

National Enteric Surveillance Program (NESP)

ANNUAL SUMMARY 2019

PROTECTING CANADIANS FROM ILLNESS



Public Health
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Canada

**TO PROMOTE AND PROTECT THE HEALTH OF CANADIANS THROUGH LEADERSHIP, PARTNERSHIP,
INNOVATION AND ACTION IN PUBLIC HEALTH.**

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NATIONAL ENTERIC SURVEILLANCE PROGRAM (NESP)

ANNUAL SUMMARY 2019

INCLUDING SEROTYPE TABLES FOR 2019, NESP AND NML

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Centre for Foodborne, Environmental and Zoonotic Infectious Diseases (CFEZID),
Public Health Agency of Canada

&

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Overview

The National Enteric Surveillance Program (NESP) is a collaborative program between the Public Health Agency of Canada (PHAC) and the Provincial Public Health Laboratories. Through NESP, weekly analysis and reporting is conducted for 14 different organisms causing enteric illness, including 10 which are nationally notifiable. The data derived from this surveillance system supports detection of multi-provincial clusters and outbreaks, guides public health interventions, and are designed to integrate with national and international efforts to limit the transmission of enteric diseases.

In 2019, a total of 15,142 isolate results were reported; a decrease from the average number of notifications received in the previous five years (15,541). *Salmonella* spp. continues to be the most common organism identified with 6,350 notifications provided in 2019, representing 42% of all isolates reported. As in previous years, *Salmonella* Enteritidis (50.87%) and *S. Typhimurium* (12.57%), remain the top two serotypes of all *Salmonella* reported to NESP in 2019. This is the first year *S. ssp* I, 4,[5],12:i:- (6.64%) was one of the top three *Salmonella* serotypes reported to NESP. Collectively, these three serotypes represent 70% of all *Salmonella* serotypes identified.

The incidence rate of shiga toxigenic *Escherichia coli* (STEC) O157 remained stable since 2010, with 1.06 cases per 100,000 population reported in 2019. An increase in the incidence rate of non-O157 isolates was observed in 2019 (2.5 cases per 100,000 population) compared to 2018 (1.42 cases per 100,000 population). This is the third consecutive year where more non-O157 isolates were reported than O157 isolates.

The incidence rate of invasive listeriosis in 2019 (0.46 per 100,000 population) is similar to what has been seen in the past 5 years. Over the 7-year period Hepatitis A has been under national surveillance, the highest incidence was reported to the program in 2019 (1.55 cases per 100,000 population). As in previous years, *Shigella sonnei* constituted the majority of *Shigella* species reported in 2019, representing 55% of all *Shigella* reported. Trends for all other *Shigella* species have remained unchanged over the past 20 years, with a slight increase in overall incidence rate reported in 2019.

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Information to the reader on the National Enteric Surveillance Program (NESP)

In Canada, the surveillance of enteric diseases is conducted through NESP and the Canadian Notifiable Diseases Surveillance System (CNDSS)^a. NESP is jointly administered by PHAC's National Microbiology Laboratory (NML) and the Centre for Foodborne, Environmental and Zoonotic Infectious Diseases (CFEZID). Since 1997, weekly analysis and reporting on laboratory-confirmed cases of enteric illness submitted by the Provincial Public Health Laboratories has been conducted through NESP.

NESP provides the first and most timely level of characterization (primarily species and serotype) of data critical to, and integrated with, other surveillance programs. Monitoring aggregated data allows for the rapid evaluation and response to enteric illness outbreaks. In addition, the data allows for the description of trends in pathogen subtypes and in the incidence of nationally notifiable enteric pathogens. CNDSS receives data that are collected by local health units, which is forwarded to provincial/territorial health authorities and collated by the Centre for Communicable Diseases and Infection Control (CCDIC). These data may be more representative of total numbers of annual illnesses; however, CNDSS is not designed to provide timely information required for cluster or outbreak detection. These two surveillance systems (CNDSS and NESP) are complementary in providing both epidemiological and laboratory results; however, discrepancies between them do exist. Due to the reporting protocols and requirements, CNDSS is a more reliable source of information in terms of total number of illnesses, while NESP data are more current and responsive to trends. A comparison of national case counts and incidence rates for enteric diseases is included (Appendix 1).

NESP is also highly complementary to another laboratory-based surveillance system, PulseNet Canada^b. Also administered by PHAC, PulseNet Canada collects high resolution data in real-time on cases of enteric diseases for the purpose of outbreak detection and response. Due to the additional testing performed (molecular or genomic subtyping), there are differences in

^a Canadian Notifiable Diseases Surveillance System, Public Health Agency of Canada: <https://diseases.canada.ca/notifiable/>

^b PulseNet Canada, National Microbiology Laboratory, Public Health Agency of Canada: <https://www.nml-lnm.gc.ca/index-eng.htm>

turnaround time compared to weekly NESP data. Further, PulseNet Canada surveillance is conducted only for a subset of the organisms that are tracked by NESP.

Data Collection

Isolates (or specimens) are submitted to provincial public health microbiology laboratories for testing and/or confirmation of the enteric pathogen. On a weekly basis, each provincial public health laboratory summarizes the number of enteric microorganisms isolated from human patients. The information details the genus, species and serotype (where appropriate). The 'report week' for NESP spans the period from Sunday to Saturday and is based on the date the laboratory test was completed, except for in Alberta, where it is based on the date received. Data are submitted to NML either directly (faxing or emailing), or by entering the data via the web-based application (webNESP) hosted on the Canadian Network for Public Health Intelligence (CNPHI). The information is submitted as soon as possible and no later than the second day after a weekend or holiday. An exception to this reporting scheme occurs when the isolate must be sent to another laboratory for completion of the identification. In this case, the isolate is reported at the level of typing or identification attained (e.g. *Salmonella* sp.) for the week in which it was sent to the reference laboratory. The NESP record is then updated when the final identification is received from the reference laboratory (e.g. report in week 35 that one "*Salmonella* sp." reported in week 33 has been confirmed as "S. Banana"). This updated information is submitted with the next weekly NESP report form.

All data submitted are aggregated by province and pathogen and do not contain any patient identifiers, locators, or other confidential information. NESP partners endeavor to include only the number of isolates from new cases identified at the laboratory that week, or updates to previously reported numbers. To avoid duplication, the provincial laboratories attempt to identify multiple, repeat, or follow-up specimens from the same individual, and consider all identical isolates from the same patient that are collected over a three month period as a single case.

Data collected for surveillance purposes are increasingly being generated using whole genome sequencing instead of by classical microbiological methods. Most of the data collected by NESP, however, can be derived from whole genome sequence data *in silico* (e.g., species identification, serotype), ensuring that the over two decades of data used for NESP analyses will remain compatible with surveillance in the genomics era. Starting in 2018, portions of the data collected and analyzed by NESP will have been generated via whole genome sequencing.

Data Analysis and Dissemination

Data analysis is conducted weekly by using an algorithm to determine if the current week case counts are significantly higher than the expected baseline. Statistical significance is based on the cumulative Poisson probability between the reported case count and the retrospective five-year median.

Results from the weekly analysis included in the “NESP Weekly Report” are disseminated to all provincial laboratories, at least one epidemiologist or Medical Officer of Health in each province/territory and multiple stakeholders at the federal level. Protocol allows sharing of the reports with other public health professionals who have an operational need to have this information, although, the weekly reports are not intended for public distribution. No response is required by public health professionals to the statistical elevations noted in the reports. The aim is to provide useful and timely information for those responsible for public health action.

In addition to the NESP Weekly Reports, partners can perform real-time data analysis, examine trends and display the data for their respective jurisdictions within webNESP. PulseNet Canada uses these data in conjunction with laboratory DNA fingerprinting data determined by pulsed-field gel electrophoresis (PFGE) and other molecular/genomic data to detect disease clusters and outbreaks. The resulting data analyses are also shared on CNPHI with provincial public health microbiology laboratories, the Canadian Food Inspection Agency (CFIA), Health Canada (HC), PHAC and provincial/territorial epidemiologists. Notably, the coordinated assessment of laboratory evidence collected through these two complementary laboratory surveillance networks allows for the interpretation of clinical microbiological evidence during multi-jurisdictional epidemiologic investigations, as described in the Food-borne Illness Outbreak Response Protocol (FIORP)^c.

Limitations

It should be noted that there are some inherent limitations of these data. For some organisms, the number of isolates reported is a subset of laboratory isolations and may not reflect the incidence of disease at the provincial or national level. For example, *Campylobacter* isolates are not routinely forwarded to provincial or central reference laboratories for further testing beyond

^c Food-borne Illness Outbreak Response Protocol (FIORP) 2010: To guide a multi-jurisdictional response. Public Health Agency of Canada: <http://www.phac-aspc.gc.ca/zoono/fiorp-pritioa/index-eng.php>

genus/species characterizations, and are therefore greatly under-represented in NESP. By contrast, *Salmonella* and *E. coli* O157 isolates captured by NESP are more representative of the true incidence of disease in Canada, as the number of cases reported to CNDSS and isolates reported to NESP show a high degree of concurrence for both diseases. There may be over-reporting of organisms in NESP due to reporting of multiple specimens from a single patient, but efforts are made to minimize this occurrence. Information regarding extra-intestinal isolation sites and foreign travel are not consistently reported to NESP from all laboratories and therefore any interpretation should be considered with caution.

Questions and correspondence may be forwarded via email to:

PHAC.NESP-PNSME.ASPC@canada.ca

Laboratory-confirmed Isolate Counts & Incidence Rates

In 2019, provincial laboratories reported the results of 15,142 isolates of enteric pathogens to NESP, a decrease from the average number of notifications in the previous five years (15,541). The most frequently reported enteric pathogen group was *Salmonella*, followed by enteric viruses (Norovirus, Hepatitis A, Rotavirus and Adenovirus), and *Campylobacter* (Table 1). Organism isolate counts reported by province and territory in 2019 can be found in Appendix 2.

Table 1. Number of isolates reported to NESP by major organism group per province or territory, 2019

GROUP	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL	% OF TOTAL ISOLATES REPORTED
<i>Salmonella</i>	959	759	175	237	2578	1156	166	144	16	152	1	7	0	6350	41.94
Viruses ¹	425	167	168	267	889	59	107	93	75	405	0	1	0	2656	17.54
<i>Campylobacter</i> ¹	39	337	170	94	123	327	238	110	35	191	0	0	0	1664	10.99
Parasites ¹	259	13	119	135	670	49	124	136	16	100	18	0	0	1639	10.82
<i>E. coli</i> ²	128	349	77	53	227	204	9	7	6	399	2	1	0	1462	9.66
<i>Shigella</i>	167	99	13	16	253	255	7	4	0	12	1	0	0	827	5.46
<i>Yersinia</i>	73	38	13	2	161	23	4	0	0	3	1	0	0	318	2.10
<i>Listeria</i>	15	10	5	7	75	54	5	2	0	1	0	0	0	174	1.15
<i>Vibrio</i>	23	7	1	0	5	6	7	2	1	0	0	0	0	52	0.34
Total	2088	1779	741	811	4981	2133	667	498	149	1263	23	9	0	15142	100.00

¹*Campylobacter*, parasitic (*Giardia*, *Cryptosporidium*, *Entamoeba histolytica/dispar* and *Cyclospora*), and viral (Norovirus, Rotavirus and Adenovirus) isolates are not routinely forwarded to the provincial or central reference laboratories and are greatly under-represented in NESP.

²*E. coli* includes O157 serotypes (397 cases), non-O157 serotypes (595 cases), CIDT positive for STX/STEC (139 isolates), and non-typed STEC (331 cases).

Annual national incidence rates for the groups of enteric pathogens reported to NESP between 2014 and 2019 are shown in Table 2 and Appendix 1. Isolates of *E. coli* O157, *Listeria monocytogenes*, *Salmonella* and *Shigella* are routinely forwarded to provincial microbiology laboratories, while isolates for *Campylobacter*, *Yersinia*, enteric parasites (*Giardia*, *Cryptosporidium*, *Entamoeba histolytica/dispar* and *Cyclospora*) and enteric viruses (Norovirus, Rotavirus and Adenovirus) are not routinely reported to the provincial or central reference laboratories. As such, NESP incidence rates are considered to be reflective of the true incidence rate for those routinely reported pathogens enabling the calculation of provincial and territorial incidence rates as shown in Table 3.

Table 2. Annual national totals and rates (per 100,000 population) for enteric pathogens and organism groups reported to NESP, 2014-2019

GROUP	2014		2015		2016		2017		2018		2019	
	Total	Rate ¹	Total	Rate ¹	Total	Rate ¹	Total	Rate ¹	Total	Rate ¹	Total	Rate ¹
<i>E. coli</i> O157	458	1.29	379	1.06	415	1.15	348	0.95	426	1.15	397	1.06
<i>E. coli</i> non-O157 ²	151	0.43	229	0.64	205	0.57	361	0.99	580	1.57	926	2.46
<i>Listeria</i>	133	0.38	125	0.35	191	0.53	109	0.30	150	0.40	174	0.46
<i>Salmonella</i>	7850	22.15	7717	21.61	7816	21.65	7313	20.01	7300	19.70	6350	16.90
<i>Shigella</i>	681	1.92	739	2.07	807	2.23	699	1.91	784	2.12	827	2.20
<i>Campylobacter</i>	1676	4.73	1514	4.24	1378	3.81	1287	3.52	1333	3.60	1664	4.43
<i>Vibrio</i>	82	0.23	85	0.24	44	0.12	54	0.15	67	0.18	52	0.14
<i>Yersinia</i>	341	0.96	383	1.07	353	0.98	387	1.06	404	1.09	318	0.85
Parasites	1811	5.11	1845	5.17	1921	5.32	1679	4.59	1675	4.52	1639	4.36
Viruses	2934	8.28	3075	8.61	2295	6.36	2600	7.12	2303	6.21	2656	7.06

¹Rates calculated using the population estimates on July 1st as reported by Statistics Canada – Table 17-10-0005-01

²*E. coli* non-O157 is not consistently reported by provinces and territories.

Table 3. Annual rates¹ (per 100,000 population) of infection per province and territory for select groups of pathogens routinely reported to NESP, 2019

GROUP	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU
<i>E. coli</i> O157	0.71	2.17	0.51	1.83	1.06	0.59	0.90	0.62	3.19	2.49	0	0	0
<i>E. coli</i> non-O157 ²	1.50	5.83	6.05	2.04	0.50	0.41	0.26	0.10	0.64	72.48	2.45	2.23	0
<i>Listeria</i>	0.30	0.23	0.43	0.51	0.51	0.64	0.64	0.21	0	0.19	0	0	0
<i>Salmonella</i>	18.91	17.39	14.90	17.31	17.70	13.62	21.37	14.82	10.19	29.14	2.45	15.62	0
<i>Shigella</i>	3.29	2.29	1.11	1.17	1.74	3.01	0.90	0.41	0	2.30	2.45	0	0

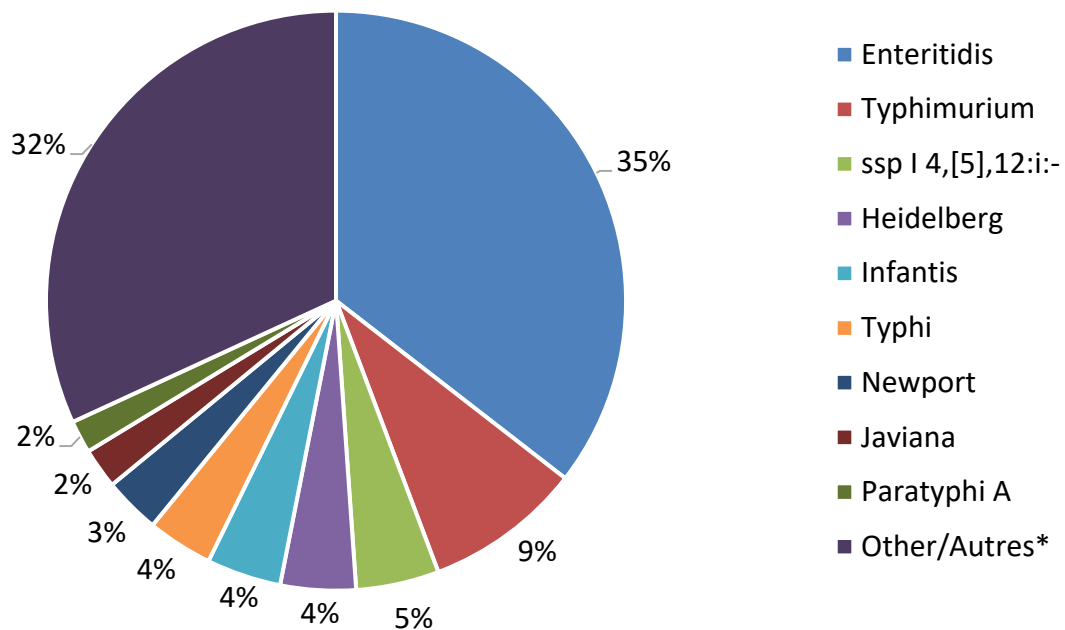
¹Rates calculated using the population estimates on July 1st as reported by Statistics Canada – Table 17-10-0005-01

²*E. coli* non-O157 is not consistently reported by provinces and territories.

Salmonella

A total of 6,350 *Salmonella* isolates representing 203 serotypes were reported in 2019. *Salmonella* Enteritidis accounted for 35% of all human salmonellosis, and together with the nine remaining most common serotypes (Figure 1), they constituted 68% of all *Salmonella* infections reported. National, provincial and territorial case counts for *Salmonella* reported in 2019 are shown in Table 4 and Appendix 2.

Figure 1. Proportion of *Salmonella* serotypes causing human illness as reported to NESP, 2019 (n=6,350)



*Other serotypes (2,024 isolates) were divided among 194 serotypes and 140 isolates were reported as unspecified *Salmonella* species.

Table 4. Number of isolates reported to NESP per province and territory for the ten most commonly reported *Salmonella* serotypes, 2019

GROUP	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL	% of <i>Salmonella</i> total
Enteritidis	437	264	77	71	829	415	74	65	13	6	1	2	0	2254	50.87
Typhimurium	36	61	18	21	281	102	19	16	2	1	0	0	0	557	12.57
ssp I 4,[5],12:i:-	43	21	6	8	114	95	3	4	0	0	0	0	0	294	6.64
Heidelberg	8	27	6	5	102	81	20	16	1	1	0	0	0	267	6.03
Infantis	27	27	2	17	118	57	6	5	3	0	0	2	0	264	5.96
Typhi	45	29	3	11	127	15	1	1	0	0	0	0	0	232	5.24
Newport	34	36	8	10	77	28	3	4	0	0	0	0	0	200	4.51
Javiana	22	15	1	4	55	39	5	2	0	0	0	0	0	143	3.23
Paratyphi A	34	24	4	1	47	6	0	0	0	0	0	0	0	116	2.62
Oranienburg	7	9	8	7	46	25	0	2	0	0	0	0	0	104	2.35
Total	693	513	133	155	1796	863	131	115	19	8	1	4	0	4431	100.00

Compared to the average number of *Salmonella* notifications received between 2014 and 2018 (7,599 cases), there was a 17.9% decrease observed in 2019 (6,350) (Figure 2). While *S. Enteritidis* remained the most common serotype over this time period, changes were observed among the other most commonly reported *Salmonella* serotypes (Table 5).

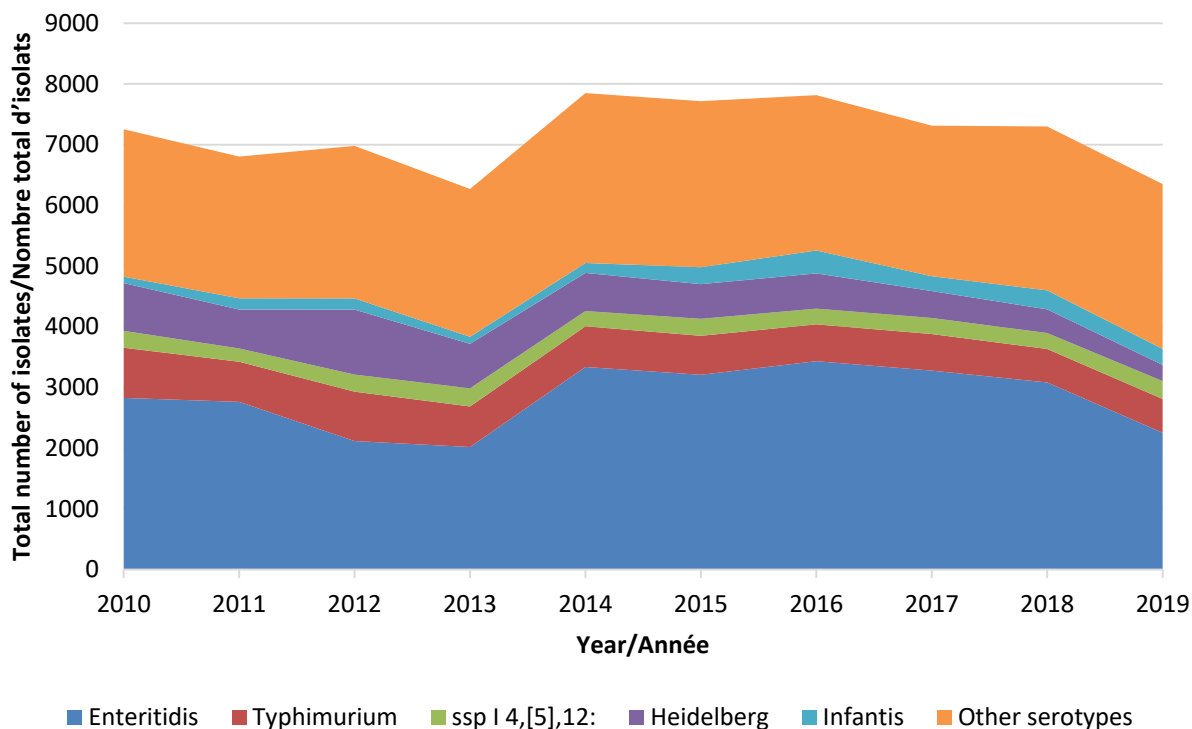
Figure 2. Annual counts between 2010 and 2019 for the top five *Salmonella* serotypes reported to NESP in 2019

Table 5. National total counts (overall rank) for the ten most commonly reported *Salmonella* serotypes to NESP, 2014-2019

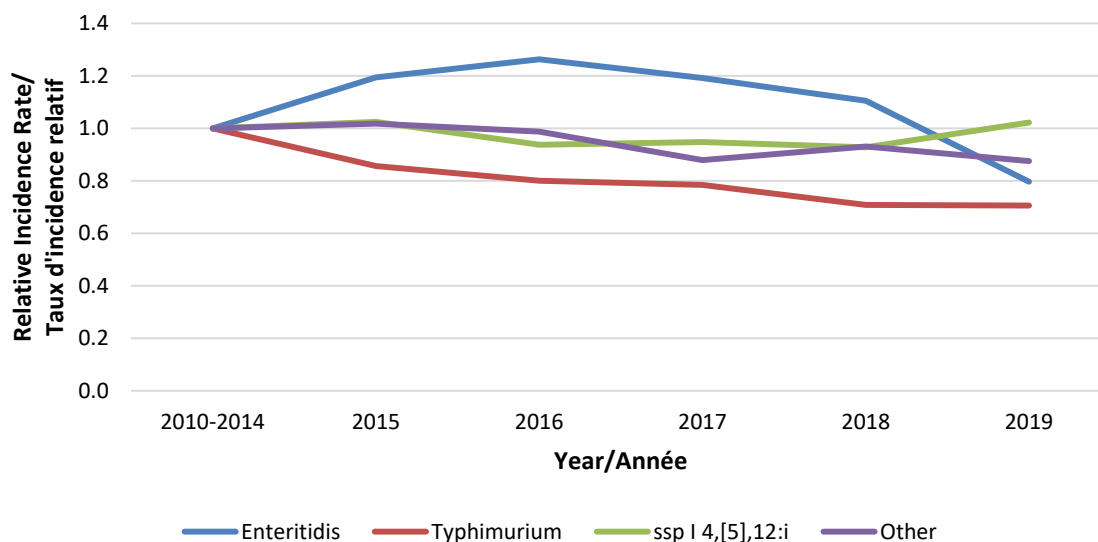
Serotypes	2014	2015	2016	2017	2018	2019	Average no. of isolates (2014-2018)
Enteritidis	3337	3209	3433	3278	3083	2254	3268
Typhimurium	671	642	607	602	551	557	615
ssp I 4,[5],12:i:-	251	280	259	265	263	294	264
Heidelberg	628	571	580	444	390	267	523
Infantis	164	279	378	244	313	264	276
Typhi	140	121	136	181	198	232	155
Newport	224	235	198	143	192	200	198
Javiana	133	136	114	111	118	143	122
Paratyphi A	64	77	62	62	56	116	64
Oranienburg	81	68	61	53	113	104	75
Thompson	392	311	290	135	148	98	255
Braenderup	71	123	81	145	127	101	109
Agona	78	63	120	103	125	125	98
Saintpaul	131	108	70	87	87	99	97

In May 2017, PulseNet Canada began performing WGS on all *Salmonella* isolates submitted for routine laboratory-based surveillance, providing high discriminatory genomic subtype data for outbreak detection and response. The potential impacts of this change on NESP data collection and analysis are currently under assessment.

Salmonella Enteritidis

In 2019, 2,254 isolates of *S. Enteritidis*, 35% of all *Salmonella* submissions, were reported to NESP. The incidence rate observed in 2019 was 7.4% lower (6.0 cases per 100,000 population) relative to the 2010-2014 baseline period (7.5 cases per 100,000 population). A decrease in incidence can be seen from 2016-2018 (Figure 3).

Figure 3. Relative incidence rates¹ of *S. Enteritidis*, *S. Typhimurium*, *S. ssp I 4,[5],12:i:-*, and other *Salmonella* serotype reported to NESP by Year, 2015-2019 compared to the 2010-2014 baseline period



¹ Rates are compared to the 2010-2014 baseline period.

Salmonella Typhimurium

Compared to the 2010-2014 baseline period, a 33% decrease in the incidence of *S. Typhimurium* cases was noted in 2019 (2.1 versus 1.5 cases per 100,000 population, respectively). From 2015-2019, a slight decreasing trend can be seen in the incidence of *S. Typhimurium* (Figure 3). Although *S. Typhimurium* continues to rank among the top 3 most common serotypes causing human salmonellosis in Canada, it represents only 9% of all *Salmonella* isolates reported to NESP in 2019 (Table 4 and Table 5).

Salmonella ssp I 4,[5],12:i:-

Salmonella ssp I 4,[5],12:i:-, for the first time ever was the third most common serotype in Canada, which represented 5% of all human *Salmonella* isolates reported to NESP in 2019. The 2019 overall incidence (0.8 per 100,000 population) was the same as the 2010-2014 baseline period (0.8 per 100,000 population) (Figure 3).

Escherichia coli

The current rate of Shiga toxinogenic *Escherichia coli* (STEC) O157 (1.06 cases per 100,000 population) has remained relatively stable since 2010 (1.2 cases per 100,000 population) (Figure 4). In 2019, several provinces reported incidence rates higher than the national reported incidence rate: Alberta (2.17 cases per 100,000 population), Manitoba (1.83 cases per 100,000 population), Prince Edward Island (3.19 cases per 100,000 population), and Newfoundland (2.49 cases per 100,000 population) (Table 3). The incidence rate of *E. coli* non-O157 increased in 2019 (2.5 cases per 100,000 population) from 2018 (1.6 cases per 100,000 population) (Figure 4). This is the third consecutive year where the proportion of non-O157 isolates reported has exceeded the proportion of O157 isolates. It should be noted that *E. coli* non-O157 are reported less consistently than *E. coli* O157 to NESP and therefore any changes observed over time are a reflection in testing practices by some provincial laboratories. Further, 8% of isolates were identified using culture-independent diagnostic tests (CIDT), which are PCR-based tests used for the identification of organisms without an isolate cultured. Reflex culture of a CIDT positive sample would obtain an isolate for further sub-typing.

Among non-O157 isolates, in 2019, 41% of these were represented by five serotypes: *E. coli* O26, *E. coli* O111, *E. coli* O103, *E. coli* O118, and *E. coli* O121 (Figure 5). In 2019, 41% of *E. coli* non-O157 did not have additional sub-type information. In 2017, a request was submitted by NML to provincial public health laboratories to report the testing method used for the identification of organisms, as the use of CIDTs are becoming more prevalent in Canada.

An increase in incidence rate was seen in *E. coli* O26 (0.21 cases per 100,000 population in 2018, 0.4 cases per 100,000 population in 2019), *E. coli* O111 (0.09 in 2018, 0.25 in 2019), *E. coli* O103 (0.09 in 2018, 0.21 in 2019), and *E. coli* O118 (0.04 in 2018, 0.08 in 2019). A small decrease in incidence rate was seen in *E. coli* O121 (0.11 in 2018, 0.08 in 2019) (Figure 6). All *E. coli* serotypes, including confirmed non-O157 STEC isolates, are summarized in Appendix 2.

Figure 4. Incidence rate (per 100,000 population) of *E. coli* O157, *E. coli* non-O157, & *E. coli* Non-Typed Serotypes reported to NESP, 1997-2019

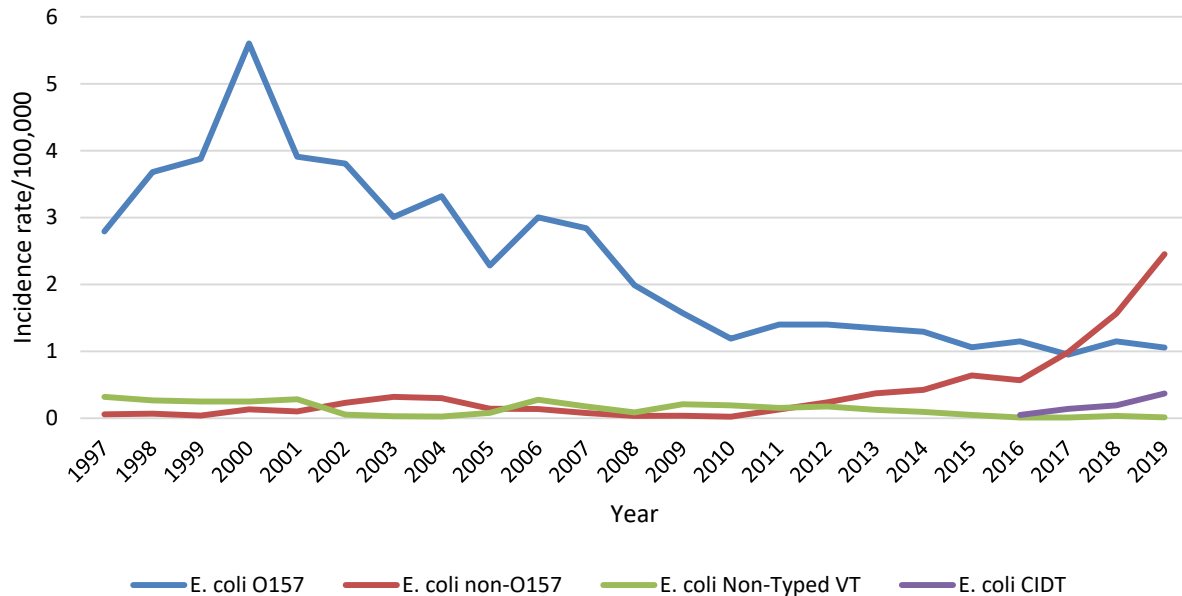
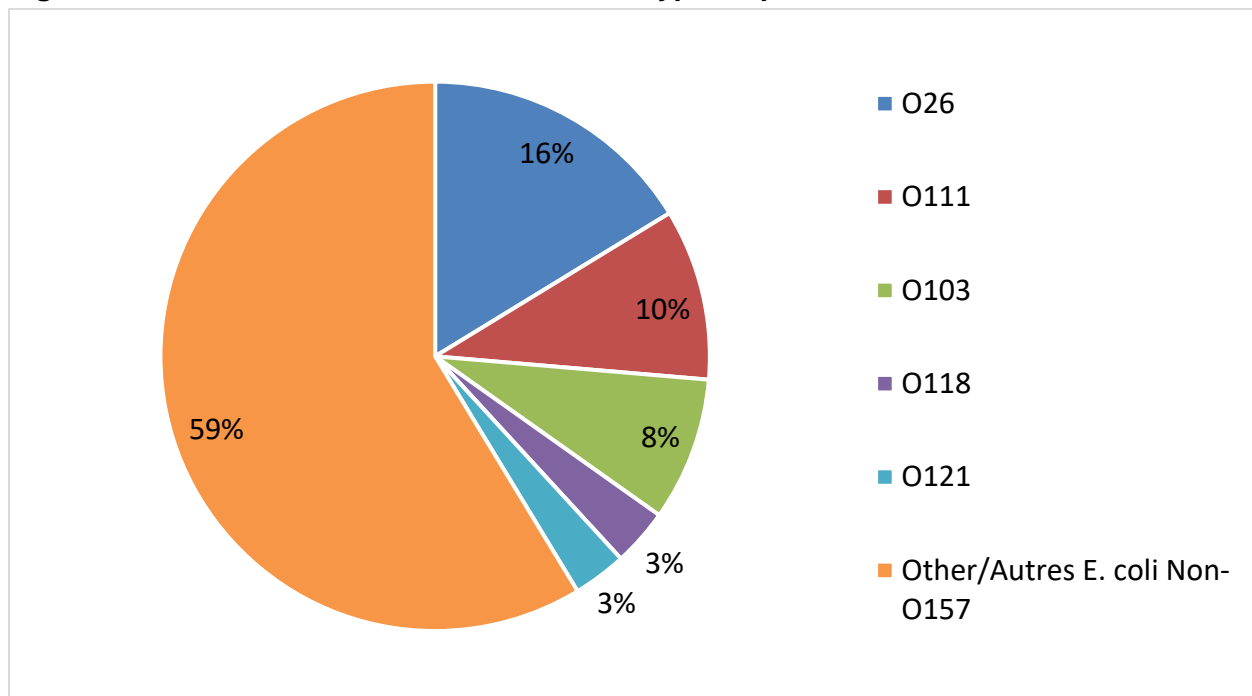
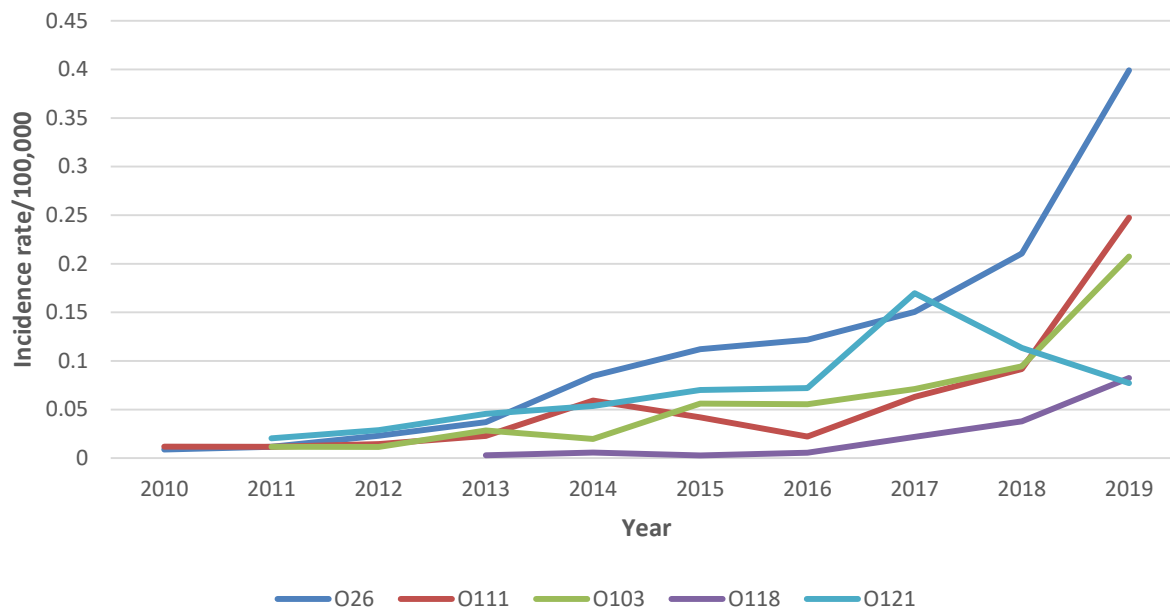


Figure 5. Distribution of *E. coli* non-O157 serotypes reported to NESP in 2019



*Other serotypes (541 isolates) were divided among 51 serotypes and 376 isolates were reported as unspecified *E. coli* non-O157 species.

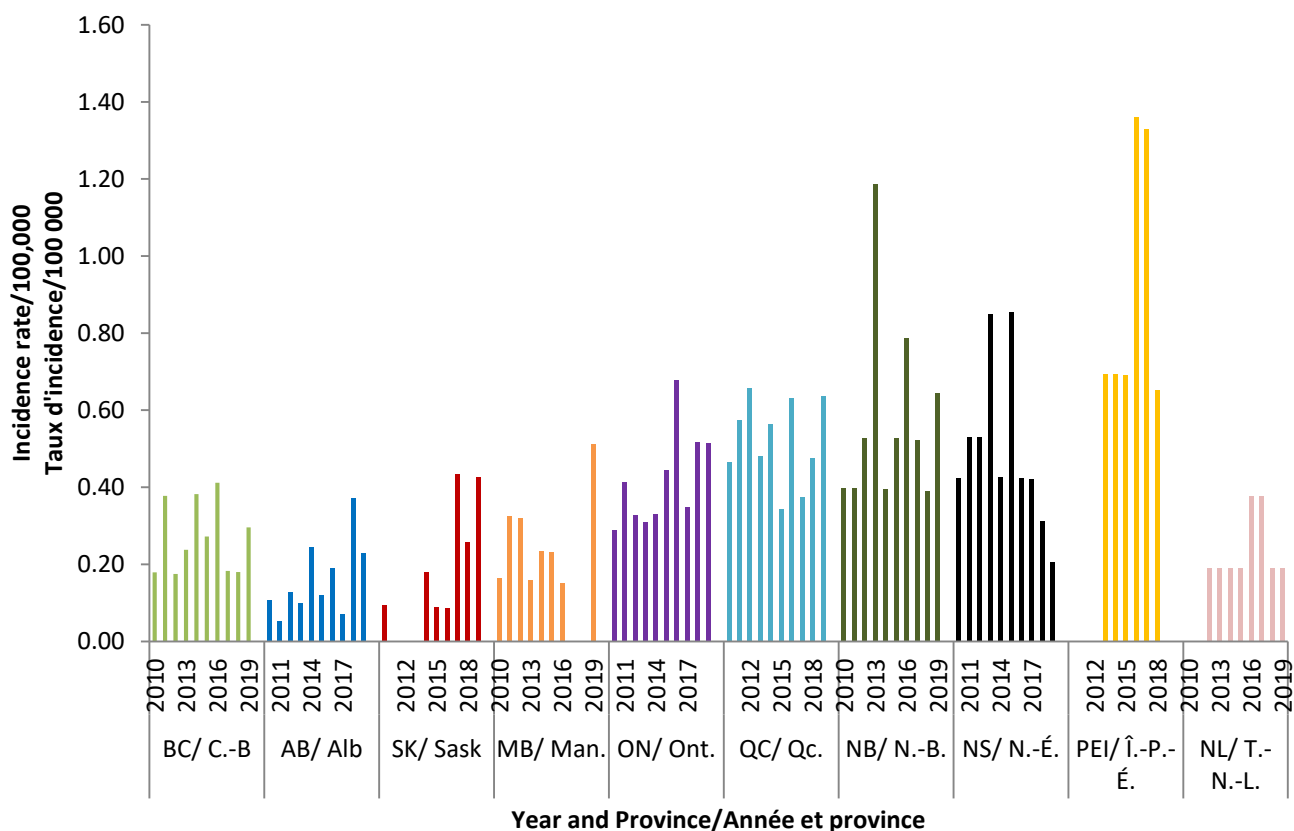
Figure 6. Incidence rate (per 100,000 population) of the top five *E. coli* non-O157 serotypes reported to NESP, 2010-2019



Listeria monocytogenes

As per the case definition for invasive listeriosis, only isolates obtained from a normally sterile site or placental/fetal tissues should be reported. An increased number of isolates for invasive listeriosis were reported in 2019 (174) compared to 2018 (150). As there are small numbers of cases of invasive listeriosis within most jurisdictions, the magnitude of the change is greatly affected with a difference of even one case (Figure 7). There were no cases of invasive listeriosis reported in 2019 by Prince Edward Island, Yukon, Northwest Territories, and Nunavut.

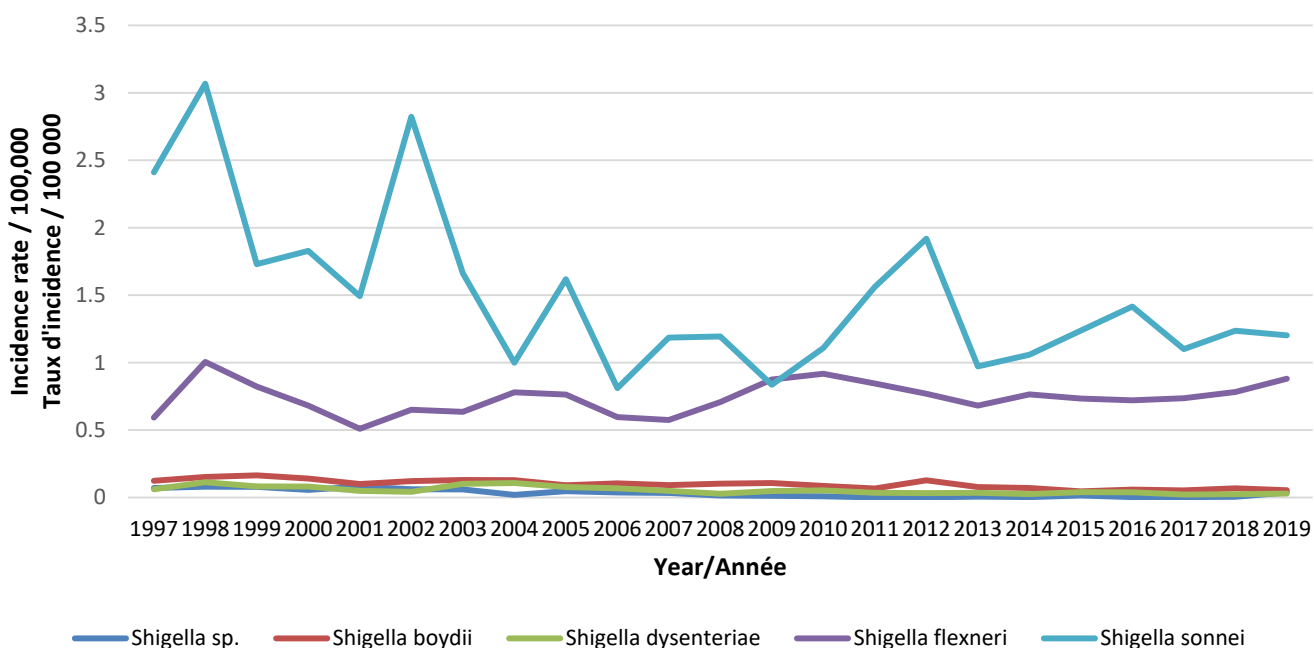
Figure 7. Incidence rate (per 100,000 population) of invasive listeriosis reported to NESP by province, 2010-2019



Shigella

There were 827 isolates of *Shigella* reported in 2019, representing a rate of 2.02 cases per 100,000 population compared to an average of 2.05 cases per 100,000 population reported between 2014 and 2018 (Figure 8). Isolates of *Shigella sonnei* and *Shigella flexneri* comprised 55% and 40% of total notifications respectively. Overall trends for *Shigella* are driven by the incidence of *S. sonnei* (1.20 cases per 100,000 population) (Figure 8). Among the other *Shigella* species, incidence trends over time have remained relatively unchanged with an incidence of 0.88 cases per 100,000 population for *Shigella flexneri*, 0.05 cases per 100,000 population for *Shigella boydii*, and 0.03 cases per 100,000 population for *Shigella dysenteriae* observed in 2018 (Figure 8).

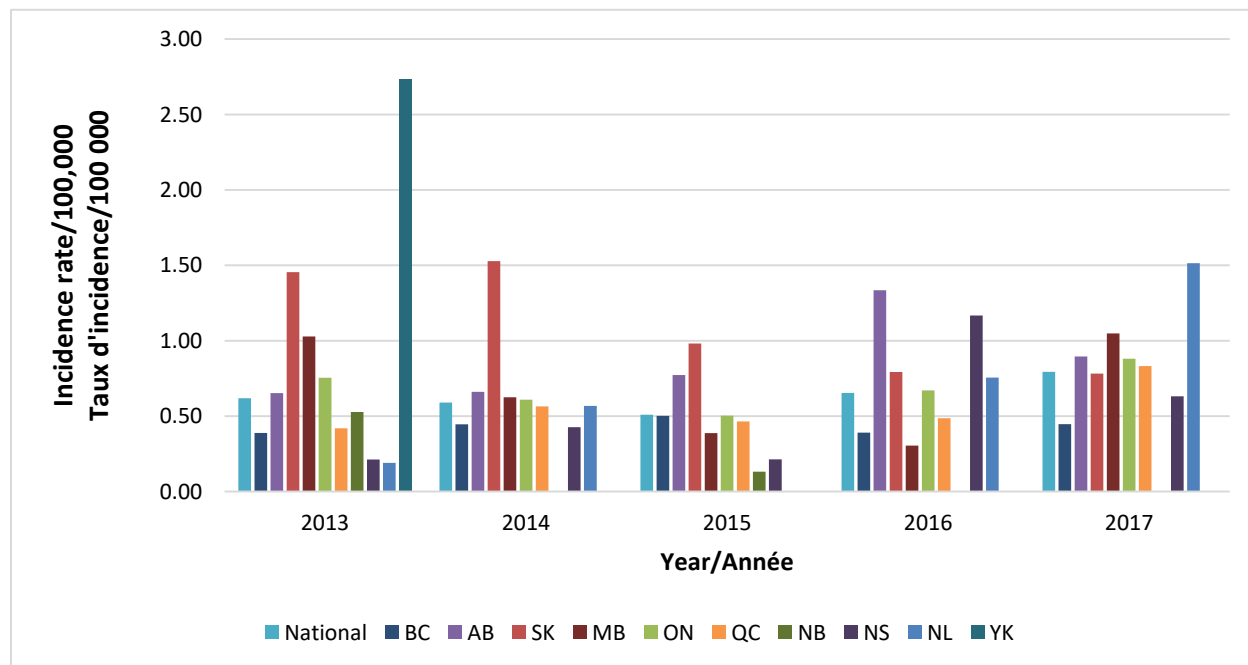
Figure 8. Incidence rate (per 100,000 population) of *Shigella* species reported to NESP, 1997-2019

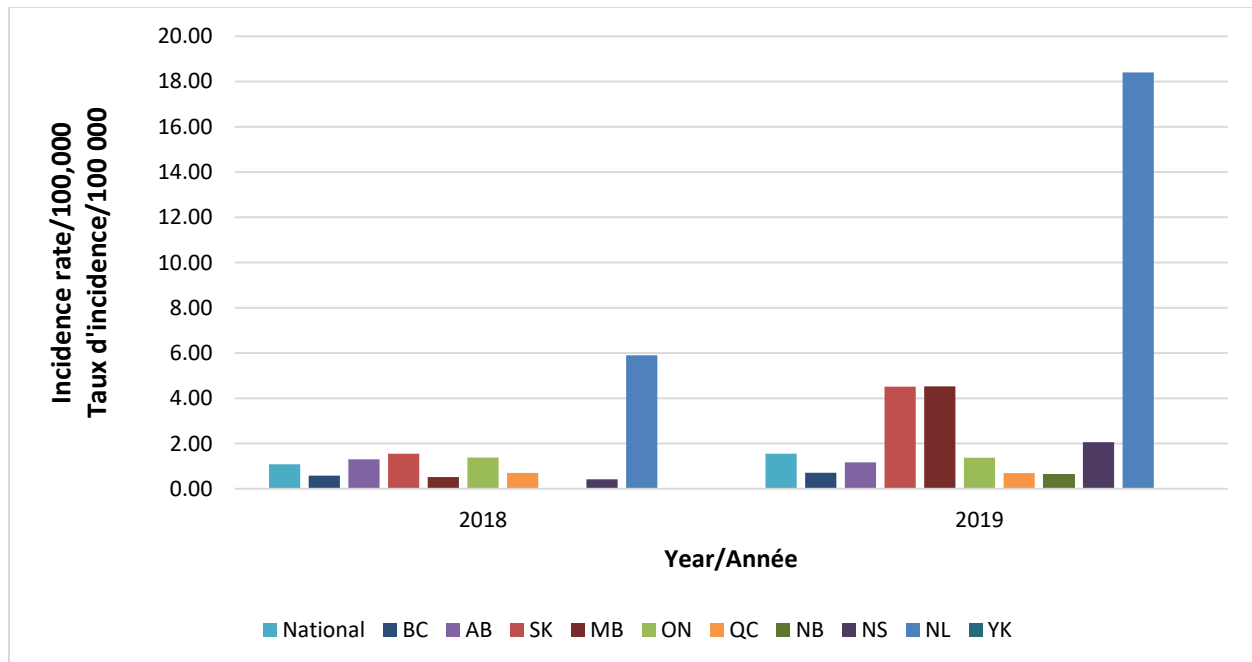


Hepatitis A

The national incidence rate for Hepatitis A in 2019 was the highest since its inclusion in NESP in 2012, with a rate of 1.55 cases per 100,000 population (Figure 9). Each provincial and territorial laboratory determines whether to report a case based solely on laboratory testing, without public health follow-up. A positive IgM result could be due to false positive or recent immunization. When local public health follow up occurs it is then determined whether case meets a confirmed case definition or not. If local public health determines it is not a case (e.g. recent immunization), this information may not always be relayed back to the laboratory, and therefore, our surveillance figures are not corrected. The drastic increases observed in Figure 9 could be a result of change of laboratory detection methods. Conversely, since not all specimens/isolates are referred from the regional and local laboratories to the provincial public health laboratories, viruses, including Hepatitis A, are under-represented in NESP and reported case counts are not representative of the true incidence of the disease in Canada.

Figure 9. National and provincial incidence rate (per 100,000 population) of Hepatitis A reported to NESP, 2013-2019





Appendix 1. Comparison of national totals, incidence per 100 000 population and proportion captured between the Canadian Notifiable Disease Surveillance System (CNDSS) and the National Enteric Surveillance Program (NESP) for enteric diseases, 2018¹

Enteric, Food and Waterborne Diseases	Canadian Notifiable Disease Surveillance System (CNDSS)		National Enteric Surveillance Program (NESP)		% of CNDSS cases captured in NESP (NESP isolations / CNDSS cases ⁸)
	N	Rate per 100,000 population	N	Rate per 100,000 population	
2018					
Botulism	8	0.02	-	-	N/A
Campylobacteriosis ²	10215	27.57	1333	-	13.0
Cholera ³	0	0	2	0.005	0
Cryptosporidiosis ²	1305	3.52	398	-	30.5
Cyclosporiasis ²	337	0.91	46	-	13.6
Giardiasis ²	3903	10.53	770	-	19.9
Hepatitis A	380	1.03	402	1.08	112.6 ⁸
Invasive Listeriosis	158	0.43	150	0.4	94.9
Norovirus ^{2,4,5}	560	11.42	1432	-	N/A
Paralytic Shellfish Poisoning ⁶	2	0.01	-	-	N/A
Salmonellosis	7131	19.24	7300	19.7	102.4 ⁸
Shigellosis	863	2.33	784	2.12	90.8
Typhoid ⁷	191	0.52	198	0.53	103.7 ⁸
Shiga toxinogenic <i>Escherichia coli</i> Infection	1088	2.94	1091	2.94	100.9 ⁸

¹CNDSS data for 2019 was not available at the time this summary was produced.

²*Campylobacter*, parasites (*Cryptosporidium*, *Cyclospora* and *Giardia*) and Norovirus are not routinely reported to provincial or central reference laboratories and are greatly under-represented in NESP; therefore no rate was calculated for NESP.

³Includes *Vibrio cholerae* serotype O1 or O139.

⁴AB, MB, NB, NS, NT, ON, PEI, QC and SK did not report on norovirus in 2018. The populations of these provinces and territory have been removed for rate calculation.

⁵For Norovirus some provinces/territories report only on aggregated outbreak related data; these data are not included here.

⁶AB, MB, NT, QC and SK did not report on paralytic shellfish poisoning in 2018. The populations of these provinces and territory have been removed for rate calculation.

⁷Typhoid includes lab confirmation of *Salmonella* Typhi; *Salmonella* Paratyphi A, B and C are reported under salmonellosis.

⁸Cases reported through the CNDSS and laboratory-confirmed isolations through NESP have not been linked, this is the degree of concurrence represented as a percentage of NESP isolations compared to the case count reported by the CNDSS. Percentages greater than 100 likely reflect cases with more than one isolate.

Appendix 2. Species and serotype data reported to NESP by province and territory, 2019

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL
Campylobacter														
<i>Campylobacter coli</i>	1	25	10	16	9	32	4	9	3	0	0	0	0	109
<i>Campylobacter concisus</i>	2	1	0	0	0	3	0	0	0	0	0	0	0	6
<i>Campylobacter curvus</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	1
<i>Campylobacter fetus</i>	1	3	0	0	2	19	0	0	0	0	0	0	0	25
<i>Campylobacter gracilis</i>	4	0	0	0	0	6	0	0	0	0	0	0	0	10
<i>Campylobacter hyointestinalis</i>	0	1	0	0	1	2	0	0	0	0	0	0	0	4
<i>Campylobacter jejuni</i>	20	301	159	78	60	227	172	92	29	0	0	0	0	1138
<i>Campylobacter lari</i>	4	0	0	0	5	11	9	0	1	0	0	0	0	30
<i>Campylobacter rectus</i>	0	0	0	0	0	3	0	0	0	0	0	0	0	3
<i>Campylobacter sp</i>	0	0	0	0	0	3	51	1	0	191	0	0	0	246
<i>Campylobacter upsaliensis</i>	5	5	1	0	46	9	2	7	2	0	0	0	0	77
<i>Campylobacter ureolyticus</i>	2	1	0	0	0	12	0	0	0	0	0	0	0	15
Total Campylobacter	39	337	170	94	123	327	238	110	35	191	0	0	0	1664
Escherichia coli														
<i>E. coli</i>	0	0	0	0	0	0	0	0	0	2	0	0	0	2
<i>E. coli</i> CIDT Positive for STX/STEC	14	0	0	0	0	119	0	0	0	6	0	0	0	139
<i>E. coli</i> Non-O157 VTEC	2	0	8	22	0	18	0	0	0	0	0	0	0	50
<i>E. coli</i> Non-Typed EAEC	0	0	0	0	0	0	0	0	0	67	0	0	0	67
<i>E. coli</i> Non-Typed EPEC	0	0	0	0	0	0	0	0	0	208	0	0	0	208
<i>E. coli</i> Non-Typed ETEC	0	0	0	0	0	0	0	0	1	50	0	0	0	51
<i>E. coli</i> Non-Typed VTEC	2	0	0	0	0	0	0	0	0	0	1	0	0	3
<i>E. coli</i> O undetermined:H2	0	0	0	0	1	0	0	0	0	3	0	0	0	4
<i>E. coli</i> O undetermined:H2 VTEC	0	3	0	0	0	0	0	0	0	0	0	0	0	3
<i>E. coli</i> O undetermined:H21 VTEC	0	2	0	0	0	0	0	0	0	0	0	0	0	2
<i>E. coli</i> O undetermined:H28	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O undetermined:H52 VTEC	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O undetermined:H8	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O undetermined:HNM	0	0	1	0	0	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O-Rough:H Nonmotile	0	0	0	0	2	0	0	0	0	0	0	0	0	2
<i>E. coli</i> O-Rough:H11	0	0	1	0	0	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O-Rough:H11 VTEC	0	2	0	0	0	0	0	0	0	0	0	0	0	2
<i>E. coli</i> O-Rough:H4	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O-Rough:H45	2	0	0	0	0	0	0	0	0	0	0	0	0	2
<i>E. coli</i> O-Rough:H52	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O100:HNM	0	0	1	0	0	0	0	0	0	0	0	0	0	1
<i>E. coli</i> O103	4	0	0	0	0	0	0	0	0	0	1	0	0	5

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL
<i>Salmonella</i> Manhattan	1	1	0	0	5	3	0	1	0	0	0	0	0	11
<i>Salmonella</i> Matopeni	0	0	0	0	2	0	0	0	0	0	0	0	0	2
<i>Salmonella</i> Mbandaka	1	2	0	0	18	4	2	0	0	0	0	0	0	27
<i>Salmonella</i> Meleagridis	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Miami	0	1	0	0	1	2	0	1	0	0	0	0	0	5
<i>Salmonella</i> Michigan	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Mikawasima	0	1	0	0	1	1	0	1	0	0	0	0	0	4
<i>Salmonella</i> Mississippi	0	0	1	0	9	1	5	1	0	0	0	0	0	17
<i>Salmonella</i> Montevideo	3	3	7	1	14	6	2	0	0	0	0	0	0	36
<i>Salmonella</i> Muenchen	10	14	2	1	37	11	3	1	1	0	0	0	0	80
<i>Salmonella</i> Muenster	4	1	1	0	4	1	0	0	0	0	0	0	0	11
<i>Salmonella</i> Nchanga	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Nessziona	0	0	0	0	2	0	0	0	0	0	0	0	0	2
<i>Salmonella</i> Newport	34	36	8	10	77	28	3	4	0	0	0	0	0	200
<i>Salmonella</i> Nigeria	0	0	0	0	1	1	0	0	0	0	0	0	0	2
<i>Salmonella</i> Nima	0	0	0	0	2	0	0	0	0	0	0	0	0	2
<i>Salmonella</i> Norwich	0	0	0	0	2	10	1	0	1	0	0	0	0	14
<i>Salmonella</i> Nottingham	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> Offa	0	1	0	0	0	1	0	0	0	0	0	0	0	2
<i>Salmonella</i> Ohio	0	0	0	0	2	1	0	0	0	0	0	0	0	3
<i>Salmonella</i> Okatie	0	0	0	0	4	0	0	0	0	0	0	0	0	4
<i>Salmonella</i> Oranienburg	7	9	8	7	46	25	0	2	0	0	0	0	0	104
<i>Salmonella</i> Orion	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Oslo	3	1	0	1	12	1	0	0	0	0	0	0	0	18
<i>Salmonella</i> Panama	3	7	1	1	17	6	0	1	0	0	0	0	0	36
<i>Salmonella</i> Paratyphi A	34	24	4	1	47	6	0	0	0	0	0	0	0	116
<i>Salmonella</i> Paratyphi B	2	0	0	1	1	0	0	0	0	0	0	0	0	4
<i>Salmonella</i> Paratyphi B var. Java	19	18	1	0	14	8	3	1	0	0	0	0	0	64
<i>Salmonella</i> Pensacola	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> Pomona	1	1	0	0	2	1	0	2	0	0	0	0	0	7
<i>Salmonella</i> Poona	4	4	1	0	7	5	0	1	0	0	0	0	0	22
<i>Salmonella</i> Potsdam	0	0	0	0	3	0	0	0	0	0	0	0	0	3
<i>Salmonella</i> Putten	0	0	0	1	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Reading	14	30	6	14	10	2	0	0	1	0	0	0	0	77
<i>Salmonella</i> Richmond	3	0	0	0	2	0	0	0	0	0	0	0	0	5
<i>Salmonella</i> Rissen	6	2	0	0	4	0	0	0	0	0	0	0	0	12
<i>Salmonella</i> Rubislaw	0	1	0	0	2	0	0	0	0	0	0	1	0	4
<i>Salmonella</i> Saintpaul	7	24	5	4	40	14	2	1	0	0	0	2	0	99
<i>Salmonella</i> San Diego	3	3	0	1	7	2	0	0	0	0	0	0	0	16
<i>Salmonella</i> Schwarzengrund	5	3	1	0	11	3	1	3	0	0	0	0	0	27

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL
<i>Shigella boydii</i> 19	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Shigella boydii</i> 2	0	0	0	0	1	3	0	0	0	0	0	0	0	4
<i>Shigella boydii</i> 20	0	1	0	0	0	1	0	0	0	0	0	0	0	2
<i>Shigella boydii</i> 4	1	0	0	0	1	0	0	0	0	0	0	0	0	2
<i>Shigella boydii</i> 8	0	0	0	0	0	2	0	0	0	0	0	0	0	2
<i>Shigella boydii</i> 9	1	1	0	0	0	0	0	0	0	0	0	0	0	2
<i>Shigella boydii</i>	3	0	0	0	0	0	0	0	0	0	0	0	0	3
<i>Shigella dysenteriae</i> 16	0	3	0	0	1	0	0	0	0	0	0	0	0	4
<i>Shigella dysenteriae</i> 2	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Shigella dysenteriae</i> 9	1	0	0	0	1	0	0	0	0	0	0	0	0	2
<i>Shigella dysenteriae</i>	1	0	0	1	0	1	0	0	0	0	0	0	0	3
<i>Shigella dysenteriae</i> Prov. SH-111	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Shigella flexneri</i> 1	3	0	0	0	10	7	0	0	0	0	0	0	0	20
<i>Shigella flexneri</i> 16	0	0	0	0	0	2	0	0	0	0	0	0	0	2
<i>Shigella flexneri</i> 1a	0	0	0	0	3	0	0	0	0	0	0	0	0	3
<i>Shigella flexneri</i> 1b	13	7	0	1	18	42	0	0	0	0	0	0	0	81
<i>Shigella flexneri</i> 2a	20	15	0	2	29	39	0	0	0	0	0	0	0	105
<i>Shigella flexneri</i> 2b	0	1	0	0	1	1	0	0	0	0	0	0	0	3
<i>Shigella flexneri</i> 3	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Shigella flexneri</i> 3a	6	3	0	0	5	4	0	0	0	0	0	0	0	18
<i>Shigella flexneri</i> 3b	1	0	0	0	1	7	0	0	0	0	0	0	0	9
<i>Shigella flexneri</i> 4	5	3	0	0	0	3	0	0	0	0	0	0	0	11
<i>Shigella flexneri</i> 4a	0	0	0	0	4	0	0	0	0	0	0	0	0	4
<i>Shigella flexneri</i> 4b	1	0	0	0	1	0	0	0	0	0	0	0	0	2
<i>Shigella flexneri</i> 4c	0	1	0	0	0	1	0	0	0	0	0	0	0	2
<i>Shigella flexneri</i> 6	1	2	0	0	5	2	0	0	0	0	0	0	0	10
<i>Shigella flexneri</i>	2	0	5	6	0	10	5	2	0	0	0	0	0	30
<i>Shigella flexneri</i> Prov. SH-104	0	3	0	0	7	4	0	0	0	0	0	0	0	14
<i>Shigella flexneri</i> var. X	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Shigella flexneri</i> var. Y	1	2	0	0	6	6	0	0	0	0	0	0	0	15
<i>Shigella sonnei</i>	103	56	8	6	157	116	2	2	0	0	1	0	0	451
Total Shigella	167	99	13	16	253	255	7	4	0	12	1	0	0	827
Vibrio														
<i>Vibrio alginolyticus</i>	2	2	0	0	1	0	0	0	1	0	0	0	0	6
<i>Vibrio cholerae</i>	0	1	0	0	0	0	1	0	0	0	0	0	0	2
<i>Vibrio cholerae</i> O1	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Vibrio cholerae</i> O1 Ogawa	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Vibrio cholerae</i> non-O1/O139	4	0	0	0	1	6	0	1	0	0	0	0	0	12
<i>Vibrio fluvialis</i>	1	1	0	0	0	0	2	1	0	0	0	0	0	5

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL
<i>Vibrio mimicus</i>	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Vibrio parahaemolyticus</i>	15	2	0	0	2	0	4	0	0	0	0	0	0	23
<i>Vibrio</i> sp	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Total Vibrio	23	7	1	0	5	6	7	2	1	0	0	0	0	52
Yersinia														
<i>Yersinia enterocolitica</i>	37	22	6	2	161	23	3	0	0	3	1	0	0	258
<i>Yersinia frederiksenii</i>	17	2	4	0	0	0	1	0	0	0	0	0	0	24
<i>Yersinia intermedia</i>	9	12	2	0	0	0	0	0	0	0	0	0	0	23
<i>Yersinia kristensenii</i>	2	2	0	0	0	0	0	0	0	0	0	0	0	4
<i>Yersinia massiliensis</i>	5	0	0	0	0	0	0	0	0	0	0	0	0	5
<i>Yersinia pseudotuberculosis</i>	3	0	1	0	0	0	0	0	0	0	0	0	0	4
Total Yersinia	73	38	13	2	161	23	4	0	0	3	1	0	0	318
Parasites														
<i>Cryptosporidium</i>	30	1	20	25	257	2	38	39	13	32	0	0	0	457
<i>Cyclospora</i>	8	0	0	1	54	0	0	1	0	1	1	0	0	66
<i>Entamoeba histolytica/dispar</i>	153	5	18	20	131	33	0	8	0	1	8	0	0	377
<i>Giardia</i>	68	7	81	89	228	14	86	88	3	66	9	0	0	739
Total Parasites	259	13	119	135	670	49	124	136	16	100	18	0	0	1639
Viruses														
Adenovirus	16	5	0	48	53	0	0	4	0	64	0	0	0	190
Astrovirus	14	0	0	0	1	0	0	0	0	68	0	0	0	83
Enterovirus	0	0	0	7	0	0	0	0	0	0	0	0	0	7
Hepatitis A	36	52	53	62	200	59	5	20	0	96	0	0	0	583
Norovirus	318	104	71	127	613	0	63	55	58	144	0	1	0	1554
Rotavirus	29	5	44	22	22	0	39	14	17	22	0	0	0	214
Sapovirus	12	1	0	1	0	0	0	0	0	11	0	0	0	25
Total Virus	425	167	168	267	889	59	107	93	75	405	0	1	0	2656