the selected time period (Statistics Canada, 2008). Details of the input and modeling approaches for each pathogen are provided (Supplementary Technical Appendix S1; Supplementary Data are available online at www.liebertpub.com/fpd). Preference was given to nationally representative data for Canada, followed by provincial data and Canadian-based published literature. If there was a gap in the Canadian-based literature, the values and references used by the U.S.-CDC estimates (Scallan *et al.*, 2011b) were generally used as a proxy for a Canadian-based input.

As per the U.S.-CDC estimates (Scallan *et al.*, 2011a), we generated an estimate for unspecified agents that cause domestically acquired foodborne illness. The estimate of unspecified agents includes illnesses not related to the 30 specified pathogens. Unspecified agents were defined using the same definition as the U.S.-CDC estimates: “Known agents with insufficient data for estimating agent-specific episodes of illness; known agents not yet recognized as causing food-borne illness; microbes, chemicals or other substances known to be in food but for which pathogenicity is unproven; and agents not yet described” (Scallan *et al.*, 2011a).

Illnesses

Laboratory-based surveillance data were available for 18 pathogens (Table 1). These data were adjusted for underdiagnosis and under-reporting using pathogen-specific multipliers. Laboratory-based surveillance data at the national level were obtained from two surveillance systems: (1)

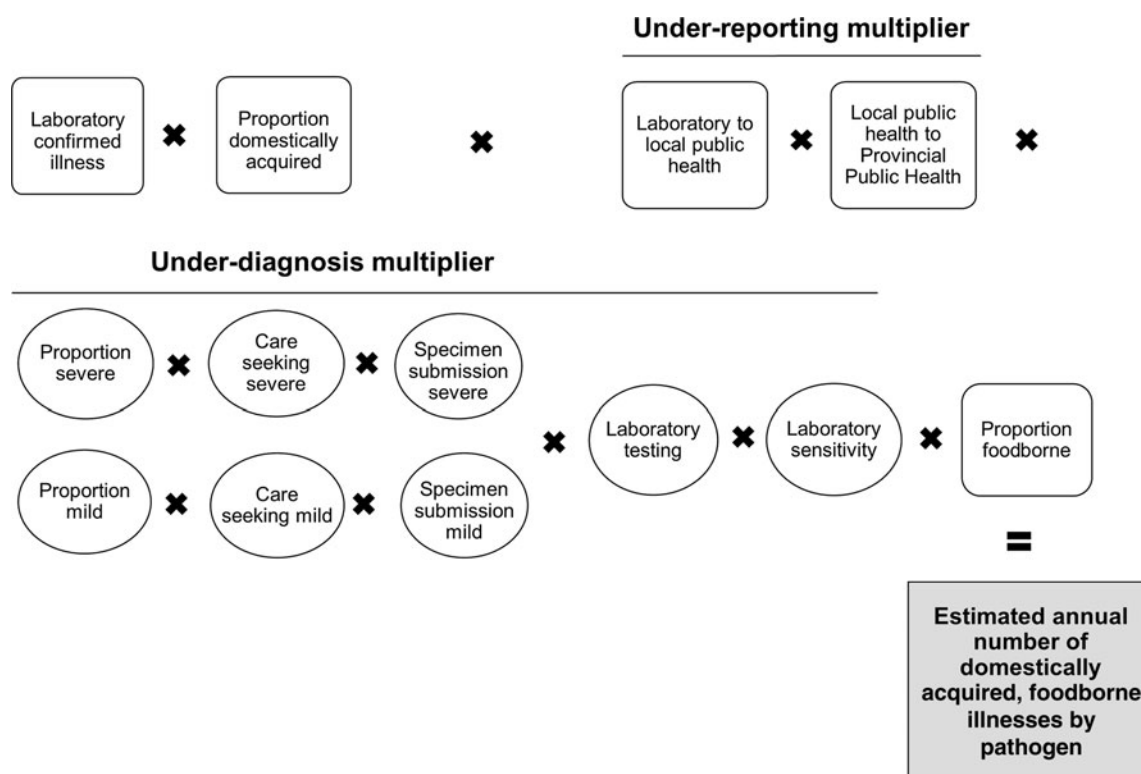


FIG. 1. Schematic of the general model used to estimate the number of cases of pathogens for which laboratory confirmed illnesses were scaled up

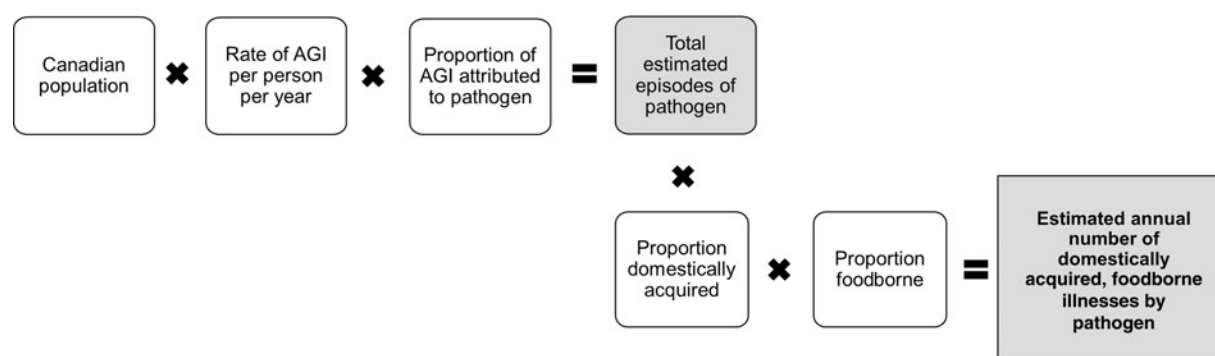


FIG. 2. Schematic of general model used to estimate the number of cases of pathogens for which the Canadian population was scaled down

Canadian Notifiable Disease Surveillance System (CNDSS) (Government of Canada, 2005; Government of Canada, 2012b), and (2) National Enteric Surveillance Program (NESP) (Government of Canada, 2012c); CNDSS data were used when available (with the exception of *Escherichia coli* O157, which relied on NESP data) followed by NESP data. Additional laboratory-based surveillance occurs at the provincial level for select pathogens.

To adjust for underdiagnosis due to medical care seeking behavior, specimen request and submission, laboratory testing, and test sensitivity, pathogen-specific multipliers were generated. Results from the National Studies on Acute Gastrointestinal Illness (NSAGI) population surveys completed in 2001–2002, 2002–2003, and 2005–2006 were combined and used to develop multiplier estimates for: medical care seeking; stool sample requests; and stool submission behaviors (Majowicz *et al.*, 2004; Thomas *et al.*, 2006; Sargeant *et al.*, 2008). This information was stratified based on symptoms to account for differences in practices when symptoms are severe or mild. We defined individuals with acute diarrheal illness to

be those who experienced ≥ 3 loose stools in 24 h with duration lasting >1 day and whose symptoms did not result from pregnancy, medication, food allergy, and/or medical conditions previously diagnosed by a doctor (e.g., colitis, diverticulitis, Crohn's disease, irritable bowel syndrome). Those who met the case definition for acute diarrheal illness and had bloody diarrhea or diarrhea that lasted greater than 7 days were considered to be severe, and proportions of those seeking medical care and stool sample submission were 44% and 27%, respectively. Those who met the case definition of acute diarrheal illness but did not experience bloody diarrhea and whose duration of illness was ≤ 7 days were considered to be mild, and proportions of those seeking medical care and stool sample submission were 14% and 20%, respectively.

For each pathogen, the proportion of laboratory-confirmed illnesses with severe and mild illness was estimated. Data from C-EnterNet (Canada's integrated enteric disease surveillance system based on sentinel sites) (Government of Canada, 2012a) were used to estimate the proportion of cases that experience bloody diarrhea or duration >7 days (i.e.,

TABLE 1. MODELING APPROACHES USED TO ESTIMATE THE TOTAL NUMBER OF ILLNESSES FOR DIFFERENT TYPES OF DATA, CANADA

Pathogens for which laboratory-confirmed illnesses were scaled up		Pathogens for which Canadian population scaled down	
National reportable disease data	Provincial reportable disease data		Other methods
<i>Brucella</i> spp.	<i>Trichinella</i> spp.	Adenovirus	<i>Escherichia coli</i> , other diarrheagenic
<i>Campylobacter</i> spp.	<i>Listeria monocytogenes</i>	Astrovirus	ETEC
<i>Clostridium botulinum</i>	<i>Vibrio parahaemolyticus</i>	Norovirus	VTEC non-O157
<i>Cryptosporidium</i> spp.	<i>Yersinia enterocolitica</i>	Rotavirus	<i>Bacillus cereus</i>
<i>Cyclospora cayentanensis</i>		Sapovirus	<i>Staphylococcus aureus</i>
VTEC O157		<i>Toxoplasma gondii</i>	
<i>Giardia</i> sp.		<i>Clostridium perfringens</i>	
Hepatitis A			
<i>Salmonella</i> spp., nontyphoidal			
<i>Salmonella</i> Typhi			
<i>Shigella</i> spp.			
<i>Vibrio cholerae</i>			
<i>Vibrio</i> spp., other ^a			
<i>Vibrio vulnificus</i> ^a			

^aThese pathogens are reported to the laboratory-based system of NESP and are not considered to be reportable to CNDSS. VTEC, verotoxigenic *Escherichia coli*; ETEC, enterotoxigenic *Escherichia coli*.

severe) and those that did not experience bloody diarrhea and had a duration of ≤ 7 days (i.e., mild) for most pathogens captured in this surveillance system. For those pathogens where C-EnterNet data were not available or appropriate due to small case counts, values from the U.S. estimates (Scallan *et al.*, 2011b) were used as a proxy for proportion severe. For certain pathogens, bloody diarrhea or long duration may not be typical (e.g., *Vibrio parahaemolyticus*, *Brucella* spp.); however, the care-seeking and sample submission behaviors were still based on these symptoms as a proxy.

Due to the severe nature of certain pathogens, the proportions of seeking medical care and sample submission for severe cases were altered to be 90% and 80%, respectively. This applied to *Vibrio vulnificus*, *Clostridium botulinum*, *Listeria monocytogenes* and hepatitis A (Scallan *et al.*, 2011b).

To account for clinical laboratory testing practices and test sensitivity, data from the NSAGI Laboratory Survey (Flint, 2002; Government of Canada, 2002), available literature, and consultation with the Canadian Public Health Laboratory Network (CPHLN) directors were used to determine input values (Supplementary Technical Appendix S2).

To account for under-reporting from a clinical laboratory to a provincial public health authority, we used data from the NSAGI Laboratory and Public Health Reporting surveys (Flint, 2002; Government of Canada, 2002; Flint *et al.*, 2004). For pathogens not included in these surveys, we used the under-reporting multiplier for nontyphoidal *Salmonella* spp. as a proxy. It was assumed that there was no under-reporting from provincial to national public health reporting systems.

Alternative approaches were used for the 12 pathogens not reported by routine surveillance or where data were not considered to be complete. Adenovirus, astrovirus, norovirus, rotavirus, sapovirus, and *C. perfringens* were estimated using incidence estimates from a community-based study completed in the United Kingdom (UK) 2008–2009 (Tam *et al.*, 2011; Tam *et al.*, 2012). They were applied to estimates of acute gastrointestinal illness (AGI) from NSAGI population surveys in Canada. Provincial reported disease data from two provinces for *Bacillus cereus*, *Staphylococcus aureus* and *C. perfringens* were extrapolated to estimate a national annual case count for each pathogen. The ratios of the mean extrapolated national case counts of *B. cereus* and *S. aureus* to *C. perfringens* were applied to the population-level estimate of *C. perfringens* (based on the UK community-based study [Tam *et al.*, 2011; Tam *et al.*, 2012]) to generate an estimate of total illnesses related to *Bacillus cereus* and *Staphylococcus aureus*. Verotoxigenic *E. coli* (VTEC) non-O157, enterotoxigenic *E. coli*, and other diarrheagenic *E. coli* non-VTEC and non-enterotoxigenic *E. coli* were all estimated relative to the estimate of domestic foodborne cases of VTEC O157 based on literature reports (Chui *et al.*, 2011; Scallan *et al.*, 2011b). *Toxoplasma gondii* was estimated based on the incidence estimated from nationally representative serologic data from the U.S. National Health and Nutrition Examination Survey (Jones *et al.*, 2007; Scallan *et al.*, 2011b) and then applied to the Canadian population. The proportion symptomatic was based on literature (WHO, 1969); however, as most symptomatic infections are thought to be mild, further estimates were made specific to the number of cases resulting in ocular disease and the number of congenital infections experiencing symptoms (Kemmeren *et al.*, 2006; Havelaar *et al.*, 2007).

Domestically acquired foodborne illness

Data from C-EnterNet surveillance (2005–2010) and the British Columbia reportable disease systems (2008–2010) (Taylor *et al.*, 2010; Government of Canada, 2012a) were used to estimate the proportion of travel-related cases by pathogen. This proportion was subtracted from the total laboratory-confirmed cases (i.e., prior to incorporating the under-reporting and underdiagnosis multipliers), assuming that the underascertainment of travel-related cases would be different from domestic cases (i.e., those with symptoms and who have traveled may be more likely to seek medical care, have a sample requested, and to submit a sample, thus altering the underdiagnosis multiplier). The proportion of cases attributed to food was determined based on a Canadian expert elicitation (Ravel *et al.*, 2010) and other relevant literature (Supplementary Technical Appendix S3).

Unspecified agents

To estimate the number of cases of AGI attributed to unspecified agents, NSAGI population survey data from 2001 to 2002, 2002 to 2003, and 2005 to 2006 (Majowicz *et al.*, 2004; Thomas *et al.*, 2006; Sargeant *et al.*, 2008) were used (Supplementary Technical Appendix S4). We estimated the proportion of individuals with AGI to be those who experienced ≥ 3 loose stools in 24 hours or any vomiting in the past 28 days, excluding those with chronic conditions, or concurrent symptoms of coughing, sneezing, sore throat, or runny nose. Data were standardized by gender and 5-year age categories to the 2006 Canadian census population (Statistics Canada, 2008), with an estimated rate of 0.630 (95% confidence intervals 0.574–0.689) episodes per person-year. This incidence was applied to the approximated 2006 Canadian population to estimate the total annual number of episodes of AGI.

The number of cases attributed to the 25 pathogens known to cause symptoms of vomiting or diarrhea was subtracted from the estimated total number of episodes of AGI to generate an estimate of the total number of cases of AGI related to unspecified agents. Five pathogens were not included since they do not typically cause symptoms of AGI (i.e., *Toxoplasma gondii*, hepatitis A, *L. monocytogenes*, *Brucella* spp., and *C. botulinum*). The estimated proportions domestically acquired and foodborne for the 25 known pathogens that cause symptoms of vomiting and diarrhea were used as a proxy for the proportion domestically acquired and proportion foodborne related to unspecified agents. These were applied to the estimate of the total number of cases of AGI related to unspecified agents to estimate the total number of domestically acquired, foodborne illnesses attributed to unspecified agents.

Uncertainty analysis

To capture the uncertainty associated with the estimates, inputs were described using probability distributions that captured the range (minimum, maximum) and most likely value. Empirical data were used to inform these distributions whenever possible; however, in situations where data were unavailable, expert opinion was used. In both situations, the minimum, maximum, and most likely values for the variable were developed (using the PERT distribution) (Supplementary Technical Appendix S1) (Vose, 2008). The final estimates

TABLE 2. ESTIMATED ANNUAL NUMBER OF CASES OF DOMESTICALLY ACQUIRED FOODBORNE ILLNESS FOR 30 PATHOGENS, UNDER-REPORTING AND UNDERDIAGNOSIS MULTIPLIERS, CANADA CIRCA 2006

Pathogen	Laboratory confirmed	Travel-related	Domestically acquired laboratory confirmed	Multipliers		Domestically acquired			Domestically acquired foodborne				
				Under-reporting	Underdiagnosis	Total	Mean	90% CrI (low)	90% CrI (high)	Foodborne	Mean	90% CrI (low)	90% CrI (high)
Bacteria													
<i>Bacillus cereus</i>	n/a	0%	n/a	n/a	n/a	n/a	36,275	19,520	55,381	100%	36,269	19,517	55,371
<i>Brucella</i> spp. ^a	8	80%	2	1.1	25.1	26.8	43	13	90	50%	22	6	45
<i>Campylobacter</i> spp.	10,344	24%	7861	1.1	25.2	27.2	213,749	144,288	308,837	68%	145,350	95,686	212,971
<i>Clostridium botulinum</i>	5	0%	5	1.1	2.5	2.7	14	0	27	100%	14	0	27
<i>Clostridium perfringens</i>	n/a	0%	n/a	n/a	n/a	n/a	176,992	95,239	270,211	100%	176,963	95,225	270,160
VTEC O157	883	5%	844	1.1	18.4	20.1	16,913	6968	29,668	76%	12,827	5225	22,750
VTEC, non-O157	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	20,523	8361	36,400
ETEC	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	3848	1568	6825
<i>Escherichia coli</i> , other diarrheagenic	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	2565	1045	4550
<i>Listeria monocytogenes</i>	131	6%	122	1.1	1.6	1.7	212	147	335	84%	178	122	283
<i>Salmonella</i> spp., nontyphoidal	5676	26%	4191	1.1	24.5	26.1	109,384	74,530	154,994	80%	87,510	58,832	125,525
<i>Salmonella</i> Typhi	117	76%	28	1.1	11.9	12.7	358	195	605	80%	287	155	487
<i>Shigella</i> spp.	886	57%	381	1.0	16.8	17.5	6675	3746	10,927	18%	1202	561	2151
<i>Staphylococcus aureus</i>	n/a	0%	n/a	n/a	n/a	n/a	25,114	13,514	38,341	100%	25,110	13,512	38,334
<i>Vibrio cholerae</i> , toxigenic	5	99%	0	1.0	11.9	11.9	0	0	1	100%	0	0	1
<i>Vibrio vulnificus</i>	1	2%	1	1.2	1.9	2.3	1	0	4	82%	1	0	3
<i>Vibrio parahaemolyticus</i>	27	13%	24	1.2	75.4	92.0	2193	1075	3995	82%	1798	869	3305
<i>Vibrio</i> spp., other	17	11%	15	1.2	75.4	92.0	1356	715	2308	82%	1112	578	1911
<i>Yersinia enterocolitica</i>	975	16%	824	1.1	36.4	39.3	32,394	19,788	49,597	80%	25,915	15,344	40,457
Subtotal							621,675		49,597		541,495		
Parasites													
<i>Cryptosporidium</i> spp.	746	30%	522	1.3	36.9	48.5	25,318	14,331	45,955	9%	2321	1012	4530
<i>Cyclospora cayentensis</i>	159	71%	46	1.4	36.9	53.5	2,475	1475	3867	99%	2450	1460	3829
<i>Giardia</i> sp.	4374	39%	2668	1.1	36.9	40.7	108,507	70,532	158,740	7%	7776	4742	11,874
<i>Toxoplasma gondii</i>	n/a	3%	n/a	n/a	n/a	n/a	18,265	14,418	22,566	50%	9132	6953	11,628
<i>Trichinella</i> spp. ^a	5	4%	5	1.1	11.7	12.5	63	0	235	100%	63	0	235
Subtotal							154,627		235		21,743		
Viruses													
Adenovirus	n/a	0%	n/a	n/a	n/a	n/a	747,805	576,880	929,637	1%	3739	1367	6398
Astrovirus	n/a	0%	n/a	n/a	n/a	n/a	382,447	260,748	516,572	1%	1912	671	3409
Hepatitis A virus	393	33%	262	1.1	12.2	13.9	3640	1953	6053	7%	271	115	516
Norovirus	n/a	0%	n/a	n/a	n/a	n/a	3,379,990	3,002,927	3,778,461	31%	1,047,733	679,576	1,434,048
Rotavirus	n/a	0%	n/a	n/a	n/a	n/a	850,233	665,213	1,045,617	1%	4252	1559	7206
Sapovirus	n/a	0%	n/a	n/a	n/a	n/a	1,898,561	1,619,335	2,195,201	1%	9491	3539	15,698
Subtotal							7,262,676		2,195,201		1,067,398		
Total mean and 90% CrI							8,038,978	7,461,815	8,631,524		1,630,636	1,237,848	2,042,713

^aPathogens for which Canadian foodborne transmission is thought to be from wild-game consumption due to surveillance and eradication programs in domestic food animals. CrI, 90% credible intervals; n/a, not applicable; VTEC, verotoxigenic *Escherichia coli*; ETEC, enterotoxigenic *Escherichia coli*.

(reported as mean with 90%CrI around the mean) were generated using Monte Carlo simulation (100,000 iterations using @Risk software, an add-in for Microsoft Excel).

Results

The combined estimate for 30 specified pathogens and unspecified agents is an annual estimate of 4.0 million (90%CrI: 3.1–5.0 million) episodes of domestically acquired, foodborne illness in Canada circa 2006. We estimate each year that there are 1.6 million (90%CrI: 1.2–2.0 million) episodes of domestically acquired foodborne illness related to 30 specified pathogens (Table 2). The pathogens that cause the greatest number of illnesses are norovirus (1 million), *C. perfringens* (177,000), *Campylobacter* spp. (145,000), and nontyphoidal *Salmonella* spp. (88,000) (Table 3). It is estimated that there are 9132 domestically acquired, foodborne toxoplasmosis cases annually in Canada, of which 293 (90%CrI: 203–388) present as ocular disease and 31 (90%CrI: 14–50) and 34 (90% CrI 14–58) present as symptomatic congenital infections in the first year of life and years 1–20, respectively. We estimate there are 2.4 million (90%CrI: 1.8–3.0 million) episodes of domestically acquired foodborne illness related to unspecified agents (Supplementary Technical Appendix S3).

Discussion

We estimate that in Canada there are 4.0 million episodes of domestically acquired foodborne illnesses each year, circa 2006, attributed to 30 known pathogens as well as unspecified agents that cause symptoms of AGI. The main pathogens associated with illnesses are norovirus, *C. perfringens*, *Campylobacter* spp., and nontyphoidal *Salmonella* spp., representing 90% of the total pathogen-specific illnesses. Unspecified agents are the main contributor to the total estimate of domestically acquired foodborne illnesses.

This estimate differs from the previous Canadian estimate of 11 million (Thomas *et al.*, 2008), which used values from earlier U.S. estimates (Mead *et al.*, 1999) applied to the total Canadian population and an incidence estimate of 1.3 episodes per person-year based on a sensitive AGI case definition of “any vomiting or diarrhea in the past 4 weeks” and did not exclude travel-related illnesses. The new approach uses a more specific case definition for AGI (that is more consistent with the U.S.-CDC estimates [Scallan *et al.*, 2011b]) and thus the incidence of AGI is lower as well. This estimate cannot be compared with the estimate of 11 million for the purpose of assessing trends. The CNDSS (Government of Canada, 2012b) provides the best national data on trends over time.

TABLE 3. TOTAL ESTIMATED DOMESTICALLY ACQUIRED FOODBORNE ILLNESS IN CANADA, ESTIMATED CASES PER 100,000 AND PATHOGEN RANK

Pathogen	Mean count	% of total (30 pathogens)	Estimated cases per 100,000	Overall rank	Rank for pathogens based primarily on Canadian data	Rank for pathogens based on limited Canadian data
Norovirus	1,047,733	65.12	3,223.79	1		1
<i>Clostridium perfringens</i>	176,963	11.00	544.50	2		2
<i>Campylobacter</i> spp.	145,350	8.42	447.23	3	1	
<i>Salmonella</i> spp., nontyphoidal	87,510	5.07	269.26	4	2	
<i>Bacillus cereus</i>	36,269	2.25	111.60	5		3
<i>Yersinia enterocolitica</i>	25,915	1.49	79.74	6	3	
<i>Staphylococcus aureus</i>	25,110	1.56	77.26	7		4
VTEC non-O157	20,523	1.19	63.15	8		5
VTEC O157	12,827	0.75	39.47	9	4	
Sapovirus	9491	0.59	29.20	10		6
<i>Toxoplasma gondii</i>	9132	0.57	28.10	11		7
<i>Giardia</i> spp.	7776	0.45	23.93	12	5	
Rotavirus	4252	0.26	13.08	13		8
ETEC	3848	0.22	11.84	14		9
Adenovirus	3739	0.23	11.51	15		10
<i>Escherichia coli</i> , other diarrheagenic	2565	0.15	7.89	16		11
<i>Cyclospora cayentanensis</i>	2450	0.14	7.54	17	6	
<i>Cryptosporidium</i> spp.	2321	0.13	7.14	18	7	
Astrovirus	1912	0.12	5.88	19		12
<i>Vibrio parahaemolyticus</i>	1798	0.10	5.53	20	8	
<i>Shigella</i> spp.	1202	0.07	3.70	21	9	
<i>Vibrio</i> , other spp.	1112	0.06	3.42	22	10	
<i>Salmonella</i> Typhi	287	0.02	0.88	23	11	
Hepatitis A	271	0.02	0.83	24	12	
<i>Listeria monocytogenes</i>	178	0.01	0.55	25	13	
<i>Trichinella</i> spp.	63	<0.01	0.19	26	14	
<i>Brucella</i> spp.	22	<0.01	0.07	27	15	
<i>Clostridium botulinum</i>	14	<0.01	0.04	28	16	
<i>Vibrio vulnificus</i>	1	<0.01	0.00	29	17	
<i>Vibrio cholerae</i> , toxigenic	0	0.0	0.00	30	18	

VTEC, verotoxigenic *Escherichia coli*; ETEC, enterotoxigenic *Escherichia coli*.

Comparisons between different country estimates are difficult to make, given the inherent differences in methodological approaches and data sources. However, the pathogen-specific results presented here are similar to other country estimates (United States, Australia, the Netherlands, New Zealand, and France) that also found norovirus (Vaillant *et al.*, 2005; Hall *et al.*, 2005; Cressey *et al.*, 2011; Scallan *et al.*, 2011b; Havelaar *et al.*, 2012) to be a main contributor and *Campylobacter* spp. and nontyphoidal *Salmonella* spp. (United States, Australia, New Zealand, France, the UK, and Greece) (Adak *et al.*, 2002; Hall *et al.*, 2005; Vaillant *et al.*, 2005; Cressey *et al.*, 2011; Gkogka *et al.*, 2011; Scallan *et al.*, 2011b) to be leading bacterial pathogens in national foodborne illness estimates. Food poisoning and foodborne toxin-producing pathogens (namely, *B. cereus*, *C. perfringens*, and *S. aureus*) are among the top 10 pathogens in recent national foodborne illness estimates (United States, Australia, the Netherlands, New Zealand, France, the UK and Greece) (Adak *et al.*, 2002; Hall *et al.*, 2005; Vaillant *et al.*, 2005; Cressey *et al.*, 2011; Gkogka *et al.*, 2011; Scallan *et al.*, 2011b; Havelaar *et al.*, 2012); however, estimates for these pathogens are typically based on limited information, warranting future research.

Among the national published foodborne illness estimates, the proportion foodborne for norovirus ranges from around 11% in the United Kingdom (Adak *et al.*, 2002) to 39% in New Zealand (Cressey *et al.*, 2011). As identified in the U.S.-CDC estimates (Scallan *et al.*, 2011b), the estimate of the proportion foodborne for norovirus can have a substantial impact on the overall estimate. Estimates of the incidence of foodborne illness due to nontyphoidal *Salmonella* spp. and *Campylobacter* spp. in Australia (Hall *et al.*, 2005) and New Zealand (Cressey *et al.*, 2011) are substantially greater than those in Canada and the U.S.-CDC estimates (Scallan *et al.*, 2011b). This is likely due to the high laboratory-confirmed incidence rate of these pathogens in Australia and New Zealand, suggesting that although they are leading bacterial causes of foodborne illness in all four countries, the actual incidence of these pathogens is lower in North America compared with Australia and New Zealand.

Comparison between the Canadian and the U.S.-CDC estimates (Scallan *et al.*, 2011b) shows that the top four pathogens are identical (i.e., norovirus, *C. perfringens*, *Campylobacter* spp., and nontyphoidal *Salmonella* spp.) and account for nearly 90% of the total pathogen-specific burden, though their relative order changes between the two estimates. The overall total estimate (specified pathogens and unspecified agents) for Canada is slightly less than the U.S.-CDC estimate; approximately one in eight Canadians compared to one in six Americans experience foodborne illness per year.

A key difference between the United States and Canadian approaches is the incorporation of duration of illness to define severity by pathogen. Duration and presence of bloody diarrhea has been used in Australia (Hall *et al.*, 2008) to determine severity of illness by pathogen and has been shown to influence the likelihood of seeking care (MacDougall *et al.*, 2008). The measure of severity is used to describe differences in behavior, which contribute to differences in the underdiagnosis of a pathogen. By incorporating duration with bloody diarrhea, the proportion of cases considered severe is higher, resulting in a lower estimate of underascertainment and the pathogen-specific total.

An additional difference between the United States and Canadian approaches was the decision to estimate rotavirus,

astrovirus, and sapovirus for the total population, rather than only for those under the age of 5 years (Scallan *et al.*, 2011b). Evidence suggests that illnesses associated with these viruses do occur in adults (Svenungsson *et al.*, 2000; de Wit *et al.*, 2001; Anderson *et al.*, 2004; Pang *et al.*, 2009; Bresee *et al.*, 2012; Anderson *et al.*, 2012). This decision effectively reduced the number of cases estimated in the unspecified portion, as they are accounted for among these viruses. Since these viruses are not thought to be primarily foodborne, the final proportion of foodborne related to specified pathogens is less, which in turn reduces the estimated total for foodborne-unspecified agents. The inclusion of adenovirus in the Canadian estimate effectively reduces the unspecified agent estimate for Canada in comparison with that of the U.S.-CDC estimate.

Because toxoplasmosis is often mild with nonspecific symptoms (i.e., lymphadenopathy, fatigue, and general malaise), estimates of congenital toxoplasmosis (i.e., symptoms of chorioretinitis, intracranial calcifications and hydrocephalus, and central nervous system abnormalities in the first year of life and the development of chorioretinitis in the first 20 years of life) and acquired ocular toxoplasmosis were generated as a subset of the full estimate, to demonstrate specific severe outcomes (Kimball *et al.*, 1971; Alford *et al.*, 1974; Koppe *et al.*, 1986; Guerina *et al.*, 1994; Gratzl *et al.*, 1998; Lopez *et al.*, 2000; Binquet *et al.*, 2003; Kemmeren *et al.*, 2006; Havelaar *et al.*, 2007). Primary infection during pregnancy can also result in spontaneous abortion and stillbirth; however these are not explicitly captured in the estimate of toxoplasmosis (Kemmeren *et al.*, 2006; Havelaar *et al.*, 2007).

The approach for the bacterial toxins (*B. cereus*, *C. perfringens*, and *S. aureus*) was also different from the U.S. approach. Though Canadian data to estimate an outbreak to sporadic ratio were explored, they were deemed not suitable for these estimates. Instead, the ratio of these pathogens from the reported provincial data was used in addition to the estimate obtained through the population incidence of *C. perfringens* from the U.K. study (Tam *et al.*, 2011; Tam *et al.*, 2012).

There are many limitations in the approach used to estimate total domestically acquired foodborne illness. The proportion severe for many pathogens is based on information from the C-EnterNet surveillance program (Government of Canada, 2012a); however, these data are based on only one sentinel site and may not reflect the Canadian population.

Data on frequency of laboratory testing were based in part on a 2001 survey of Canadian Laboratories (Flint, 2002; Government of Canada, 2002) and vetted by members of the Canadian Public Health Laboratory Network; however, it is likely that laboratory practices have changed since 2001. Furthermore, there was little information in the literature to determine laboratory test sensitivity, warranting future research. Though not incorporated in these estimates or other national foodborne illness estimates, test specificity (false positives) should be explored.

The use of population surveys on self-reported illness and care-seeking behaviors related to AGI is a potential limitation. Recall bias and case definitions can alter the results (Majowicz *et al.*, 2008; Cantwell *et al.*, 2010; Thomas *et al.*, 2011). Non-infectious causes of vomiting and diarrhea and illness associated with respiratory symptoms were excluded. A highly specific case definition was used (Hall *et al.*, 2010; Majowicz *et al.*, 2004; Sargeant *et al.*, 2008; Thomas *et al.*, 2006), yet cases may have been misclassified. The exclusion of cases with

symptoms of runny nose or sore throat may have resulted in an overly conservative case definition, which may be a limitation.

For the estimation of norovirus, rotavirus, astrovirus, sapovirus, adenovirus; and *C. perfringens*, data from the U.K. cohort study were used (Tam *et al.*, 2011; Tam *et al.*, 2012). The UK study population differs somewhat from the Canadian population, with a higher proportion of participants in the 55 years and greater age group and fewer in the 15–44 years age group (compared with the 2006 Canadian census population). Also, the incidence of these pathogens in the United Kingdom may differ from that of Canada; however, at the time of this work, no suitable Canadian data were available.

Data on the proportion of travel-related cases is based on two Canadian geographical areas, which may not represent the rest of Canada. The case definition for travel-related episodes varied between the two surveillance databases used.

The proportion of illnesses transmitted by food greatly affects the estimates, but there is a paucity of data on which to base these values. One expert elicitation (Ravel *et al.*, 2010) was used for many proportion estimates, but may be prone to bias. For pathogens not included in the expert elicitation, the U.S.-CDC estimates were used. This may not accurately reflect the Canadian situation. With full national implementation of Canadian Outbreak Summaries (currently implemented in some provinces only) (Savelli *et al.*, 2009), future estimates could incorporate information from outbreak-related databases.

The estimate of domestically acquired foodborne illness related to unspecified agents is highly dependent on the accuracy of the estimates related to the 25 known AGI-causing pathogens. As the number of cases attributed to the 25 known pathogens increases, the number of cases attributed to the unspecified agents decreases. Furthermore, the proportion domestic and foodborne based on 25 known pathogens may not be the same for unspecified agents. This approach is consistent with the U.S. estimates (Scallan *et al.*, 2011a; Scallan *et al.*, 2011b) and thus allows for comparison.

To estimate the number of cases related to unspecified agents, it was necessary to subtract the total number of illnesses related to 25 known AGI pathogens. For simplicity and consistency with the U.S. methods (Scallan *et al.*, 2011a; Scallan *et al.*, 2011b), the same multiplier was applied to travel-related cases to subtract a total pathogen-specific estimate from the total estimate of AGI. Future work will be necessary to develop an estimate of travel-related foodborne illness in Canada.

With full implementation of surveillance programs like C-EnterNet (Government of Canada, 2012a) and Outbreak Summaries for Canada (Savelli *et al.*, 2009), critical information will be collected to inform a reassessment of the annual burden of foodborne illness in Canada. A survey of Canadian clinical laboratories would refine our understanding of current laboratory practices and test sensitivities. Test specificity should be explored in future. As noted in Table 3, estimates of certain pathogens relied more heavily on non-Canadian data sources, indicating a Canadian data gap and that these estimates should be interpreted carefully.

Conclusions

As incidence of pathogens, availability of data, and laboratory practices change with time, re-estimating the number

of episodes of foodborne illness in the future will be important to determine what pathogens are contributing to the overall burden, while assessing how identified data gaps have been addressed. Currently, efforts are focusing on estimating the number of hospitalizations and deaths related to foodborne illness, estimating costs and related Disability Adjusted Life Years, and estimating attribution of foodborne illness.

These revised estimates of domestically acquired foodborne illness for Canada represent the most accurate and current values and utilized rigorous and robust methodology. This information will be useful for policy-makers to direct prevention and control activities to those pathogens that cause the most illness. The estimates could inform education campaigns for consumers, provide information to industry and academics for research programs, and be incorporated in food-safety risk assessments.

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Address correspondence to:
M. Kate Thomas, MSc, PhD
120-255 Woodlawn Road W
Guelph, Ontario N1H 8J1
Canada

E-mail: Kate.Thomas@phac-aspc.gc.ca