National Enteric Surveillance Program (NESP)

Annual Summary 2022

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The National Microbiology Laboratory (NML) and
Centre for Foodborne, Environmental and Zoonotic Infectious Diseases (CFEZID),
Public Health Agency of Canada

&

Provincial Public Health Laboratories

Acknowledgements

National Enteric Surveillance Program (NESP) Coordination Team:

Celine Nadon, Director, Division of Enteric Diseases, National Microbiology Laboratory (NML)
Sara Christianson, Chief, Diagnostic and Reference Services Section, Division of Enteric Diseases, NML
Lori Lozinski, Surveillance Clerk, Division of Enteric Diseases, NML
Brent Avery, A/Surveillance Manager, Foodborne Disease and AMR Surveillance Division (FDASD), Centre for Foodborne, Environmental and Zoonotic Infectious Diseases (CFEZID)
Lauren Sherk, Epidemiologist, FDASD, CFEZID

Provincial Laboratory Partners:

BC Centre for Disease Control Public Health Laboratory
Alberta Precision Laboratories
Roy Romanow Provincial Laboratory (Saskatchewan)
Cadham Provincial Microbiology Laboratory (Manitoba)
Public Health Ontario
Laboratoire de santé publique du Québec (LSPQ)
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Prince Edward Island Public Health Laboratories
Newfoundland and Labrador Public Health Laboratory

Provincial/Territorial Epidemiology Partners:

British Columbia Centre for Disease Control
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Ministère de la santé et des services sociaux du Québec
New Brunswick Health
Nova Scotia Department of Health and Wellness
Prince Edward Island Department of Health and Wellness
Newfoundland and Labrador Department of Health and Community Services
Yukon Health and Social Services
Northwest Territories Department Health and Social Services
Nunavut Health and Social Services

Overview

The National Enteric Surveillance Program (NESP) is a collaboration 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 organisms that are nationally notifiable. The data and information 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 2022, a total of 12,523 isolate results were reported to NESP; a similar number as the average number of notifications received in the previous five years (12,677). However, this number remains lower than the 2015 to 2019 (pre-COVID-19 pandemic) five-year average number of notifications (15,313). *Salmonella* spp. continues to be the most common organism identified with 4,826 notifications provided in 2022, representing 39% of all isolates reported to NESP. As in previous years, *Salmonella* Enteritidis (1,840 isolates; 38%) and *S.* Typhimurium (319 isolates; 7%), represent the top two serotypes among all *Salmonella* reported in 2022. In 2022, *S.* ssp I 4,[5],12:i:- (265 isolates; 5%) was the third most commonly reported serotype. Collectively, these three serotypes represent 50% of all *Salmonella* serotypes identified.

The 2022 incidence rate of Shiga toxin-producing *Escherichia coli* (STEC) O157 is slightly higher than the 2021 rate of O157 STEC with 0.77 cases per 100,000 population reported, but remains lower than the relatively stable rate seen from 2010 to 2019 (between 0.95 to 1.40 cases per 100,000 population). A slight increase was observed in the incidence rate of non-O157 STEC isolates in 2022 (1.32 cases per 100,000 population) compared to 2021 (0.98 cases per 100,000 population). However, this remains lower than an all-time high of 1.58 cases per 100,000 population reported to NESP in 2019. This is the sixth consecutive year where more non-O157 STEC isolates were reported than O157 STEC isolates.

The incidence rate of invasive listeriosis in 2022 (0.47 per 100,000 population) is slightly higher than what was reported in 2021, but similar to 2019. The incidence rate of Hepatitis A increased in 2022 (0.80 cases per 100,000 population) compared to 2021 (0.69 cases per 100,000 population). However, this is still lower than the highest incidence reported in 2019 (1.30 cases per 100,000 population). In contrast to 2019 and years before where *Shigella sonnei* represented the majority of *Shigella* species reported, 2022 followed a similar trend to 2021 and 2020 where *Shigella flexneri* represented over 50% of all *Shigella* reported. In 2022, the rate of *Shigella flexneri* (1.45 per 100,000 population) was also higher than the rate of *Shigella sonnei* (0.96 per 100,000 population). Trends for all other *Shigella* species in 2022 were similar to 2021, remaining lower compared to previous years.

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

In Canada, the national surveillance of human 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 by the provincial public health laboratories has been conducted through NESP.

NESP provides the most timely data (at a level of characterization that is primarily species and serotype) that are critical to, and integrated with other surveillance programs. Monitoring these aggregated data allows for the rapid evaluation and response to enteric illness outbreaks. In addition, these data allow 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 PHAC's 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 (i.e., whole genome sequence) data in real-time on cases of enteric diseases for the purpose of outbreak detection and response. Due to the additional testing performed (genomic subtyping, whole genome sequencing), there are differences in 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 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, pathovar

[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.canada.ca/en/public-health/programs/pulsenet-canada.html

(where appropriate) 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 (through email), 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* spp.) 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 indicates that one "*Salmonella* spp." 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 public health laboratories attempt to identify multiple, repeat, or follow-up specimens from the same individual. For example, when multiple isolates are collected from a single patient, the laboratories would consider this as a single case if all identical isolates are collected over a reasonable time period (typically three months).

Enhanced subtype data collected for surveillance purposes are primarily generated using whole genome sequencing (WGS) *in silico* predictions instead of by classical microbiological methods. This includes *in silico* predictions of species identification and serotype (where applicable). Use of WGS data for NESP analyses helps ensure this system will remain compatible with surveillance in the genomics era. Since 2018, the majority of the data collected and analyzed by NESP has been generated via WGS.

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 public health 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 NESP Weekly Reports, partners can perform real-time data analysis, examine trends and display their respective jurisdictions' data within the webNESP application. PulseNet Canada uses these data in conjunction with whole genome sequencing based subtyping data and other molecular/genomic data to detect disease clusters and outbreaks. The resulting data analyses are also shared on CNPHI with provincial public health laboratories, the Canadian Food Inspection Agency (CFIA), Health Canada (HC), PHAC and provincial/territorial epidemiologists. The coordinated assessment of laboratory evidence collected through these 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].

For this annual summary, initial 2022 data validation activities were performed in collaboration with the provinces and territories. Once the final dataset was validated and closed, summary statistics using SAS software[d] were conducted for the 14 different enteric organisms causing enteric illness that are reported to NESP.

Limitations

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 public health or central reference laboratories for further testing beyond genus/species characterizations, and are therefore greatly under-represented in NESP. By contrast, *Salmonella* and O157 STEC 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 provincial public health laboratories and therefore any interpretation should be considered with caution.

In March of 2020, the COVID-19 pandemic was declared[e] and global public health action was taken to address it. Across Canada and within specific provinces/territories and regions, various public health measures were put in place. These public health measures and the adaptations Canadians made to combat COVID-19 not only helped

[c] Food-borne Illness Outbreak Response Protocol (FIORP) 2017: To guide a multi-jurisdictional response. Public Health Agency of Canada: https://www.canada.ca/en/public-health/services/publications/health-risks-safety/canadas-foodborne-illness-outbreak-response-protocol-fiorp-guide-multi-jurisdictional-enteric-outbreak-response.html

[d] SAS software, Version 9.4 of the SAS System for Windows. Copyright © 2016 SAS Institute Inc.

[e] https://www.who.int/director-general/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020 (accessed September 13, 2021)

to reduce the transmission of COVID-19, but have also impacted other reported infectious diseases to varying degrees in various ways.

Similar to the 2020 and 2021 NESP Annual Summaries, interpretation of the data and findings in the 2022 NESP Annual Summary should be interpreted with caution, as the public health measures invoked to help limit the spread of COVID-19 likely impacted disease incidence spanning all pandemic-related years, as well as data collection and reporting to NESP (Appendix D). In addition, COVID-19 impacts on laboratory services (e.g., delays, break in service, reduced service, change in service) likely impacted the observed incidence of these enteric pathogens reported to NESP during the pandemic years.

Questions and correspondence may be forwarded via email to:

nesp-pnsme@phac-aspc.gc.ca

Laboratory-confirmed Isolate Counts & Incidence Rates

In 2022, provincial public health laboratories reported 12,523 cases of illness caused by enteric pathogens to NESP, similar to the average number of notifications reported in the previous five years (12,677). However, this number remains lower than the 2015 to 2019 (pre-COVID-19 pandemic) five-year average number of notifications (15,313). The most frequently reported enteric pathogen group was *Salmonella*, followed by enteric viruses (Norovirus, Hepatitis A, Rotavirus, Adenovirus, Astrovirus, Sapovirus and Enterovirus) and *E. coli* (Table 1). Organism isolate counts reported by province and territory in 2022 can be found in Appendix B.

Table 1. Number of isolates reported to NESP by major organism group per province or territory, 2022

Group[4]	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total	% of total isolates reported
Salmonella	781	598	146	111	1,977	949	121	80	7	46	0	8	2	4,826	38.54
Viruses[1]	258	811	223	236	569	57	151	67	30	383	0	1	3	2,789	22.27
E. coli[2]	133	325	58	156	183	154	17	1	5	296	0	0	0	1,328	10.60
Campylobacter[1]	6	164	119	135	69	186	187	84	32	105	1	0	0	1,088	8.69
Parasites[1]	147	7	88	67	432	NR[3]	102	68	19	79	21	0	0	1,030	8.22
Shigella	304	275	3	5	231	146	4	1	0	7	1	1	0	978	7.81
Yersinia	65	33	4	4	95	30	1	0	0	1	0	0	0	233	1.86
Listeria	14	14	1	5	69	59	4	12	1	4	0	0	0	183	1.46
Vibrio	27	3	3	0	17	4	11	0	3	0	0	0	0	68	0.54
Total	1,735	2,230	645	719	3,642	1,585	598	313	97	921	23	10	5	12,523	100.00

[1] *Campylobacter* isolates, parasitic detections (*Giardia, Cryptosporidium, Entamoeba histolytica/dispar* and *Cyclospora*), and viral detections (Norovirus, Rotavirus, Adenovirus, Astrovirus, Sapovirus and Enterovirus) are not routinely forwarded to the provincial public health or central reference laboratories and are greatly under-represented in NESP.
[2] *E. coli* includes O157 STEC serotypes (299 isolates), non-O157 STEC serotypes (513 isolates), CIDT positive for STX/STEC (178 detections), non-typed STEC (54 isolates), and other non-STEC pathotypes (284 detections).
[3] NR stands for Not Reported. In 2020, 2021 and 2022 due to resources being directed to COVID-19, no parasites were reported from Quebec.
[4] Cases visiting a different province or territory are captured in the total count for the province or territory where the case was detected.

Annual national incidence rates for the groups of enteric pathogens reported to NESP between 2017 and 2022 are shown in Table 2 and Appendix A. Isolates of O157 STEC, non-O157 STEC, *Listeria monocytogenes, Salmonella* spp., *Shigella* spp., and *Vibrio cholerae* are routinely forwarded to provincial public health laboratories, while isolates of *Campylobacter* spp., non-*cholerae Vibrio, Yersinia* spp., enteric parasites (*Giardia* spp., *Cryptosporidium* spp., *Entamoeba histolytica/dispar* and *Cyclospora cayetanensis*) and enteric viruses (Norovirus, Rotavirus, Adenovirus, Astrovirus, Sapovirus and Enterovirus) are not routinely forwarded to the provincial public health or central reference laboratories. As such, NESP incidence rates are considered to be reflective of the true incidence rate for those pathogens that are routinely reported, enabling the calculation of provincial and territorial incidence rates as shown in Table 3.

Table 2. Annual national totals and rates[1] (per 100,000 population) for enteric pathogens and organism groups reported to NESP, 2017 to 2022

Group	2017		2018		2019		2020		2021		2022	
	Total	Rate[1]	Total	Rate[1]	Total	Rate[1]	Total	Rate[1]	Total	Rate[1]	Total	Rate[1]
O157 STEC	348	0.95	426	1.15	397	1.06	237	0.62	260	0.68	299	0.77
Non-O157 STEC[2]	361	0.99	525	1.42	595	1.58	320	0.84	373	0.98	513	1.32
Listeria	109	0.30	150	0.40	174	0.46	158	0.42	154	0.40	183	0.47
Salmonella	7,313	20.01	7,300	19.70	6,350	16.89	4,919	12.94	3,360	8.79	4,826	12.40
Shigella	699	1.91	784	2.12	828	2.20	393	1.03	416	1.09	978	2.51
Campylobacter	1,287	3.52	1,333	3.60	1,664	4.43	1,289	3.39	1,255	3.28	1,088	2.79
Vibrio	54	0.15	67	0.18	52	0.14	44	0.12	51	0.13	68	0.17
Yersinia	387	1.06	404	1.09	318	0.85	283	0.74	298	0.78	233	0.60
Parasites	1,679	4.59	1,675	4.52	1,639	4.36	1,017	2.68	1,020	2.67	1,030	2.65
Viruses	2,593	7.10	2,273	6.13	2,564	6.82	1,035	2.72	938	2.45	2,789	7.16

[1]Rates calculated using the population estimates on July 1st as reported by Statistics Canada – Table 17-10-0005-01. Accessed November 17, 2023. https://doi.org/10.25318/1710000501-eng

[2]Unless otherwise indicated, it is assumed that all *E. coli* samples reported to NESP from the provinces and territories are Shiga toxin-producing *Escherichia coli* (STEC). This value does not include any non-typed *E. coli.*

Table 3. Annual rates[1] (per 100,000 population) of infection per province and territory for select groups of pathogens routinely reported to NESP, 2022

Group[2]	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU
O157 STEC	0.24	2.22	0.75	0.28	0.78	0.48	0.74	0.10	2.93	0.00	0.00	0.00	0.00
Non-O157 STEC	1.75	4.89	4.10	2.55	0.43	0.47	0.74	0.00	0.00	0.19	0.00	0.00	0.00
Listeria	0.26	0.31	0.08	0.35	0.46	0.68	0.49	1.18	0.59	0.76	0.00	0.00	0.00
Salmonella	14.68	13.16	12.22	7.88	13.08	10.91	14.90	7.85	4.10	8.75	0.00	17.54	4.94
Shigella	5.72	6.05	0.25	0.35	1.53	1.68	0.49	0.10	0.00	1.33	2.28	2.19	0.00

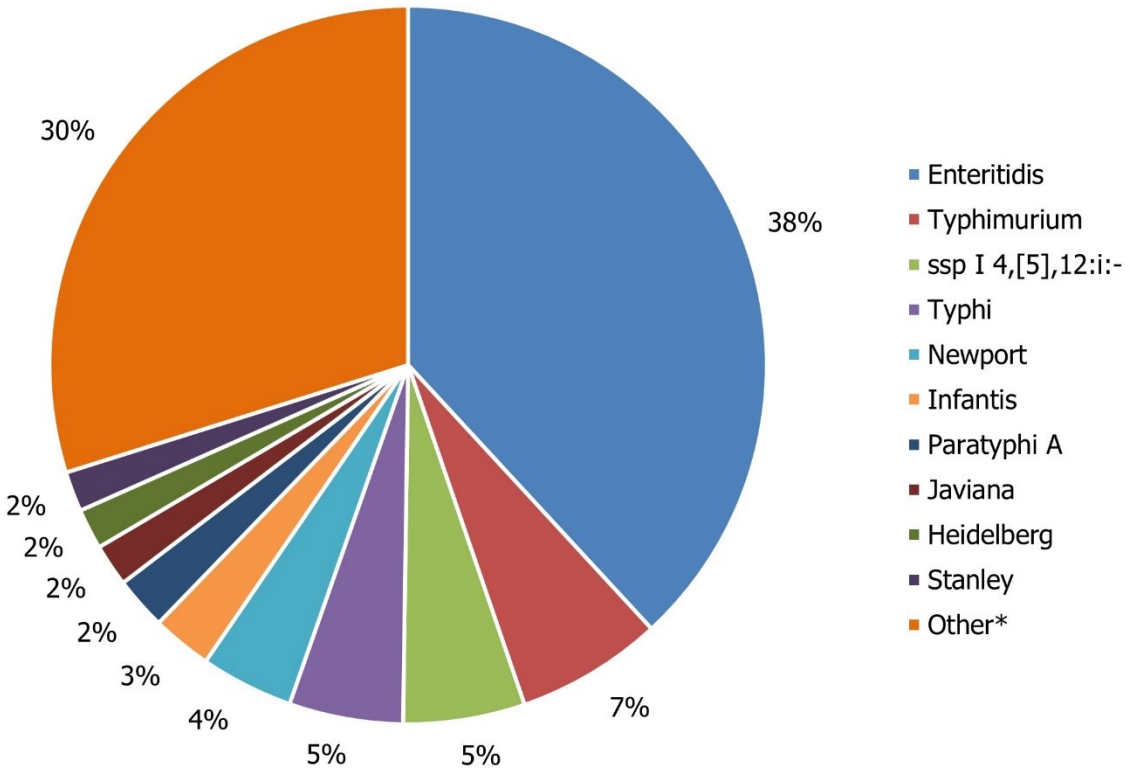
[1]Rates calculated using the population estimates on July 1st as reported by Statistics Canada – Table 17-10-0005-01. Accessed November 17, 2023. https://doi.org/10.25318/1710000501-eng

[2]Cases visiting a different province or territory are captured in the total count for the province or territory where the case was detected.

Salmonella

A total of 4,826 *Salmonella* isolates representing 217 serotypes were reported to NESP in 2022. *Salmonella* Enteritidis accounted for 38% of all human salmonellosis, and together with the nine remaining most common serotypes (Figure 1), they made up 70% of all *Salmonella* infections reported. National, provincial and territorial case counts for *Salmonella* reported in 2022 are shown in Table 4 and Appendix B.

Figure 1. Proportion of *Salmonella* serotypes causing human illness as reported to NESP, 2022 (n=4,826)



*Other serotypes (1,440 isolates) were divided among 207 serotypes or incomplete antigenic profiles, and 22 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, 2022

Serotype	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total	% of total *Salmonella* (n=4,826)
Enteritidis	365	221	34	32	661	380	78	43	4	20	0	2	0	1,840	38.13%
Typhimurium	29	66	7	10	113	81	3	7	0	2	0	1	0	319	6.61%
ssp I 4,[5],12:i:-	19	20	3	6	109	96	9	1	0	0	0	1	1	265	5.49%
Typhi	46	33	6	10	134	13	2	1	1	2	0	0	0	248	5.14%
Newport	39	37	2	4	86	30	2	2	0	0	0	0	0	202	4.18%
Infantis	11	16	6	4	56	26	5	4	1	1	0	0	0	130	2.69%
Paratyphi A	26	15	2	5	60	5	0	1	0	1	0	0	0	115	2.38%
Javiana	8	10	0	4	39	26	0	0	0	5	0	0	0	92	1.91%
Heidelberg	5	5	4	0	34	32	6	2	0	0	0	0	0	88	1.82%
Stanley	9	6	44	2	17	8	0	0	0	0	0	0	1	87	1.80%
Total	557	429	108	77	1,309	697	105	61	6	31	0	4	2	3,386	70.16%

Compared to the average number of *Salmonella* notifications received from 2017 through 2021 (5,848 cases), there was a 17% decrease observed in 2022 (4,826 cases). The national incidence rate of *Salmonella* (12.40 cases per 100,000 population) increased in comparison to 2021 (8.79 cases per 100,000 population), but remained lower than the previous five years, likely due to the impacts of the COVID-19 pandemic and the continued impact of the CFIA regulation[f] implemented in April 2019 to address *Salmonella* in raw frozen breaded chicken products (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).

In 2022, five provinces/territories reported incidence rates of *Salmonella* higher than the national reported incidence rate: British Columbia (14.68 cases per 100,000 population), Alberta (13.16 cases per 100,000 population), Ontario (13.08 cases per 100,000 population), New Brunswick (14.90 cases per 100,000 population), and Northwest Territories (17.54 cases per 100,000 population) (Table 3).

In May 2017, PulseNet Canada began performing WGS on all *Salmonella* isolates submitted for routine laboratory-based surveillance, providing highly discriminatory genomic subtype data for outbreak detection and response.

[f]Salmonella control options in frozen raw breaded chicken products. Canadian Food Inspection Agency: https://inspection.canada.ca/preventive-controls/meat/salmonella-in-frozen-raw-breaded-chicken/eng/1531254524193/1531254524999

Figure 2. Annual counts between 2013 to 2022 for the top five non-typhoidal *Salmonella* serotypes reported to NESP in 2022

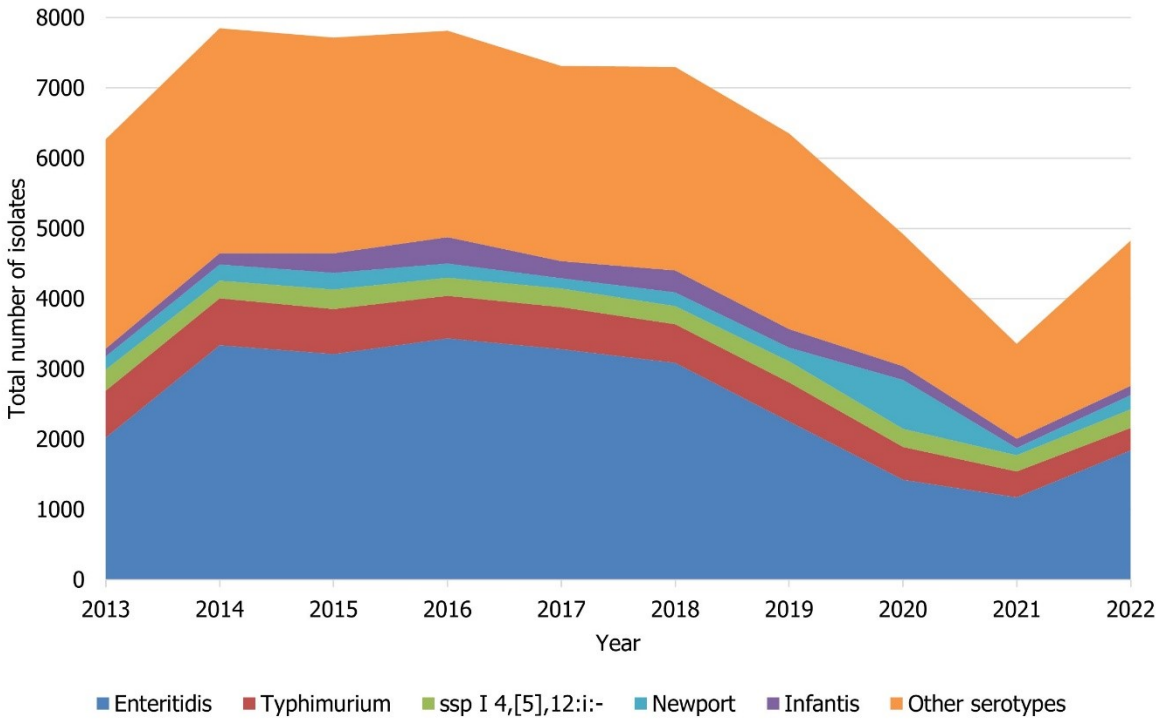


Table 5. National total counts (overall rank) for the ten most commonly reported *Salmonella* serotypes to NESP, 2017 to 2022

Serotypes	2017	2018	2019	2020	2021	2022	Average no. of isolates (2017-2021)
Enteritidis	3,278 (1)	3,083 (1)	2,254 (1)	1,422 (1)	1,172 (1)	1,840 (1)	2,242
Typhimurium	602 (2)	551 (2)	557 (2)	468 (3)	370 (2)	319 (2)	510
ssp I 4,[5],12:i:-	265 (4)	263 (5)	294 (3)	256 (4)	231 (3)	265 (3)	262
Typhi	181 (6)	198 (6)	232 (6)	113 (8)	57 (8)	248 (4)	156
Newport	143 (8)	192 (7)	200 (7)	693 (2)	99 (5)	202 (5)	265
Infantis	244 (5)	313 (4)	264 (5)	198 (6)	138 (4)	130 (6)	231
Paratyphi A	62	56	116 (9)	59	19	115 (7)	62
Javiana	111 (10)	118	143 (8)	50	49	92 (8)	94
Heidelberg	444 (3)	390 (3)	267 (4)	207 (5)	97 (6)	88 (9)	281
Stanley	65	101	87	29	31	87 (10)	63
Thompson	135 (9)	148 (8)	98	126 (7)	95 (7)	85	120
Muenchen	89	53	80	55	56 (9)	44	67
Oranienburg	53	113	104 (10)	71 (10)	55 (10)	56	79
Braenderup	145 (7)	127 (9)	102	81 (9)	42	73	99
Agona	103	125 (10)	101	35	24	50	78

Salmonella Enteritidis

In 2022, 1,840 isolates of *S.* Enteritidis, 38% of all *Salmonella* submissions, were reported to NESP. The incidence rate observed in 2022 was 45% lower (4.73 cases per 100,000 population) relative to the 2013-2017 baseline period (8.53 cases per 100,000 population). A general decrease in incidence can be seen from 2018-2021, and the incidence rate in 2022 increased slightly in comparison to 2020 and 2021. However, the rate observed in 2022 remains lower than that seen in 2018 and 2019, suggesting that this is part of an ongoing trend unrelated to the impacts of COVID-19 (Figure 3) and was also likely a continuation of impacts of relatively recent CFIA poultry product regulations[g].

Salmonella Typhimurium

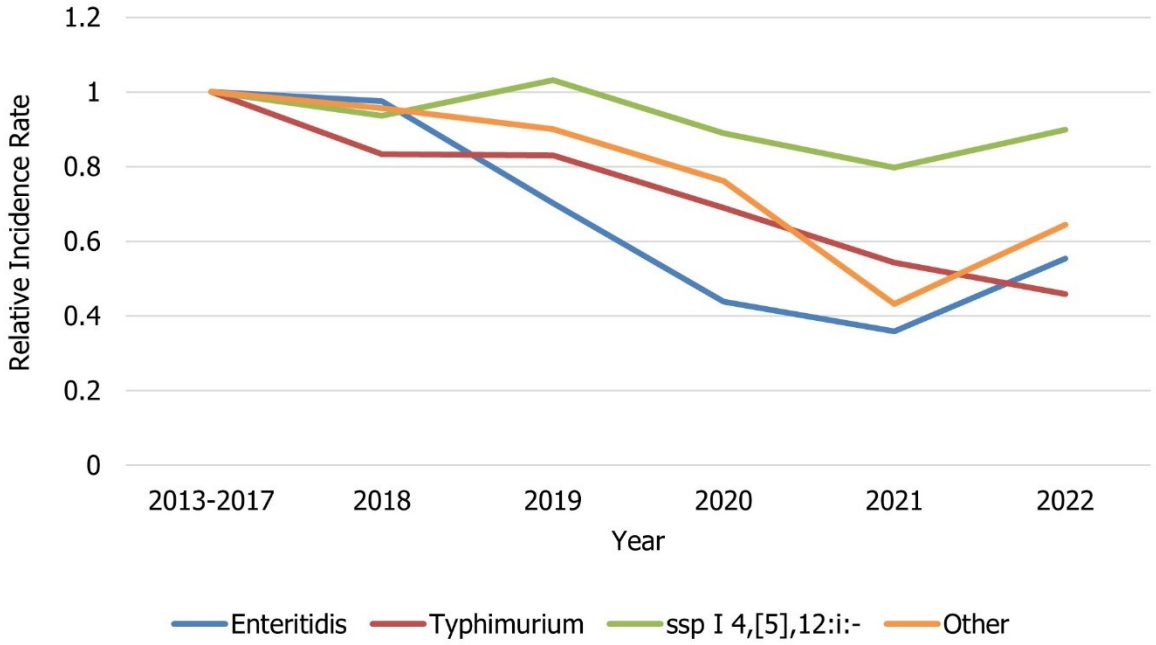
Compared to the 2013-2017 baseline period (1.78 cases per 100,000 population), a 54% decrease in the incidence of *S.* Typhimurium cases was noted in 2022 (0.82 cases per 100,000 population). From 2018-2022, a slight decreasing trend can be seen in the incidence of *S.* Typhimurium (Figure 3). Although *S.* Typhimurium continues to rank among the top 3 most common serotypes causing human salmonellosis in Canada, it represents only 6.61% of all *Salmonella* isolates reported to NESP in 2022 (Figure 1 and Table 5).

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

Salmonella ssp I 4,[5],12:i:-, for the third time since NESP was launched in 1997 (first time being 2019 and second time being 2021), was the third most common serotype in Canada, representing 5.49% of all human *Salmonella* isolates reported to NESP in 2022. The 2022 overall incidence (0.68 cases per 100,000 population) was 11% lower than the 2013-2017 baseline period (0.76 cases per 100,000 population).

[g]Salmonella control options in frozen raw breaded chicken products. Canadian Food Inspection Agency: https://inspection.canada.ca/preventive-controls/meat/salmonella-in-frozen-raw-breaded-chicken/eng/1531254524193/1531254524999

Figure 3. Relative incidence rates[1] (per 100,000 population) of *S.* Enteritidis, *S.* Typhimurium, *S.* ssp I 4,[5],12:i:-, and other *Salmonella* serotypes reported to NESP by year, 2018 to 2022 compared to the 2013 to 2017 baseline period



[1] Rates are compared to the 2013 to 2017 baseline period.

Escherichia coli

Unless otherwise indicated, it is assumed that all *E. coli* isolates reported to NESP from the provinces and territories are Shiga toxin-producing *Escherichia coli* (STEC). The 2022 rate of O157 STEC (0.77 cases per 100,000 population) is slightly higher than the 2021 rate of O157 STEC, but lower than the relatively stable rates seen between 2010 to 2019, which is likely due to the impacts of COVID-19 during 2020 to 2022 (Figure 4). In 2022, three provinces reported incidence rates of O157 STEC higher than the national reported incidence rate: Alberta (2.22 cases per 100,000 population), Ontario (0.78 cases per 100,000 population), and Prince Edward Island (2.93 cases per 100,000 population) (Table 3). The incidence rate of non-O157 STEC increased slightly in 2022 (1.32 cases per 100,000 population) from 2021 (0.98 cases per 100,000 population). However, this rate remains lower than in comparison to 2019 (1.58 cases per 100,000 population) likely due to the impacts of the pandemic (Figure 4). Data from 2022 represent the sixth consecutive year where the proportion of non-O157 STEC reported has exceeded the proportion of O157 STEC isolates. It should be noted that non-O157 STEC are suspected to be reported less consistently than O157 STEC to NESP due to laboratory testing biases that select for *E. coli* O157. Therefore, any changes observed over time may also be a reflection in testing practices by some provincial public health laboratories[h].

Further, 178 *E. coli* cases reported to NESP by 4 provinces were identified using culture-independent diagnostic tests (CIDT), and were not later updated with reflex culture, as seen in Appendix B. CIDTs can detect a specific antigen or genetic sequence of the organism, without isolating or culturing the living organism[i]. According to national guidance[hj], reflex cultures are to be obtained from CIDT-positive samples for public health and clinical management, especially when the Shiga toxin type is unknown (i.e., unable to differentiate between *stx*1 and *stx*2). However, sometimes organisms may not grow upon reflex culture. Reflex culture of a CIDT-positive sample can help obtain an isolate for further sub-typing, which would be updated in NESP.

Among non-O157 STEC isolates serotyped in 2022, 52% of these were represented by five O-antigen serogroups: O26, O103, O121, O111, and O5 (Figure 5). In 2022, 20% of non-O157 STEC did not have additional serotype information.

[h]Public Health Agency of Canada. CPHLN recommendations for the laboratory detection of Shiga toxin-producing *Escherichia coli* (O157 and non-O157). *Can Commun Dis Rep* 2018;44(11):304-7. https://doi.org/10.14745/ccdr.v44i11a06
[i]Centers for Disease Control and Prevention (CDC). Foodborne illness and culture-independent diagnostic tests (CIDTs). 2015 May 14. Available from: https://www.cdc.gov/foodnet/reports/cidt-questions-and-answers-2015.html
[j]Public Health Agency of Canada. National case definition: Shiga toxin-producing *Escherichia coil* (STEC) infection. December 2023. Available from: https://www.canada.ca/en/public-health/services/diseases/e-coli/health-professionals-e-coli/national-case-definition.html

Of the top 5 serogroups from the broader list of the non-O157 STEC isolates where a serotype result was available, O26, O111 and O5 showed an increased rate per 100,000 population in 2022 compared to 2021. With the exception of O121 and O5, the top five serogroups among serotyped *E. coli* isolates showed a decreased rate in 2022 compared to 2019, likely due to the impacts of COVID-19 (Figure 6). All *E. coli* serotypes, including confirmed non-O157 STEC isolates, and any other reported pathotypes are summarized in Appendix B.

Figure 4. Incidence rates (per 100,000 population) of O157 STEC, non-O157 STEC, and other non-typed *E. coli* reported to NESP, 1997 to 2022

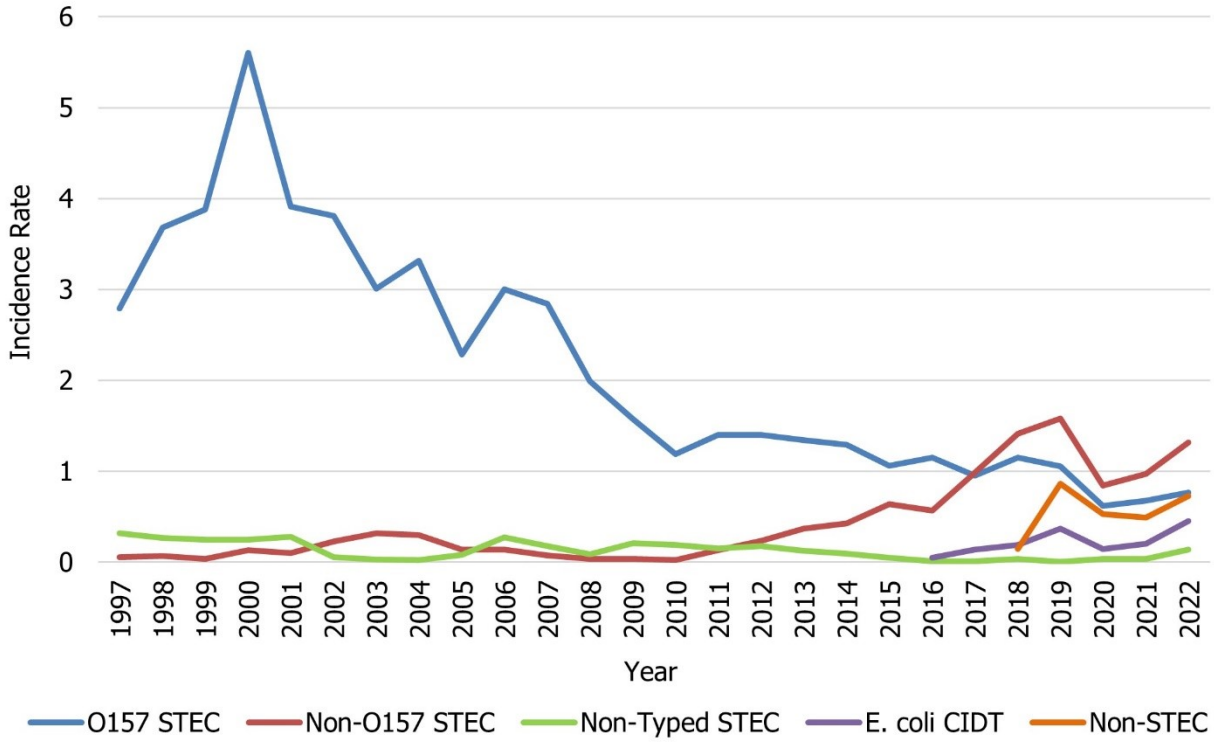
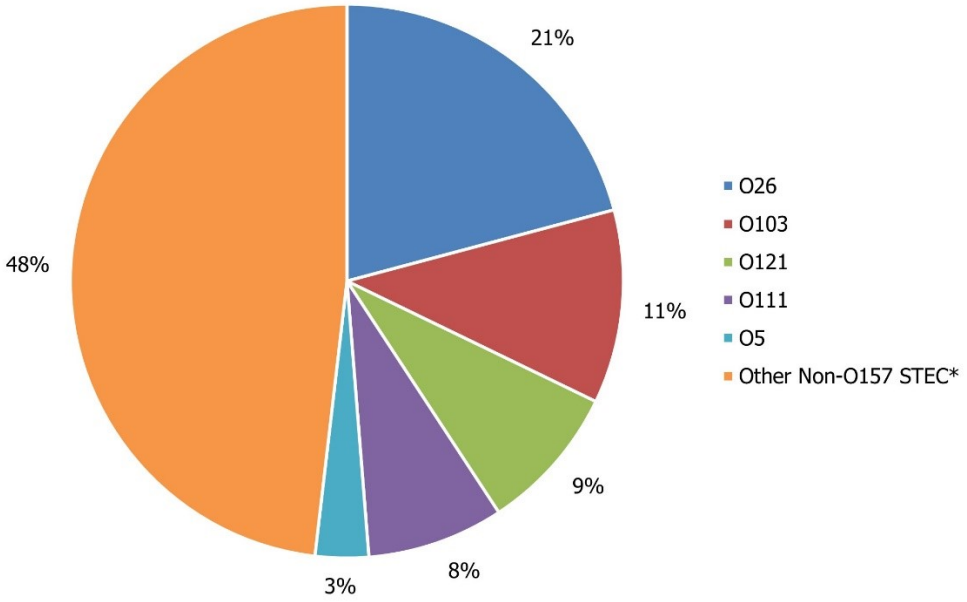
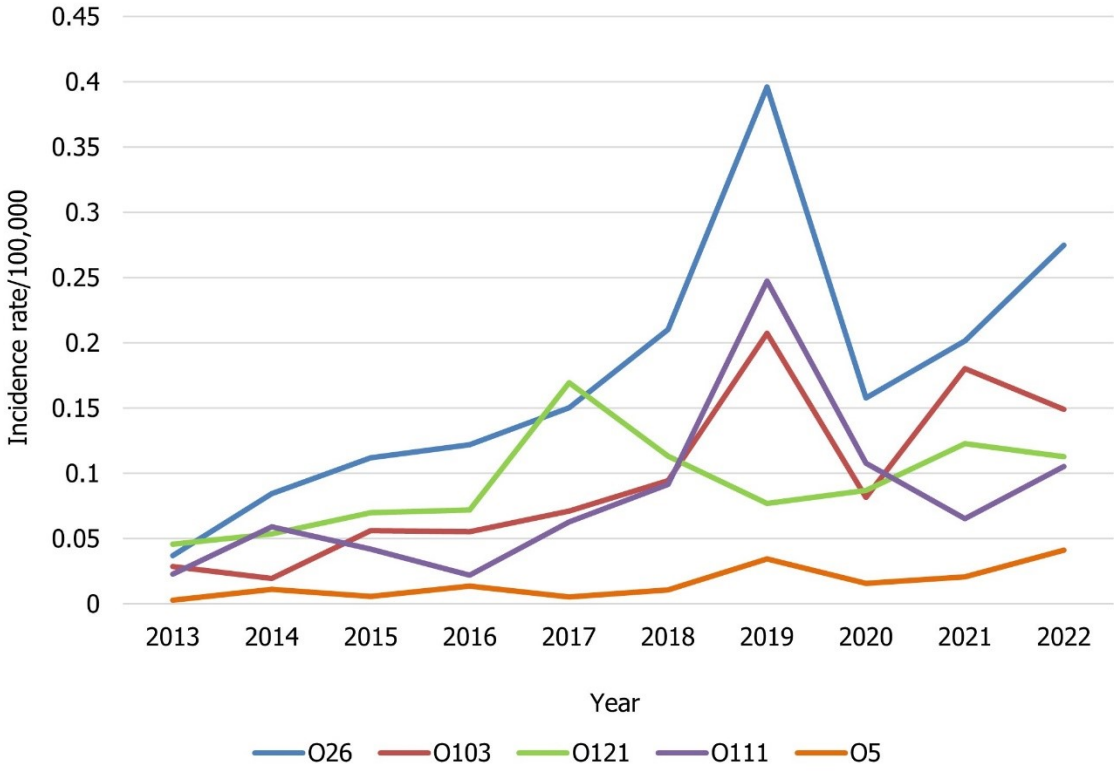


Figure 5. Distribution of non-O157 STEC serogroups reported to NESP in 2022 (n=513)



*Other serotypes (247 isolates) were divided among 55 serogroups and 102 isolates were reported as unspecified non-O157 STEC.

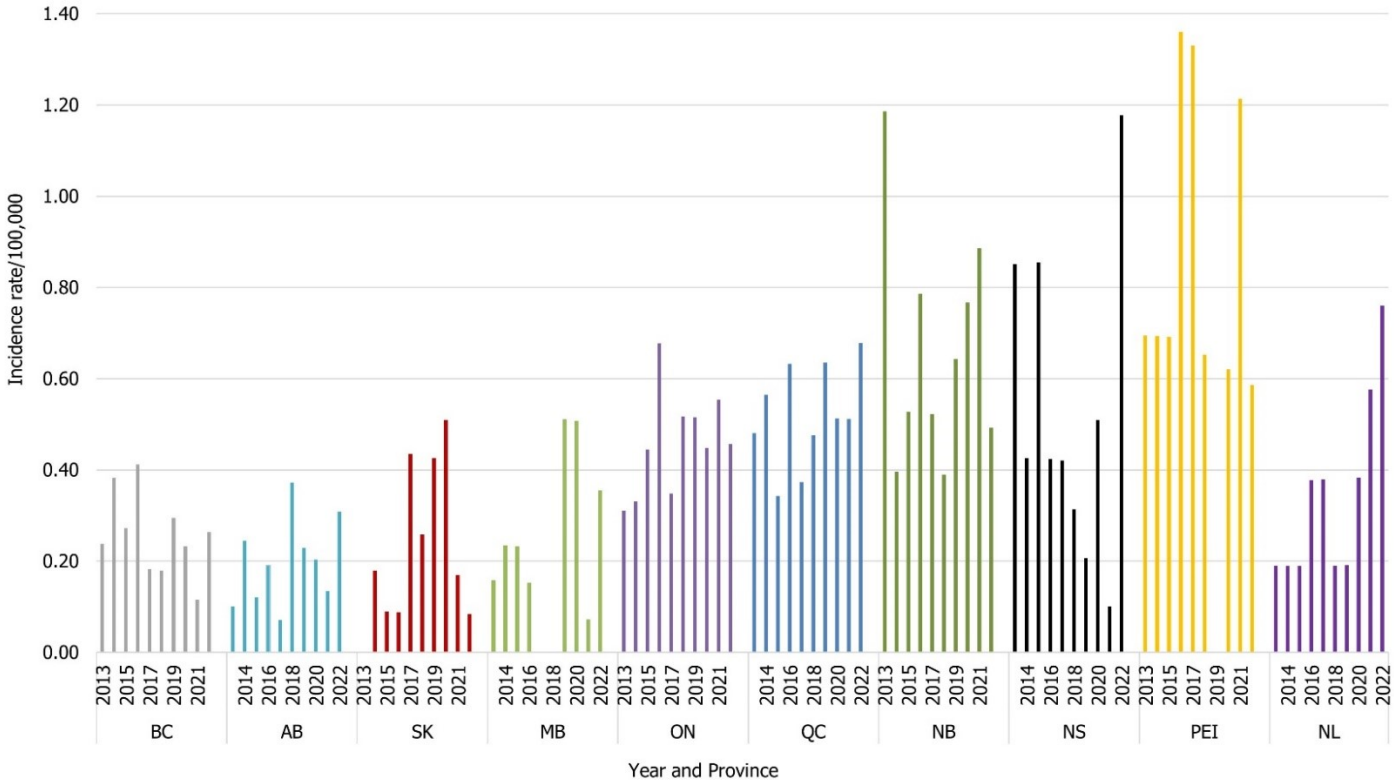
Figure 6. Incidence rate (per 100,000 population) of the top five serotyped non-O157 STEC serogroups reported to NESP, 2013 to 2022



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. The national incidence rate of *Listeria monocytogenes* increased in 2022 (0.47 cases per 100,000 population) compared to 2021 (0.40 cases per 100,000 population). However, the 2022 rate is similar to the rate seen in 2019 pre-COVID-19 pandemic (0.46 cases per 100,000 population). 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 remain wide differences in the incidence rate of invasive listeriosis across the country, with some provinces reporting an incidence rate more than ten times that of others. In 2022, five provinces reported incidence rates of *Listeria monocytogenes* higher than the national reported incidence rate: Québec (0.68 cases per 100,000 population), New Brunswick (0.49 cases per 100,000 population), Nova Scotia (1.18 cases per 100,000 population), Prince Edward Island (0.59 cases per 100,000 population), and Newfoundland and Labrador (0.76 cases per 100,000 population) (Table 3).

Figure 7. Incidence rate (per 100,000 population) of invasive listeriosis reported to NESP by province, 2013 to 2022[1]



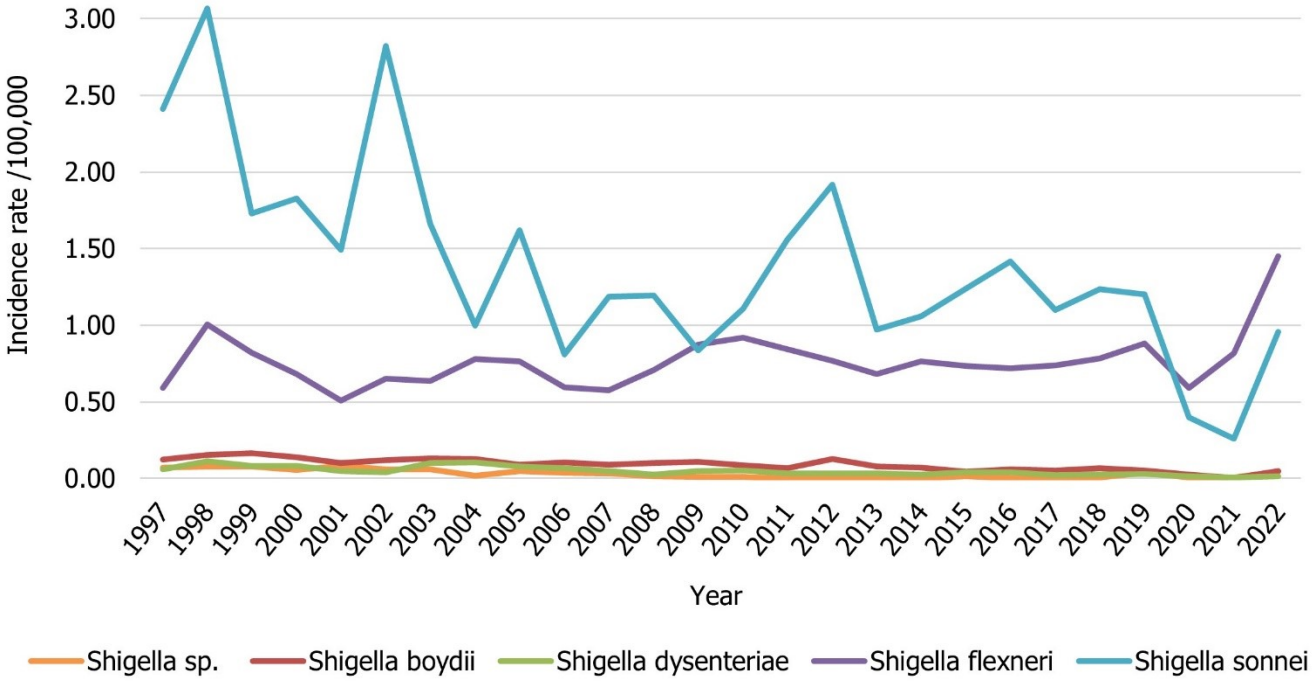
[1]There were no cases of invasive listeriosis reported in 2022 by Yukon, Northwest Territories, and Nunavut.

Shigella

There were 978 isolates of *Shigella* reported in 2022, representing a rate of 2.51 cases per 100,000 population which is over double the 2021 rate of 1.09 cases per 100,000 population. This rate is higher than the average of 2.11 cases per 100,000 population reported between 2015 and 2019 (Figure 8). In 2022, two provinces reported an incidence rate of *Shigella* higher than the national reported incidence rate: British Columbia with 5.72 cases per 100,000 population and Alberta with 6.05 cases per 100,000 population.

Isolates of *Shigella sonnei* and *Shigella flexneri* comprised 38% and 58% of total notifications respectively. Overall trends for *Shigella* have historically been driven by the incidence of *S. sonnei* (0.96 cases per 100,000 population in 2022). However, the rate of *S. flexneri* (1.45 cases per 100,000 population in 2022) surpassed that of S. *sonnei* in 2020 and has remained higher since then (Figure 8). Among the other *Shigella* species, incidence trends over time have remained relatively unchanged with an incidence of 0.05 cases per 100,000 population for *Shigella boydii* and 0.02 cases per 100,000 population for *Shigella dysenteriae* observed in 2022 (Figure 8). Rates of all species of *Shigella* increased in 2022 compared to 2020 and 2021, likely due to the impacts of COVID-19 (Figure 8).

Figure 8. Incidence rate (per 100,000 population) of *Shigella* species reported to NESP, 1997 to 2022

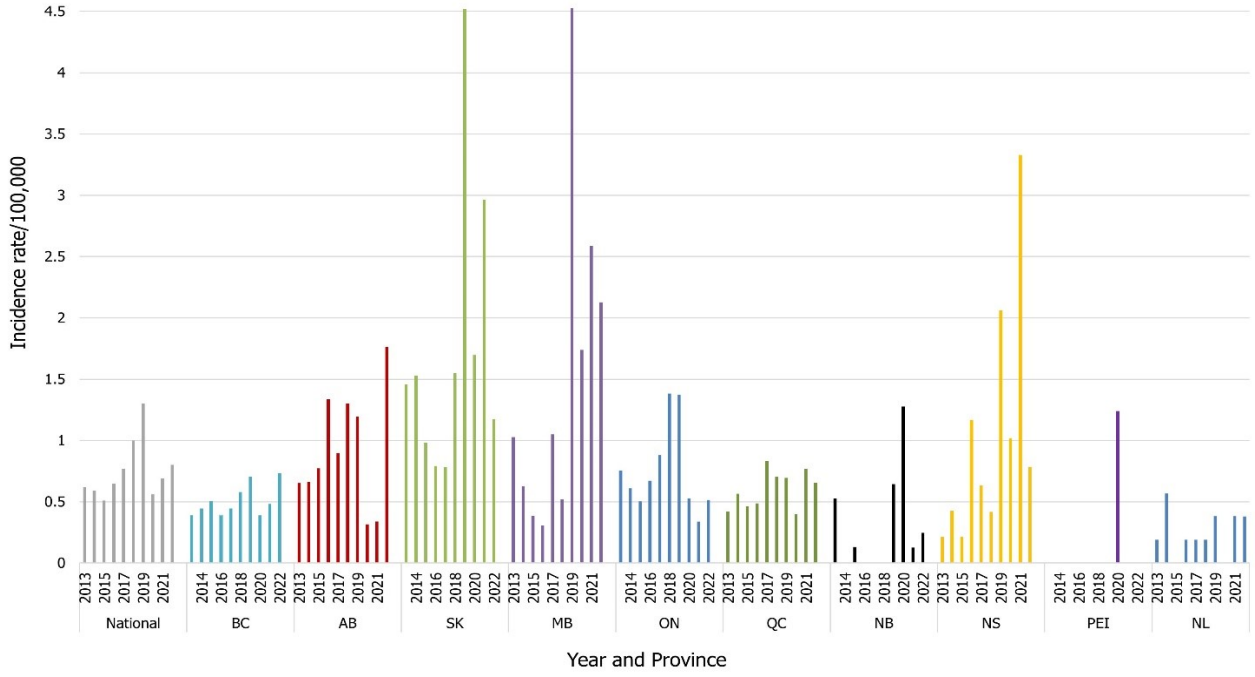


Hepatitis A

The national incidence rate for Hepatitis A in 2022 was higher than in 2021 (0.80 cases per 100,000 population in 2022 compared to 0.69 in 2021). However, this is still lower than the 2019 rate (1.30 cases per 100,000 population) (Figure 9). In 2022, three provinces reported incidence rates of Hepatitis A higher than the national reported incidence rate: Alberta (1.76 cases per 100,000 population), Manitoba (1.17 cases per 100,000 population), and Saskatchewan (2.13 cases per 100,000 population) (Figure 9).

Each provincial and territorial laboratory determines whether to report a case based solely on laboratory IgM testing, without public health follow-up. Considering that IgM testing can result in false positive results or indicate recent immunization, positive results are further investigated by local public health to determine if the case meets the definition of a "confirmed case". If the case does not meet this definition upon follow-up, the data is not always relayed back to the laboratory. Therefore, Hepatitis A data reported through NESP would not be corrected in this scenario and may result in over-reporting of confirmed cases for this virus. Hepatitis A rates appear to be increasing in some provinces since 2018, as seen in Figure 9. These increases observed in Figure 9 could be a result of change of laboratory detection methods, or over-reporting. Conversely, since not all specimens 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 to 2022



Appendix A. Canadian Notifiable Disease Surveillance System (CNDSS) and the National Enteric Surveillance Program (NESP)

Table 6. Comparison of national totals, incidence per 100,000 population and proportion captured between CNDSS and NESP for enteric diseases, 2021[1,2]

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[7])
2021	N	Rate per 100,000 population	N	Rate per 100,000 population	
Botulism	6	0.02	-	-	N/A
Campylobacteriosis[3]	7,796	20.39	1,255	-	16.1
Cholera[4]	2	0.01	1	0.003	50.0
Cryptosporidiosis[3]	963	2.52	307	-	31.9
Cyclosporiasis[3]	121	0.32	32	-	26.4
Giardiasis[3]	2,320	6.07	515	-	22.2
Hepatitis A	177	0.46	263	0.69	148.6[7]
Invasive Listeriosis	158	0.41	154	0.40	97.5
Norovirus[3,5]	199	4.4	443	-	N/A
Paralytic Shellfish Poisoning	0	0	-	-	N/A
Salmonellosis	3,318	8.68	3,303	8.64	99.5
Shigellosis	492	1.29	416	1.09	84.6
Typhoid[6]	57	0.15	57	0.15	100.0
Shiga toxigenic *Escherichia coli* Infection	772	2.02	633[8]	1.66	82.0

[1]CNDSS data for 2022 was not available at the time this summary was produced.
[2]Data for 2021 should be interpreted with caution due to the possible impacts of the COVID-19 pandemic on public health surveillance and access to healthcare services in Canada.
[3]*Campylobacter*, parasites (*Cryptosporidium*, *Cyclospora* and *Giardia*) and Norovirus are not routinely reported to provincial public health or central reference laboratories and are greatly under-represented in NESP; therefore, no rate was calculated for NESP.
[4]Includes *Vibrio cholerae* serotype O1 or O139.
[5]For Norovirus some provinces/territories report only on aggregated outbreak related data; these data are not included here.
[6]Typhoid includes lab confirmation of *Salmonella* Typhi; *Salmonella* Paratyphi A, B and C are reported under salmonellosis.
[7]Cases 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.
[8]Unless otherwise indicated, it is assumed that all the samples reported to NESP from the provinces and territories are Shiga toxigenic *Escherichia coli* (STEC). This value does not include any non-typed *E. coli*.

Appendix B. Species and serotype data reported to NESP by province and territory, 2022

Cases visiting a different province or territory are captured in the total count for the province or territory where the case was detected.

Table 7. *Campylobacter*

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Campylobacter coli	3	10	6	9	7	21	9	2	0	0	1	0	0	68
Campylobacter concisus	0	1	0	0	0	1	0	0	0	0	0	0	0	2
Campylobacter fetus	1	0	1	0	8	5	0	2	0	0	0	0	0	17
Campylobacter gracilis	0	1	0	0	0	1	0	0	0	0	0	0	0	2
Campylobacter hyointestinalis	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Campylobacter jejuni	1	147	112	126	47	130	125	73	31	0	0	0	0	792
Campylobacter lari	0	0	0	0	2	7	2	1	1	0	0	0	0	13
Campylobacter rectus	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Campylobacter sp	0	0	0	0	0	2	45	1	0	105	0	0	0	153
Campylobacter sputorum	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Campylobacter upsaliensis	0	5	0	0	5	6	6	5	0	0	0	0	0	27
Campylobacter ureolyticus	1	0	0	0	0	10	0	0	0	0	0	0	0	11
Total *Campylobacter*	6	164	119	135	69	186	187	84	32	105	1	0	0	1,088

Table 8. *E. coli**

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
E. coli	0	2	0	0	0	0	0	0	0	0	0	0	0	2
E. coli CIDT Positive for STX/STEC	27	0	0	78	0	71	2	0	0	0	0	0	0	178
Non-O157 STEC	2	0	49	36	0	0	6	0	0	0	0	0	0	93
E. coli Non-Typed EAEC	0	0	0	0	0	0	0	0	0	31	0	0	0	31
E. coli Non-Typed EPEC	0	0	0	0	0	0	0	0	0	222	0	0	0	222
E. coli Non-Typed ETEC	0	0	0	0	0	0	1	0	0	30	0	0	0	31
Non-Typed STEC	0	0	0	38	0	0	2	0	0	12	0	0	0	52
E. coli O undetermined:H Rough	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O undetermined:H2	1	1	0	0	1	0	0	0	0	0	0	0	0	3
E. coli O undetermined:H34	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O undetermined:H45	0	0	0	0	2	0	0	0	0	0	0	0	0	2
E. coli O-Rough:HNM	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O-Rough:H2	0	0	0	0	0	1	0	0	0	0	0	0	0	1
E. coli O1:H20	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O5:H9	2	9	0	0	0	1	0	0	0	0	0	0	0	12
E. coli O5:H19	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O5:HNM	0	0	0	0	3	0	0	0	0	0	0	0	0	3
E. coli O6:H1	0	0	0	0	0	1	0	0	0	0	0	0	0	1
E. coli O7:H18	0	0	0	0	1	0	0	0	0	0	0	0	0	1

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
E. coli O8:H8	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O8:H9	0	1	0	0	1	0	0	0	0	0	0	0	0	2
E. coli O8:H19	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O17:H45	3	0	0	0	0	0	0	0	0	0	0	0	0	3
E. coli O24:H30	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O25:H12	0	0	0	0	0	1	0	0	0	0	0	0	0	1
E. coli O26	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O26:H11	27	62	0	0	3	8	0	0	0	0	0	0	0	100
E. coli O26:HNM	2	2	0	0	0	2	0	0	0	0	0	0	0	6
E. coli O34:H40	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O38:H21	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O41:H19	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O44:H18	0	0	0	0	0	1	0	0	0	0	0	0	0	1
E. coli O45:H2	0	1	0	0	0	1	0	0	0	0	0	0	0	2
E. coli O45:HNM	0	0	0	0	0	1	0	0	0	0	0	0	0	1
E. coli O49:HNM	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O52:H45	0	1	0	0	6	2	0	0	0	0	0	0	0	9
E. coli O68:H18	0	0	0	0	0	1	0	0	0	0	0	0	0	1
E. coli O69:H11	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O71:H2	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O71:H8	0	0	0	0	2	0	0	0	0	0	0	0	0	2
E. coli O71:H11	1	1	0	0	3	1	0	0	0	0	0	0	0	6
E. coli O73:H18	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O75:H38	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O76:HNM	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O81:H21	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O84:H2	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O84:HNM	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O85:H2	0	0	0	0	3	0	0	0	0	0	0	0	0	3
E. coli O85:H4	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O87:H16	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O88:H25	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O91:H14	2	2	0	0	0	0	0	0	0	0	0	0	0	4
E. coli O91:H21	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O93:H46	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O98:HNM	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O100:H20	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O103:H2	3	21	0	0	10	4	0	0	0	1	0	0	0	39
E. coli O103:H11	0	4	0	0	0	2	0	0	0	0	0	0	0	6
E. coli O103:H25	0	7	0	0	1	3	0	0	0	0	0	0	0	11
E. coli O103:HNM	1	1	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O111:H8	2	22	0	0	3	2	0	0	0	0	0	0	0	29

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
E. coli O111:HNM	3	6	0	0	3	0	0	0	0	0	0	0	0	12
E. coli O113:H4	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O116:H21	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O116:H49	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O117:H7	5	1	0	0	0	0	0	0	0	0	0	0	0	6
E. coli O117:HNM	2	0	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O118:H2	0	4	0	0	2	1	0	0	0	0	0	0	0	7
E. coli O118:H16	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O119:H4	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O121:H19	7	29	0	0	3	4	0	0	0	0	0	0	0	43
E. coli O121:HNM	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O123:H11	0	0	0	0	0	1	0	0	0	0	0	0	0	1
E. coli O128:H2	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O128ab:H2	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O130:H11	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O136:H12	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O140:H45	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O145:H7	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O145:H12	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O145:H undetermined	0	2	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O145:HNM	1	5	0	0	2	2	0	0	0	0	0	0	0	10
E. coli O146:H21	1	2	0	0	0	0	0	0	0	0	0	0	0	3
E. coli O146:HNM	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O150:H8	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O156:H25	0	2	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O156:HNM	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O157	0	0	0	4	0	0	0	1	5	0	0	0	0	10
E. coli O157:H7	12	99	9	0	114	42	6	0	0	0	0	0	0	282
E. coli O157:H16	0	0	0	0	3	0	0	0	0	0	0	0	0	3
E. coli O157:HNM	1	2	0	0	1	0	0	0	0	0	0	0	0	4
E. coli O166:H15	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O168:H8	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O169:H8	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O169:H9	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O174:H21	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O177:H11	0	2	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O177:H25	0	3	0	0	1	0	0	0	0	0	0	0	0	4
E. coli O177:H45	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O177:HNM	0	2	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O178:H19	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O181:H49	1	1	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O183:H18	0	1	0	0	1	0	0	0	0	0	0	0	0	2

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
E. coli O186:H2	2	0	0	0	3	1	0	0	0	0	0	0	0	6
E. coli O187:H52	1	0	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O2/O50:H4	0	0	0	0	1	0	0	0	0	0	0	0	0	1
E. coli O123/O186:H2	0	5	0	0	0	0	0	0	0	0	0	0	0	5
E. coli O123:H2/O186:H2	0	1	0	0	0	0	0	0	0	0	0	0	0	1
E. coli O151/O118:H2	0	2	0	0	0	0	0	0	0	0	0	0	0	2
E. coli O151/O118:H16	0	2	0	0	0	0	0	0	0	0	0	0	0	2
Total *E. coli*	133	325	58	156	183	154	17	1	5	296	0	0	0	1,328

*Unless otherwise indicated, it is assumed that all *E. coli* samples reported to NESP from the provinces and territories are Shiga toxin-producing *Escherichia coli* (STEC).

Table 9. *Listeria monocytogenes*

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Listeria monocytogenes	14	14	1	5	69	59	4	12	1	4	0	0	0	183
Total *Listeria*	14	14	1	5	69	59	4	12	1	4	0	0	0	183

Table 10. Parasites

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Cryptosporidium	7	0	17	16	146	0	34	7	13	20	0	0	0	260
Cyclospora	4	3	0	0	57	0	0	1	0	7	0	0	0	72
Entamoeba histolytica/dispar	93	3	9	0	83	0	0	1	0	0	8	0	0	197
Giardia	43	1	62	51	146	0	68	59	6	52	13	0	0	501
Total Parasites	147	7	88	67	432	0	102	68	19	79	21	0	0	1,030

Table 11. *Salmonella*

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Salmonella Aberdeen	0	0	0	0	4	1	0	0	0	0	0	0	0	5
Salmonella Abony	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Adelaide	2	0	0	0	2	0	0	0	0	0	0	0	0	4
Salmonella Agbeni	0	0	0	0	4	3	0	1	0	0	0	0	0	8
Salmonella Agona	11	7	0	0	24	5	1	1	0	0	0	1	0	50
Salmonella Agoueve	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Alachua	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Salmonella Albany	1	0	0	0	3	0	0	0	0	0	0	0	0	4
Salmonella Altona	0	0	0	0	1	4	0	1	0	0	0	0	0	6
Salmonella Amager	1	3	0	0	0	0	0	0	0	0	0	0	0	4
Salmonella Amsterdam	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Anatum	4	3	0	1	6	8	0	0	0	0	0	0	0	22
Salmonella Arechavaleta	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Salmonella Bareilly	9	3	1	0	12	5	0	1	0	0	0	0	0	31

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Salmonella Benin	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Berta	0	1	0	0	7	1	0	0	0	0	0	0	0	9
Salmonella Bonariensis	0	1	0	0	3	0	0	0	0	0	0	0	0	4
Salmonella Bonn	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Bovismorbificans	2	2	0	1	3	3	0	0	0	0	0	0	0	11
Salmonella Braenderup	11	11	3	4	32	11	0	0	0	1	0	0	0	73
Salmonella Brancaster	1	0	0	0	1	0	0	0	0	0	0	0	0	2
Salmonella Brandenburg	11	3	2	2	23	8	0	2	0	1	0	0	0	52
Salmonella Bredeney	1	1	0	0	7	1	0	0	0	0	0	0	0	10
Salmonella Cerro	0	0	0	0	3	0	0	1	0	0	0	0	0	4
Salmonella Chester	0	0	0	0	7	6	0	0	0	0	0	0	0	13
Salmonella Choleraesuis	0	0	0	0	1	1	0	1	0	0	0	0	0	3
Salmonella Choleraesuis var Kunzendorf	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Colindale	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Salmonella Concord	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Corvallis	2	2	0	0	4	2	0	0	0	0	0	0	0	10
Salmonella Cotham	2	0	0	0	0	0	0	0	0	0	0	0	0	2
Salmonella Cubana	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Daytona	2	0	0	0	0	0	0	0	0	0	0	0	0	2
Salmonella Derby	2	0	0	1	2	2	0	0	0	0	0	0	0	7
Salmonella Dublin	1	2	1	0	6	18	0	0	0	0	0	0	0	28
Salmonella Durban	1	0	1	0	1	0	0	0	0	0	0	0	0	3
Salmonella Durham	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Ealing	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Eastbourne	0	0	1	0	3	0	0	0	0	0	0	0	0	4
Salmonella Emek	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Enteritidis	365	221	34	32	661	380	78	43	4	20	0	2	0	1,840
Salmonella Florida	0	1	0	0	0	1	0	0	0	0	0	0	0	2
Salmonella Gaminara	0	0	0	0	2	1	0	0	0	0	0	0	0	3
Salmonella Gateshead	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Gatuni	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Give	2	1	1	1	3	1	0	0	0	0	0	0	0	9
Salmonella Glostrup	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Goldcoast	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Hadar	16	5	1	0	25	12	2	2	0	4	0	0	0	67
Salmonella Haifa	0	0	0	0	5	0	0	0	0	0	0	0	0	5
Salmonella Hartford	0	1	0	0	4	3	0	0	0	0	0	0	0	8
Salmonella Hato	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Havana	3	1	0	0	5	0	0	0	0	0	0	0	0	9
Salmonella Heidelberg	5	5	4	0	34	32	6	2	0	0	0	0	0	88
Salmonella Hull	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Hvittingfoss	3	1	0	0	3	1	0	0	0	0	0	0	0	8

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Salmonella Idikan	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Indiana	0	4	0	0	0	0	0	0	0	0	0	0	0	4
Salmonella Infantis	11	16	6	4	56	26	5	4	1	1	0	0	0	130
Salmonella Isangi	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Itami	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Ivrysurseine	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Javiana	8	10	0	4	39	26	0	0	0	5	0	0	0	92
Salmonella Kaevlinge	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Kedougou	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Kentucky	4	1	1	1	6	5	0	0	0	0	0	0	0	18
Salmonella Kiambu	0	2	1	0	7	1	0	1	0	0	0	0	0	12
Salmonella Kisii	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Kottbus	0	0	0	0	4	2	0	1	0	0	0	0	0	7
Salmonella Linton	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Litchfield	1	0	0	1	11	4	0	0	0	0	0	0	0	17
Salmonella Liverpool	0	1	0	0	1	0	0	0	0	0	0	0	0	2
Salmonella Livingstone	0	1	0	0	6	2	0	0	0	0	0	0	0	9
Salmonella Llandoff	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Lomalinda	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Lome	1	1	0	1	4	0	0	0	0	0	0	0	0	7
Salmonella London	1	1	0	0	2	0	0	0	0	0	0	0	0	4
Salmonella Manhattan	1	0	0	0	2	5	0	0	0	0	0	0	0	8
Salmonella Mbandaka	0	1	2	1	15	5	0	0	0	0	0	0	0	24
Salmonella Meleagridis	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Menston	0	0	0	0	4	0	0	0	0	0	0	0	0	4
Salmonella Miami	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Salmonella Michigan	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Mikawasima	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Minnesota	2	1	0	1	2	1	0	0	0	0	0	0	0	7
Salmonella Mishmarhaemek	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Salmonella Mississippi	0	1	0	0	7	2	0	0	0	0	0	0	0	10
Salmonella Molade	1	0	0	0	1	0	0	0	0	0	0	0	0	2
Salmonella Montevideo	5	2	0	3	16	6	1	0	0	0	0	0	0	33
Salmonella Mountpleasant	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Muenchen	2	6	2	0	22	5	1	4	1	1	0	0	0	44
Salmonella Muenster	2	0	0	0	3	2	0	0	0	0	0	0	0	7
Salmonella Napoli	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Nessziona	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Newport	39	37	2	4	86	30	2	2	0	0	0	0	0	202
Salmonella Norwich	1	0	0	0	2	0	0	0	0	0	0	0	0	3
Salmonella Ohio	0	1	0	0	8	0	0	0	0	0	0	0	0	9
Salmonella Oranienburg	5	13	0	0	24	12	2	0	0	0	0	0	0	56

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Salmonella Orientalis	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Orion	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Oslo	2	0	0	0	5	3	0	0	0	0	0	0	0	10
Salmonella Panama	8	3	0	0	15	4	0	0	0	0	0	0	0	30
Salmonella Papuana	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Paratyphi A	26	15	2	5	60	5	0	1	0	1	0	0	0	115
Salmonella Paratyphi B	2	1	1	0	4	1	0	0	0	0	0	0	0	9
Salmonella Paratyphi B var. Java	11	4	1	0	13	7	0	0	0	0	0	0	0	36
Salmonella Pomona	2	1	0	0	2	1	1	0	0	0	0	0	0	7
Salmonella Poona	1	2	0	3	7	6	0	0	0	0	0	0	0	19
Salmonella Presov	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Putten	0	0	0	0	2	1	0	0	0	0	0	0	0	3
Salmonella Reading	11	16	10	2	2	0	0	0	0	0	0	2	0	43
Salmonella Remiremont	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Rissen	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Salmonella Rubislaw	1	0	0	0	1	0	0	0	0	0	0	0	0	2
Salmonella Saintpaul	12	7	2	1	30	19	0	1	0	0	0	1	0	73
Salmonella Sandiego	2	3	1	0	5	1	0	0	0	0	0	0	0	12
Salmonella Sandiego/Chester	0	0	0	0	0	7	0	0	0	0	0	0	0	7
Salmonella Sangera	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Saphra	0	2	0	0	0	0	0	0	0	0	0	0	0	2
Salmonella Schwarzengrund	3	2	1	1	5	1	0	1	0	0	0	0	0	14
Salmonella Senftenberg	5	8	1	0	6	0	1	0	0	0	0	0	0	21
Salmonella Shubra	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Singapore	1	0	0	0	1	0	0	0	0	0	0	0	0	2
Salmonella Soerenga	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Stanley	9	6	44	2	17	8	0	0	0	0	0	0	1	87
Salmonella Stanleyville	0	3	1	0	1	0	0	0	0	0	0	0	0	5
Salmonella Strathcona	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Takoradi	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Salmonella Telelkebir	0	0	0	0	5	2	0	0	0	0	0	0	0	7
Salmonella Tennessee	2	3	0	0	7	1	0	0	0	0	0	0	0	13
Salmonella Thompson	4	3	0	1	57	16	3	1	0	0	0	0	0	85
Salmonella Tilene	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella Tudu	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Typhi	46	33	6	10	134	13	2	1	1	2	0	0	0	248
Salmonella Typhimurium	29	66	7	10	113	81	3	7	0	2	0	1	0	319
Salmonella Uganda	2	1	0	0	12	2	0	0	0	1	0	0	0	18
Salmonella Urbana	0	0	0	0	3	2	0	0	0	0	0	0	0	5
Salmonella Veneziana	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Virchow	2	2	0	1	5	1	0	0	0	0	0	0	0	11
Salmonella Vitkin	0	0	0	0	2	0	0	0	0	0	0	0	0	2

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Salmonella Wandsworth	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella Waral	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Waycross	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Weltevreden	4	1	0	0	15	3	0	0	0	0	0	0	0	23
Salmonella Widemarsh	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella Worthington	0	1	0	0	1	0	0	0	0	0	0	0	0	2
Salmonella bongori 48:z81:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella sp	10	0	0	4	0	0	1	0	0	7	0	0	0	22
Salmonella ssp I 11:i:-	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 13,23:-:l,w	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 13,23:b:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 16:-:1,5	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 18:z4,z23:-	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Salmonella ssp I 3,10:-:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 4,[5],12,27:-:-	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 4,[5],12,[27]:HNM	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Salmonella ssp I 4,[5],12:-:-	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 4,[5],12:-:1,7	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 4,[5],12:b:-	1	4	1	0	19	8	0	0	0	0	0	0	0	33
Salmonella ssp I 4,[5],12:d:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 4,[5],12:i:-	19	20	3	6	109	96	9	1	0	0	0	1	1	265
Salmonella ssp I 4,[5],12:l,v:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 44:z10:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,7,14:-:-	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,7,[14]:r:-	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,7:-:1,5	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,7:c:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,7:e,h:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,8,[20]:HNM	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,8:-:1,5	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,8:d:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 6,8:e,h:-	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 9,12:-:-	1	0	0	0	2	1	0	0	0	0	0	0	0	4
Salmonella ssp I 9,12:-:1,5	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Salmonella ssp I 9,12:HNM	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 9,12:a:-	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I 9,12:l,v:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I 9,12:r:-	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp I Rough-O:-:1,5	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Salmonella ssp I Rough-O:H undetermined	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I Rough-O:HNM	1	0	0	0	6	0	0	0	0	0	0	0	0	7
Salmonella ssp I Rough-O:b:-	0	1	0	0	3	0	0	0	0	0	0	0	0	4

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Salmonella ssp I Rough-O:g,m:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I Rough-O:m,t:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I Rough-O:r:1,5	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp I Rough-O:z4,z23:-	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp II 17:b:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp II 42:b:e,n,x,z15	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp II 6,14:m,t:e	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp II 9,12:e,n,x:1,[5],7	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella ssp IIIa	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIa 41:z4,z23:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIa 44:z4,z23:-	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 16:z10:e,n,x,z15	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Salmonella ssp IIIb 38:z53:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 48:i:z	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Salmonella ssp IIIb 48:i:z:[z72]	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Salmonella ssp IIIb 48:k:1,5,7	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 50:k:z	0	2	0	0	1	0	0	0	0	0	0	0	0	3
Salmonella ssp IIIb 50:l,v:z35	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 53:z10:z35	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:l,v:-	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:l,v:1,5,7	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:l,v:1,5,7:[z57]	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:l,v:z	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:l,v:z35	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:r:z53	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:z52:1,5,7	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Salmonella ssp IIIb 61:z52:z53	0	1	0	0	0	2	0	0	0	0	0	0	0	3
Salmonella ssp IV 11:z4,z23:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IV 44:z4,z23:-	0	0	0	0	4	0	0	0	0	0	0	0	0	4
Salmonella ssp IV 48:g,z51:-	0	0	0	0	3	0	0	0	0	0	0	0	0	3
Salmonella ssp IV 48:z4,z32:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IV 50:g,z51:-	1	1	0	0	0	0	0	0	0	0	0	0	0	2
Salmonella ssp IV 50:z4,z23:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IV Rough-O:HNM	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IV Rough-O:g,z51:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Salmonella ssp IV Rough-O:g:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Total *Salmonella*	781	598	146	111	1,977	949	121	80	7	46	0	8	2	4,826

Table 12. *Shigella*

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Shigella	7	0	0	0	0	0	3	0	0	7	0	0	0	17

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Shigella boydii 10	0	0	0	0	2	0	0	0	0	0	0	0	0	2
Shigella boydii 12	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Shigella boydii 14	1	0	0	0	0	1	0	0	0	0	0	0	0	2
Shigella boydii 18	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Shigella boydii 20	1	0	0	0	1	0	0	0	0	0	0	0	0	2
Shigella boydii 4	1	0	0	0	2	0	0	0	0	0	0	0	0	3
Shigella boydii 5	0	1	0	0	1	0	0	0	0	0	0	0	0	2
Shigella boydii 7	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Shigella boydii 8	1	0	0	0	2	0	0	0	0	0	0	0	0	3
Shigella boydii	0	0	0	0	1	1	0	0	0	0	0	0	0	2
Shigella dysenteriae 1	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Shigella dysenteriae 12	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Shigella dysenteriae 2	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Shigella dysenteriae 3	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Shigella dysenteriae 9	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Shigella dysenteriae	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Shigella flexneri 1a	0	0	0	0	4	1	0	0	0	0	0	0	0	5
Shigella flexneri 1b	14	1	0	0	19	15	0	0	0	0	0	0	0	49
Shigella flexneri 2a	66	7	0	0	43	49	0	0	0	0	0	1	0	166
Shigella flexneri 2b	1	0	0	0	1	0	0	0	0	0	0	0	0	2
Shigella flexneri 3a	3	236	0	0	7	15	0	0	0	0	1	0	0	262
Shigella flexneri 3b	2	4	0	0	5	0	0	0	0	0	0	0	0	11
Shigella flexneri 4a	1	0	0	0	5	0	0	0	0	0	0	0	0	6
Shigella flexneri 4c	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Shigella flexneri 6	4	0	0	0	4	6	0	0	0	0	0	0	0	14
Shigella flexneri	0	0	2	3	0	8	1	1	0	0	0	0	0	15
Shigella flexneri Prov. SH-104	7	1	0	0	14	3	0	0	0	0	0	0	0	25
Shigella flexneri var. Y	0	2	0	0	2	4	0	0	0	0	0	0	0	8
Shigella sonnei	190	20	1	2	117	42	0	0	0	0	0	0	0	372
Total *Shigella*	304	275	3	5	231	146	4	1	0	7	1	1	0	978

Table 13. *Vibrio*

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Vibrio alginolyticus	1	3	0	0	1	0	0	0	0	0	0	0	0	5
Vibrio cholerae	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Vibrio cholerae O1	0	0	1	0	0	0	0	0	0	0	0	0	0	1
Vibrio cholerae O1 Ogawa	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Vibrio cholerae O1 bio El Tor sero	0	0	0	0	3	0	0	0	0	0	0	0	0	3
Vibrio cholerae O139	0	0	0	0	0	1	1	0	0	0	0	0	0	2
Vibrio cholerae non-O1/O139	2	0	2	0	4	3	1	0	0	0	0	0	0	12
Vibrio fluvialis	1	0	0	0	0	0	1	0	0	0	0	0	0	2

Vibrio parahaemolyticus	17	0	0	0	9	0	8	0	3	0	0	0	0	37
Vibrio sp	3	0	0	0	0	0	0	0	0	0	0	0	0	3
Vibrio vulnificus	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Total *Vibrio*	27	3	3	0	17	4	11	0	3	0	0	0	0	68

Table 14. Viruses

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Adenovirus	33	198	0	51	123	0	0	4	0	111	0	0	1	521
Astrovirus	23	41	0	19	0	0	0	0	0	61	0	0	0	144
Enterovirus	0	0	0	7	0	0	0	0	0	0	0	0	0	7
Hepatitis A	39	80	14	30	78	57	2	8	0	2	0	0	0	310
Norovirus	141	324	138	88	339	0	136	53	26	182	0	1	1	1,429
Rotavirus	6	67	71	23	29	0	12	2	4	7	0	0	0	221
Sapovirus	16	101	0	18	0	0	1	0	0	20	0	0	1	157
Total Virus	258	811	223	236	569	57	151	67	30	383	0	1	3	2,789

Table 15. *Yersinia*

	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
Yersinia enterocolitica	36	32	4	4	95	28	1	0	0	1	0	0	0	201
Yersinia frederiksenii	15	0	0	0	0	0	0	0	0	0	0	0	0	15
Yersinia intermedia	6	1	0	0	0	0	0	0	0	0	0	0	0	7
Yersinia kristensenii	4	0	0	0	0	0	0	0	0	0	0	0	0	4
Yersinia massiliensis	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Yersinia mollaretii	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Yersinia pseudotuberculosis	2	0	0	0	0	0	0	0	0	0	0	0	0	2
Yersinia sp	0	0	0	0	0	2	0	0	0	0	0	0	0	2
Total *Yersinia*	65	33	4	4	95	30	1	0	0	1	0	0	0	233

Appendix C. NESP support for outbreak investigations

NESP data supported 5 out of 7 National Outbreak Investigation Coordinating Committees (OICCs) in 2022. More information about the OICCs that NESP supported can be seen below in Table 16.

Table 16. Multi-jurisdictional outbreak investigations in 2022

Multi-jurisdictional Outbreak Investigations	Outbreak Source	Number of cases-final (Canada only)	Date of first case onset	Date of last case onset	Provinces and Territories with Cases
[2022-091] [OICC: Norovirus and GI reports associated with Spot Prawns in AB, BC, MB and ON] [May, 2022 - June, 2022]	Spot Prawns	60	2022-05-12	2022-05-23	BC 18 AB 12 MB 19 ON 11
[2022-065] [OICC: Hepatitis A in AB and SK] [May, 2022 - July, 2022]	Fresh Organic Strawberries	10	2022-04-04	2022-04-17	AB 4 SK 6
[2022-029] [OICC: GI reports associated with raw oysters in BC] [March, 2022 - May, 2022]	Oysters	339	2022-01-21	2022-04-05	BC 301 AB 3 SK 1 ON 19 MB 15
[2022-017] [OICC: E. coli O157:H7 in AB, SK, and the US] [January, 2022 - March, 2022]	Kimchi	14	2021-12-11	2022-01-07	AB 13 SK 1
[2021-180] [OICC: WGS Cluster of S. Enteritidis in BC, AB, SK, MB & ON] [October, 2021 - March, 2022]	Frozen corn	118	2021-09-06	2022-01-27 (isolation date)	BC 44 AB 55 SK 4 MB 13 ON 2

Appendix D. Impacts of COVID-19: Comparison of NESP weekly isolate counts from 2022, 2021 and 2020 compared to the 2015 to 2019 historical average for select pathogens

In March of 2020, the COVID-19 pandemic was declared[k] and global public health action was taken to address it. Across Canada and within specific provinces/territories and regions, various public health measures were put in place. These included international[l] and domestic travel restrictions, closing of non-essential businesses and activities (including restaurants, gyms, salons, places of worship, etc.), closing of in-person schools and initiating virtual learning, and mandating of face coverings in public and indoor spaces. Additionally, increased public health messaging related to hand washing and cough and sneeze etiquette, reminders about staying home if you were feeling unwell and to get tested for COVID-19 were implemented. These public health measures and the adaptations Canadians made to combat COVID-19 not only helped to reduce the transmission of COVID-19 but have also impacted other reported infectious diseases to varying degrees in various ways. These measures were first implemented in 2020, and many remained in place or were re-instated in 2021 and 2022. Similar to the 2020 and 2021 NESP Annual Summaries, interpretation of the data and findings in the 2022 NESP Annual Summary must be interpreted with caution, as the public health measures invoked to help limit the spread of COVID-19 likely impacted disease incidence as well as data collection and reporting to NESP. Figures 10-17 compare 2022, 2021 and 2020 NESP data with the pre-pandemic period five-year (2015-2019) average for select pathogens.

The impact that the public health measures for COVID-19 had on the pathogens reported through NESP in 2022 was variable. For all *Salmonella* serotypes (Figure 10), the 2022 NESP counts remain lower than the 2015-2019 historical average throughout the year. However, generally counts appear higher in 2022 than in 2020 and 2021, excluding the early months in 2020. This is likely due to the absence of COVID-19 public health measures prior to March 2020.

Focusing on certain *Salmonella* serotypes and groupings, the magnitude of the difference between the 2022 NESP data and the pre-pandemic historical average is greater for *Salmonella* Enteritidis (Figure 12) compared to all other *Salmonella* serotypes excluding *S.* Enteritidis (Figure 11). In 2022, *Salmonella* Enteritidis case counts increased in comparison to 2020 and 2021, but still remain lower than the 2015 to 2019 historical average. The decrease in *S.* Enteritidis data is likely related to both the impacts of COVID-19 public health measures as well as the continued positive impact related to the Canadian Food Inspection Agency's regulation implemented in April 2019 to address *Salmonella* in raw frozen breaded chicken products[m].

[k] https://www.who.int/director-general/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19---11-march-2020 (accessed September 13, 2021)
[l] https://pm.gc.ca/en/news/news-releases/2020/03/16/prime-minister-announces-new-actions-under-canadas-covid-19-response (accessed October 20, 2021).
[m] Salmonella control options in frozen raw breaded chicken products. Canadian Food Inspection Agency: https://inspection.canada.ca/preventive-controls/meat/salmonella-in-frozen-raw-breaded-chicken/eng/1531254524193/1531254524999

Regarding O157 STEC (Figure 13) and non-O157 STEC (Figure 14), 2022 case counts appear generally comparable to the pre-pandemic historical average. Cases of non-O157 STEC in 2022 surpass the pre-pandemic historical average overall, whereas cases of O157 STEC remain similar to the historical average over the same time period. The divergence of trends in O157 STEC and non-O157 STEC over this time period may be related to the overall increased frequency of non-O157 STEC reported to NESP over the last several years (i.e. since 2018; data not shown).

Trends in data for *Listeria monocytogenes* reported to NESP in 2022 (Figure 15) are comparable to trends observed in 2020, 2021, and to the pre-pandemic historical average for 2015-2019. This suggests that the impact of the public health measures put in place to combat COVID-19 may have had less of an effect on *L. monocytogenes.* Possible explanations for this are that *L. monocytogenes* is generally less associated with travel-acquired infection (i.e. less travel in the pandemic period) and considering the severe illness this organism often causes – reporting of cases may have been less affected than other organisms that often cause less-severe illness[n].

For *Shigella*, the number of cases reported in 2022 generally rebounded back to levels similar to and sometimes higher than the pre-pandemic historical average (Figure 16). These trends are higher than the reduced counts of *Shigella* reported in 2020 and 2021. Shigellosis is frequently travel-related and this microorganism is often transmitted through person-to-person contact, and thus the impact of COVID-19 public health measures in place likely played a role in the lower levels of *Shigella* observed in 2020 and 2021.

In general, compared to pre-pandemic counts, larger decreases were seen in 2020 and 2021 for pathogens that typically are more often associated with travel, are typically milder symptom-wise or less invasive, or are more frequently transmitted via person-to-person contact. The main exception to this finding relates to *Listeria monocytogenes* which is typically more severe and is much less likely to be associated with travel or acquired through person-to-person contact; thus, the frequency of cases of *Listeria* reported to NESP during 2020, 2021 and 2022 did not appear to differ compared to the pre-pandemic period.

The public health measures that were implemented in response to the COVID-19 pandemic were multifaceted; thus, it is challenging to attribute specific measures to specific enteric disease impacts (perhaps with the exception of the impacts of travel restrictions)[n]. Considering that some public health measures also caused a major shift in food consumption patterns (i.e., decreasing food purchased and consumed outside the home) further complicates our ability to easily discern these individual impacts. Finally, possible deviations in medical

[n]Dougherty et al., 2023. Impact of the COVID-19 Pandemic on the Reported Incidence of Select Bacterial Enteric Diseases in Canada, 2020. DOI:10.1089/fpd.2022.0064.

care-seeking behaviour among Canadians as a result of stay-at-home orders and local healthcare system changes may have also influenced specimen submission and thus, reporting of isolates to NESP during the pandemic period.

Figure 10. All *Salmonella* reported to NESP in 2022, 2021 and 2020 compared to the 2015 to 2019 historical average

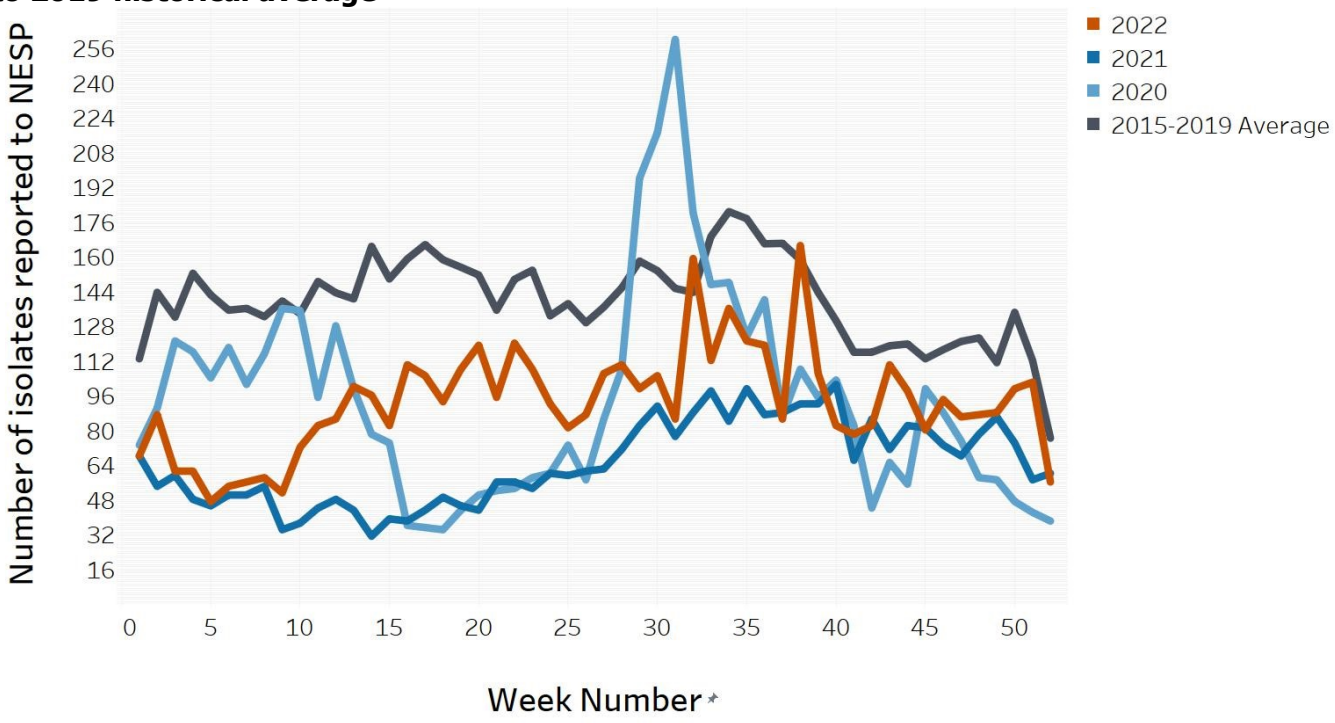


Figure 11. All *Salmonella* reported to NESP excluding *Salmonella* Enteritidis in 2022, 2021 and 2020 compared to the 2015 to 2019 historical average

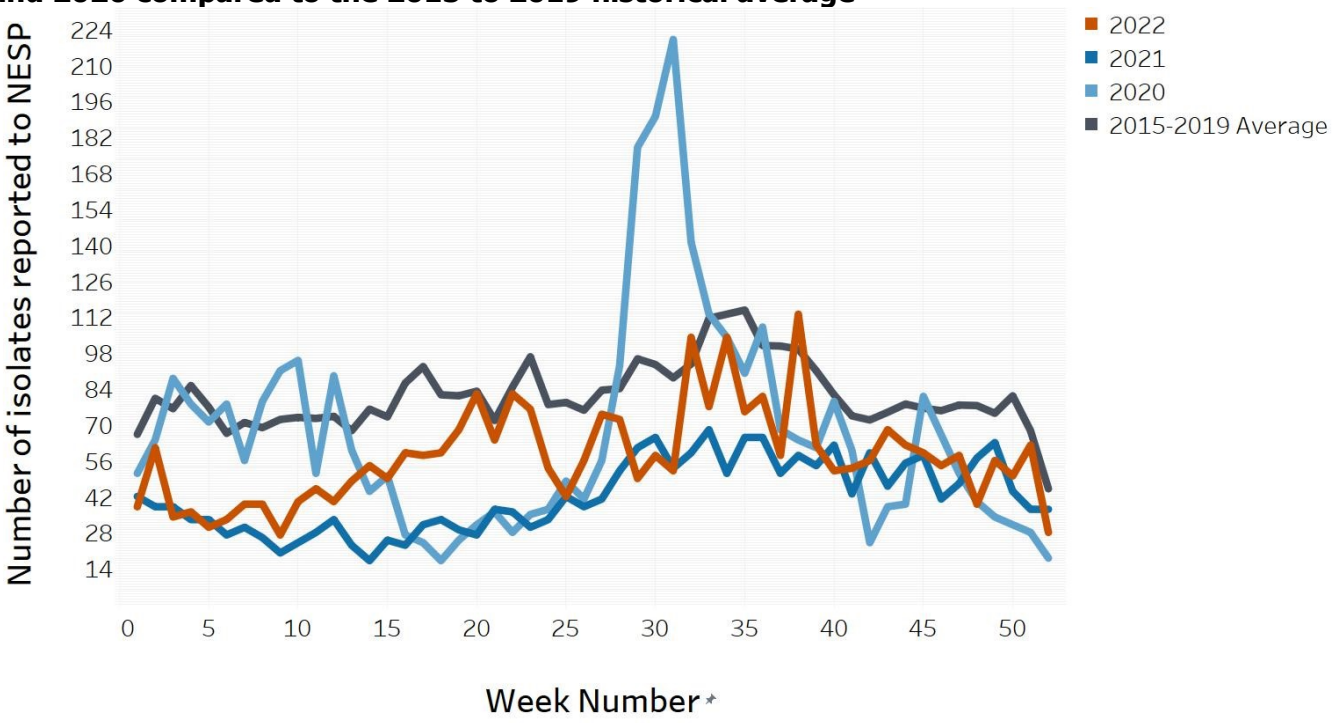


Figure 12. *Salmonella* Enteritidis reported to NESP in 2022, 2021 and 2020 compared to the 2015 to 2019 historical average

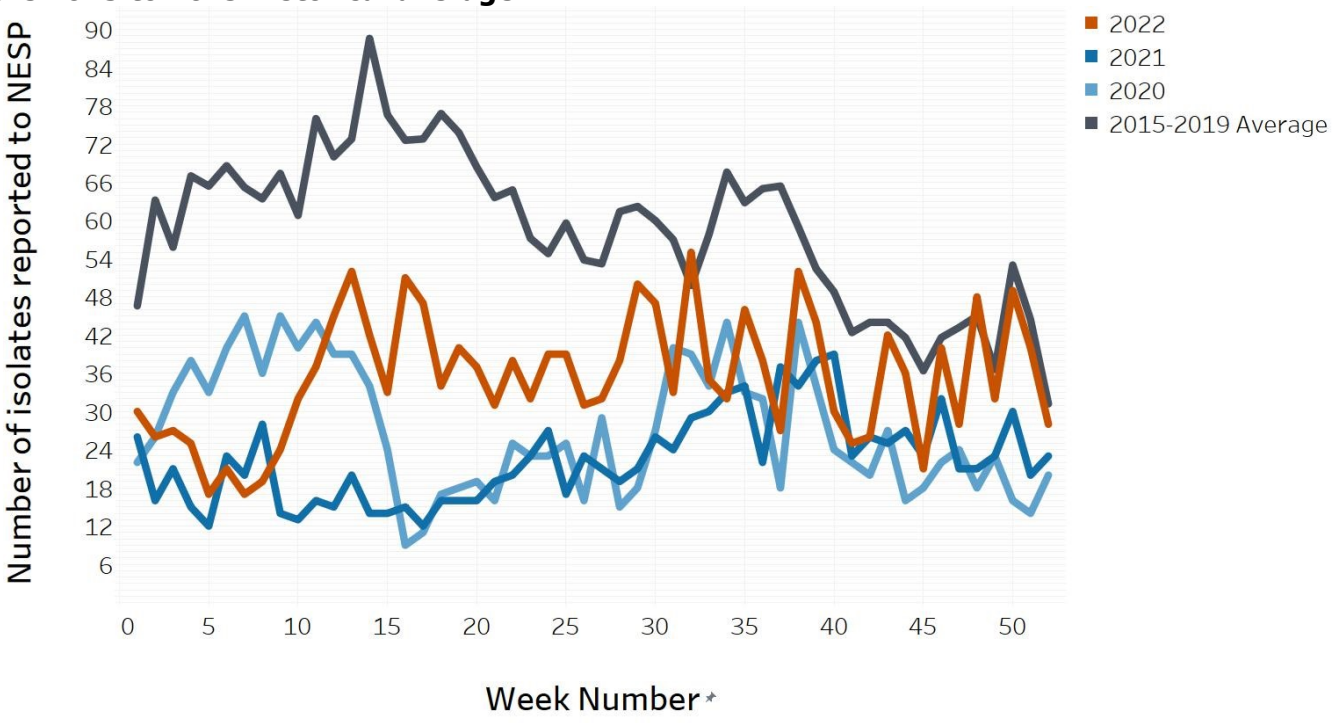


Figure 13. O157 STEC reported to NESP in 2022, 2021 and 2020 compared to the 2015 to 2019 historical average

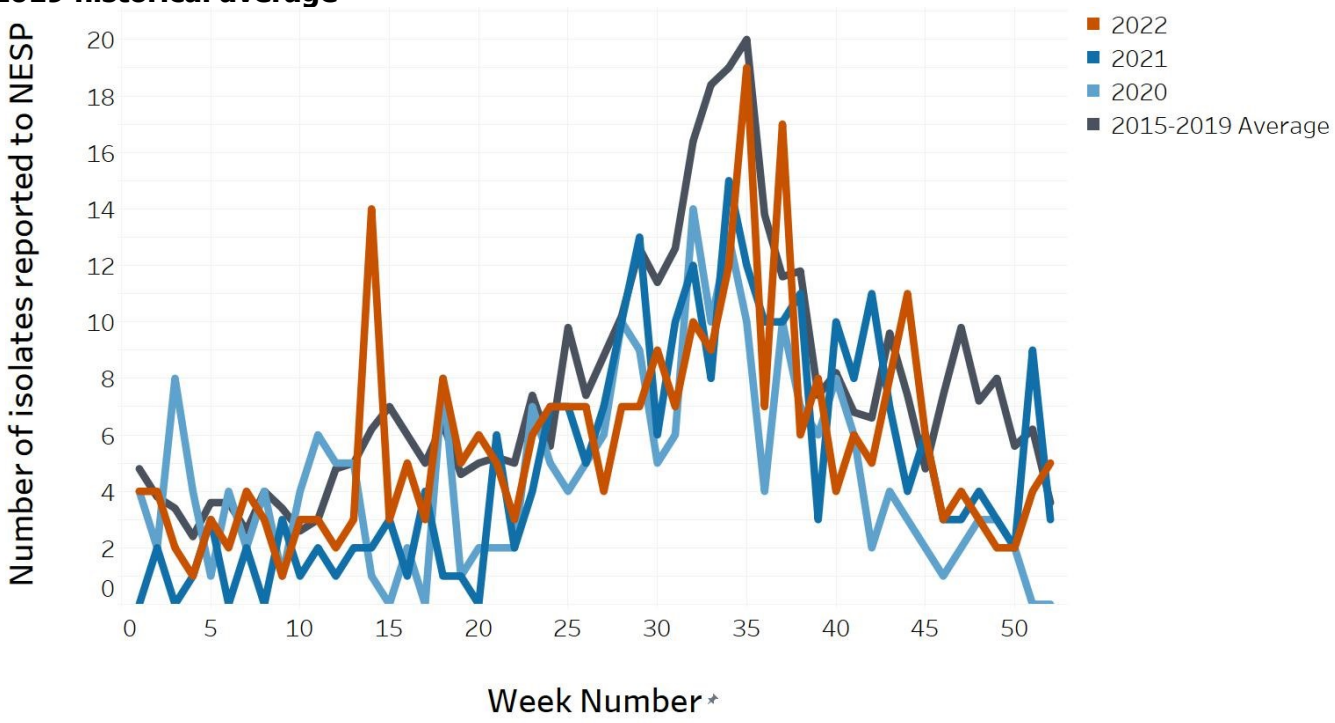


Figure 14. Non-O157 STEC reported to NESP in 2022, 2021 and 2020 compared to the 2015 to 2019 historical average

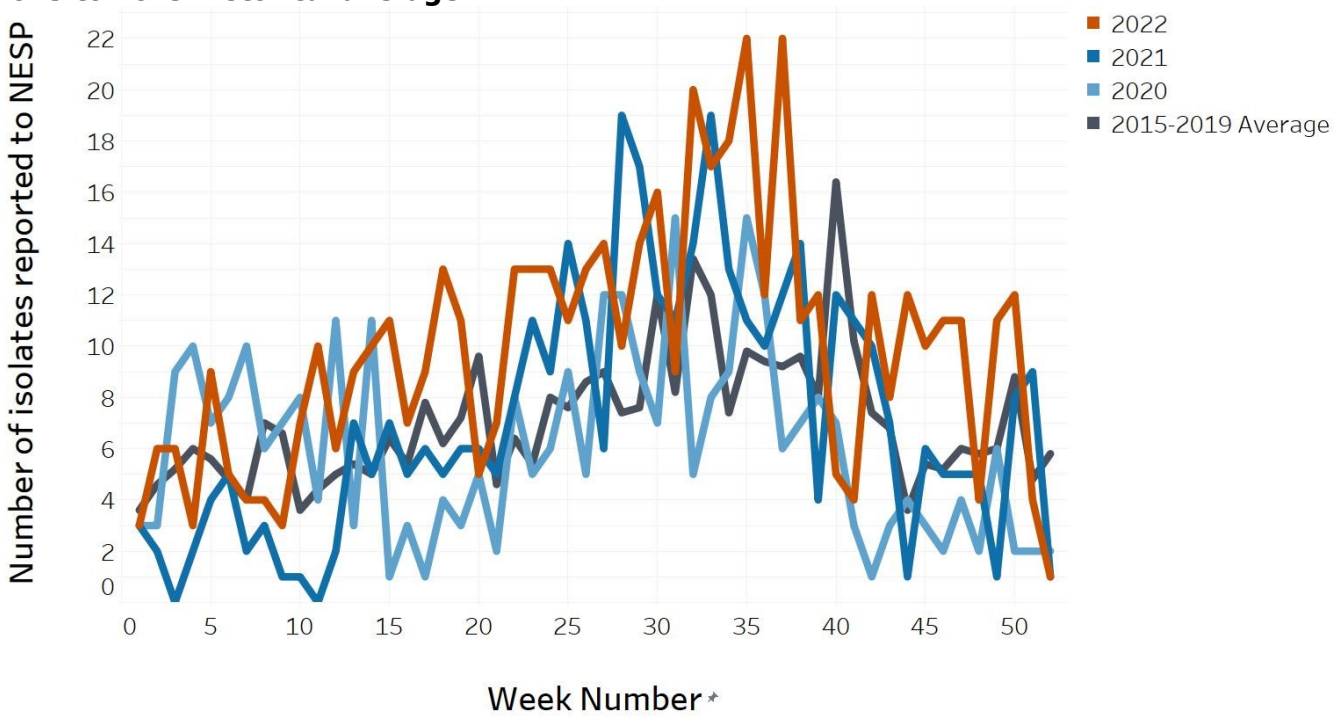


Figure 15. *Listeria monocytogenes* reported to NESP in 2022, 2021 and 2020 compared to the 2015 to 2019 historical average

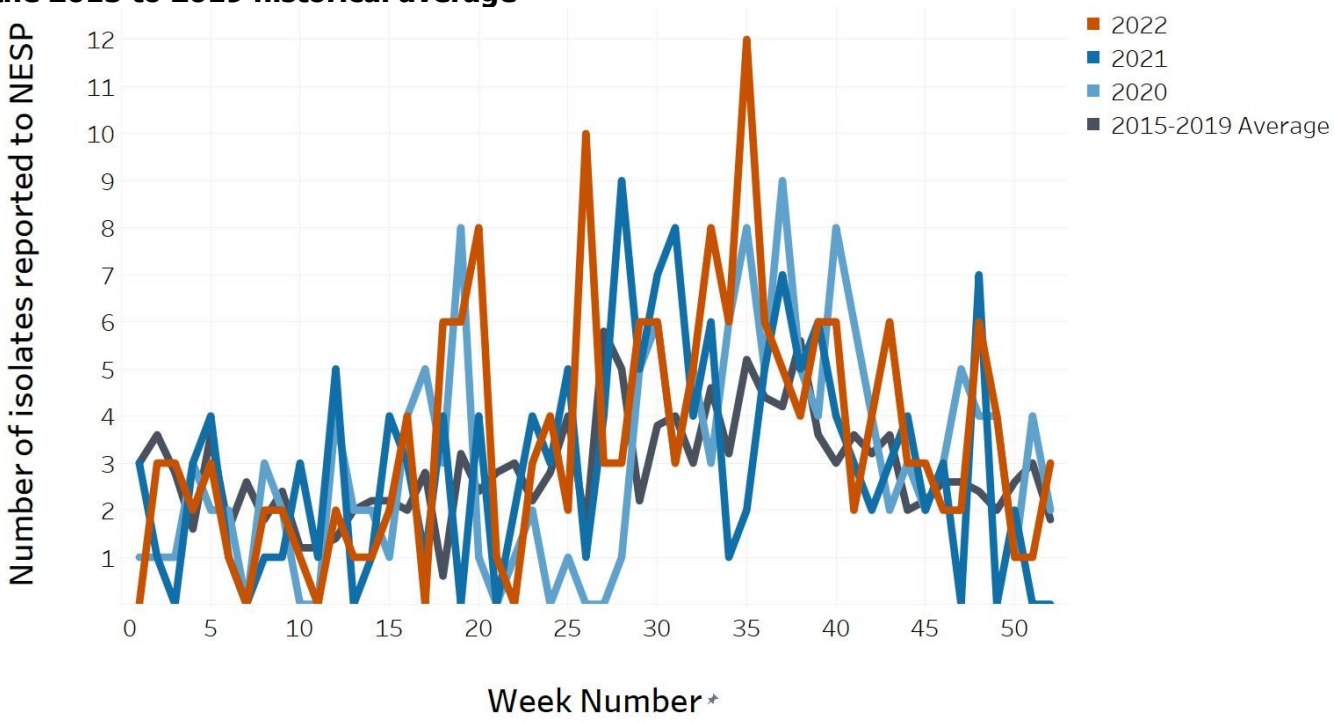


Figure 16. *Shigella* reported to NESP in 2022, 2021 and 2020 compared to the 2015 to 2019 historical average