

# National Enteric Surveillance Program (NESP)

ANNUAL SUMMARY 2021

PROTECTING CANADIANS FROM ILLNESS



Public Health  
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Programme national de surveillance des maladies entériques (PNSME) – rapport sommaire 2021

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Publication date: July 2023

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Cat.: HP37-15E-PDF  
ISBN: 2292-8561  
Pub.: 230114

# NATIONAL ENTERIC SURVEILLANCE PROGRAM (NESP)

## ANNUAL SUMMARY 2021

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

&

Provincial Public Health Laboratories

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## 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 2021, a total of 8,276 isolate results were reported to NESP; a 41% decrease from the average number of notifications received in the previous five years (14,085). This decrease is in part due to the impacts of the COVID-19 pandemic. *Salmonella* spp. continues to be the most common organism identified with 3,360 notifications provided in 2021, representing 40.60% of all isolates reported to NESP. As in previous years, *Salmonella* Enteritidis (1,172 isolates; 35%) and *S. Typhimurium* (370 isolates; 11%), represent the top two serotypes among all *Salmonella* reported in 2021. In 2021, *S. ssp* I 4,[5],12:i:- (231 isolates; 7%) was the third most commonly reported serotype. Collectively, these three serotypes represent 53% of all *Salmonella* serotypes identified.

The 2021 incidence rate of Shiga toxinogenic *Escherichia coli* (STEC) O157 is similar to the 2020 rate of O157 with 0.68 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 2021 (0.98 cases per 100,000 population) compared to 2020 (0.84 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 fifth consecutive year where more non-O157 STEC isolates were reported than *E. coli* O157 isolates.

The incidence rate of invasive listeriosis in 2021 (0.40 per 100,000 population) is similar to what has been seen in the past three years. The incidence rate of Hepatitis A increased in 2021 (0.91 cases per 100,000 population) compared to 2020 (0.67 cases per 100,000 population). Over the 9-year period that Hepatitis A has been reported to NESP, the highest incidence was reported in 2019 (1.55 cases per 100,000 population). In contrast to 2019 and years before where *Shigella sonnei* represented the majority of *Shigella* species reported, 2021 followed a similar trend to 2020 where *Shigella flexneri* represented 75% of all *Shigella* reported. In 2021, the rate of *Shigella flexneri* (0.82 per 100,000 population) was also higher than the rate of *Shigella sonnei* (0.26 per 100,000 population). Trends for all other *Shigella* species in 2021 were similar to 2020, remaining lower compared to previous years.

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## Information to the reader about 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)<sup>a</sup>. 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<sup>b</sup>. 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), 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.

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

<sup>b</sup> PulseNet Canada, National Microbiology Laboratory, Public Health Agency of Canada: <https://www.canada.ca/en/public-health/programs/pulsenet-canada.html>



## 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 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* 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 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, 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 primarily generated using whole genome sequencing (WGS) 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. 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)<sup>c</sup>.

For this annual summary, initial 2021 data validation activities were performed in collaboration with the provinces and territories. Once the final dataset was validated and closed, summary statistics were conducted for the 14 different organisms causing enteric illness that are reported to NESP using SAS software<sup>d</sup>.

## 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 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 *E. coli* O157 isolates captured by NESP are more representative of the true incidence of disease in Canada, as the number of

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<sup>c</sup> 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>

<sup>d</sup> SAS software, Version 9.4 of the SAS System for Windows. Copyright © 2016 SAS Institute Inc.

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<sup>e</sup> 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 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 NESP Annual Summary, interpretation of the data and findings in the 2021 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 (Appendix 4).

**Questions and correspondence may be forwarded via email to:**

**[nesp-pnsme@phac-aspc.gc.ca](mailto:nesp-pnsme@phac-aspc.gc.ca)**

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<sup>e</sup> <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)

## Laboratory-confirmed Isolate Counts & Incidence Rates

In 2021, provincial public health laboratories reported the results of 8,276 isolates of enteric pathogens to NESP, a decrease from the average number of notifications in the previous five years (14,085). The most frequently reported enteric pathogen group was *Salmonella*, followed by *Campylobacter*, and enteric viruses (Norovirus, Hepatitis A, Rotavirus, Adenovirus, Astrovirus, Sapovirus and Enterovirus) (Table 1). Organism isolate counts reported by province and territory in 2021 can be found in Appendix 2.

**Table 1. Number of isolates reported to NESP by major organism group per province or territory, 2021**

GROUP <sup>4</sup>	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL	% OF TOTAL ISOLATES REPORTED
<i>Salmonella</i>	544	436	97	81	1,246	675	95	107	12	65	2	0	0	3,360	40.60
<i>Campylobacter</i> <sup>1</sup>	21	261	147	45	101	241	190	123	52	67	7	0	0	1,255	15.16
Viruses <sup>1</sup>	68	320	112	74	146	66	23	43	17	66	1	0	2	938	11.33
<i>E. coli</i> <sup>2</sup>	97	232	45	29	154	134	7	3	2	208	1	0	0	912	11.02
Parasites <sup>1</sup>	155	5	63	53	365	NR <sup>3</sup>	87	62	11	77	14	0	0	892	10.78
<i>Shigella</i>	207	20	2	5	97	79	2	3	1	0	0	0	0	416	5.03
<i>Yersinia</i>	129	34	5	4	103	17	2	0	1	1	2	0	0	298	3.60
<i>Listeria</i>	6	6	2	1	82	44	7	1	2	3	0	0	0	154	1.86
<i>Vibrio</i>	13	5	0	2	10	0	16	2	3	0	0	0	0	51	0.62
<b>Total</b>	<b>1,240</b>	<b>1,319</b>	<b>473</b>	<b>294</b>	<b>2,304</b>	<b>1,256</b>	<b>429</b>	<b>344</b>	<b>101</b>	<b>487</b>	<b>27</b>	<b>0</b>	<b>2</b>	<b>8,276</b>	<b>100.00</b>

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

<sup>2</sup>*E. coli* includes O157 serotypes (260 cases), non-O157 STEC serotypes (373 cases), CIDT positive for STX/STEC (77 isolates), non-typed STEC (14 cases), and non-STEC (188 cases).

<sup>3</sup>NR stands for Not Reported. In 2021 due to resources being directed to COVID-19, no parasites were reported from Quebec.

<sup>4</sup>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 2016 and 2021 are shown in Table 2 and Appendix 1. Isolates of *E. coli* O157 or non-O157 STEC, *Listeria monocytogenes*, *Salmonella* and *Shigella* are routinely forwarded to provincial public health laboratories, while isolates of *Campylobacter*, *Yersinia*, enteric parasites (*Giardia*, *Cryptosporidium*, *Entamoeba histolytica/dispar* and *Cyclospora*) and enteric viruses (Norovirus, Rotavirus, Adenovirus, Astrovirus, Sapovirus and Enterovirus) are not routinely reported 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 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, 2016-2021**

GROUP	2016		2017		2018		2019		2020		2021	
	Total	Rate <sup>1</sup>	Total	Rate <sup>1</sup>	Total	Rate <sup>1</sup>	Total	Rate <sup>1</sup>	Total	Rate <sup>1</sup>	Total	Rate <sup>1</sup>
<i>E. coli</i> O157	415	1.15	348	0.95	426	1.15	397	1.06	237	0.62	260	0.68
Non-O157 STEC <sup>2</sup>	205	0.57	361	0.99	525	1.42	595	1.58	320	0.84	373	0.98
<i>Listeria</i>	191	0.53	109	0.30	150	0.40	174	0.46	158	0.42	154	0.40
<i>Salmonella</i>	7,816	21.65	7,313	20.01	7,300	19.70	6,350	16.89	4,919	12.94	3,360	8.79
<i>Shigella</i>	807	2.23	699	1.91	784	2.12	828	2.20	393	1.03	416	1.09
<i>Campylobacter</i>	1,378	3.82	1,287	3.52	1,333	3.60	1,664	4.43	1,289	3.39	1,255	3.28
<i>Vibrio</i>	44	0.12	54	0.15	67	0.18	52	0.14	44	0.12	51	0.13
<i>Yersinia</i>	353	0.98	387	1.06	404	1.09	318	0.85	283	0.74	298	0.78
Parasites	1,921	5.32	1,679	4.59	1,675	4.52	1,639	4.36	1,017	2.68	892	2.33
Viruses	2,292	6.35	2,593	7.10	2,273	6.13	2,564	6.82	1,035	2.72	938	2.45

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

<sup>2</sup>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<sup>1</sup> (per 100,000 population) of infection per province and territory for select groups of pathogens routinely reported to NESP, 2021**

GROUP <sup>2</sup>	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU
<i>E. coli</i> O157	0.48	1.51	0.42	0.93	0.62	0.58	0.38	0.30	1.21	0.00	0.00	0.00	0.00
Non-O157 STEC	1.13	3.65	3.39	1.15	0.42	0.26	0.51	0.00	0.00	1.54	0.00	0.00	0.00
<i>Listeria</i>	0.12	0.14	0.17	0.07	0.55	0.51	0.89	0.10	1.21	0.58	0.00	0.00	0.00
<i>Salmonella</i>	10.46	9.81	8.21	5.82	8.41	7.85	12.02	10.80	7.28	12.49	4.62	0.00	0.00
<i>Shigella</i>	3.98	0.45	0.17	0.36	0.65	0.92	0.25	0.30	0.61	0.00	0.00	0.00	0.00

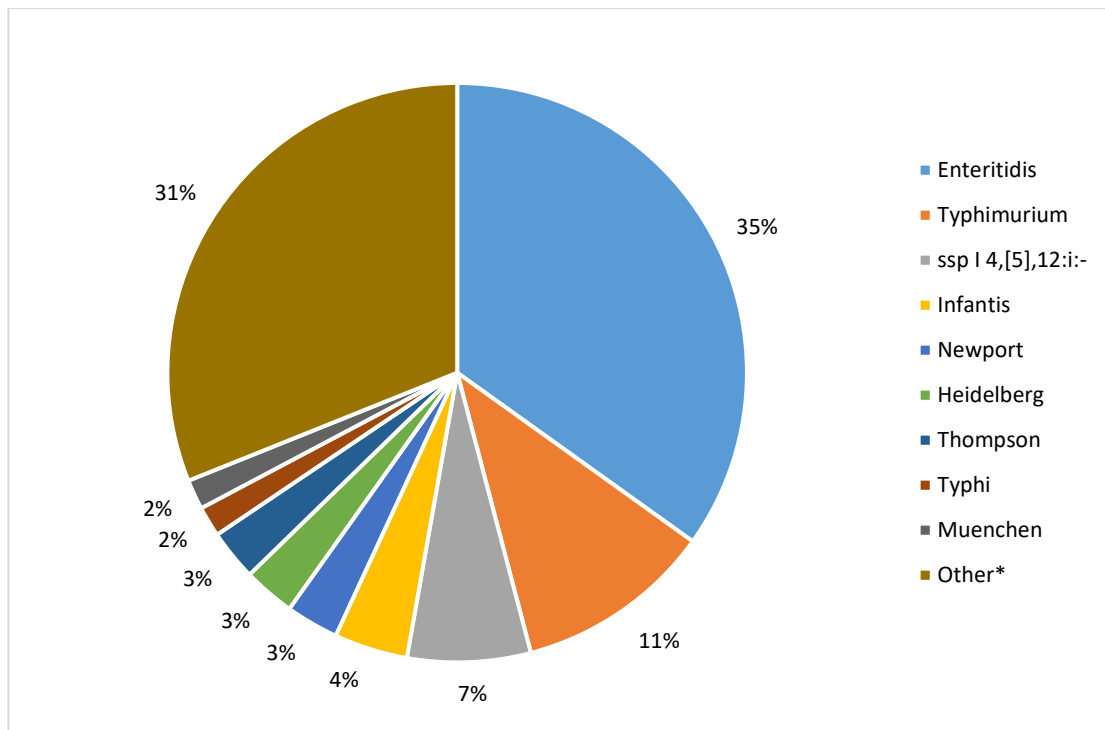
<sup>1</sup>Rates calculated using the population estimates on July 1st as reported by Statistics Canada – Table 17-10-0005-01

<sup>2</sup>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 3,360 *Salmonella* isolates representing 177 serotypes were reported to NESP in 2021. *Salmonella* Enteritidis accounted for 35% of all human salmonellosis, and together with the eight remaining most common serotypes (Figure 1), they constituted 69% of all *Salmonella* infections reported. National, provincial and territorial case counts for *Salmonella* reported in 2021 are shown in Table 4 and Appendix 2.

**Figure 1. Proportion of *Salmonella* serotypes causing human illness as reported to NESP, 2021 (n=3,360)**



\*Other serotypes (1,045 isolates) were divided among 168 serotypes or incomplete antigenic profiles, and 18 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, 2021**

Serotype	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL	% of <i>Salmonella</i> total (n=3,360)
Enteritidis	303	176	39	34	269	188	50	68	6	37	2	0	0	1,172	34.88
Typhimurium	36	60	10	10	155	81	10	5	1	2	0	0	0	370	11.01
ssp I 4,[5],12:i:-	15	17	9	2	78	99	6	5	0	0	0	0	0	231	6.88
Infantis	11	11	2	5	72	31	2	3	1	0	0	0	0	138	4.11
Newport	12	17	5	3	45	13	0	2	0	2	0	0	0	99	2.95
Heidelberg	3	7	2	0	43	35	4	3	0	0	0	0	0	97	2.89
Thompson	4	12	0	1	53	24	1	0	0	0	0	0	0	95	2.83
Typhi	11	8	0	1	31	4	2	0	0	0	0	0	0	57	1.70
Muenchen	3	4	1	0	29	12	1	4	0	2	0	0	0	56	1.67
Oranienburg	8	4	1	1	17	20	3	1	0	0	0	0	0	55	1.64
<b>Total</b>	<b>406</b>	<b>316</b>	<b>69</b>	<b>57</b>	<b>792</b>	<b>507</b>	<b>79</b>	<b>91</b>	<b>8</b>	<b>43</b>	<b>2</b>	<b>0</b>	<b>0</b>	<b>2,370</b>	<b>70.54</b>

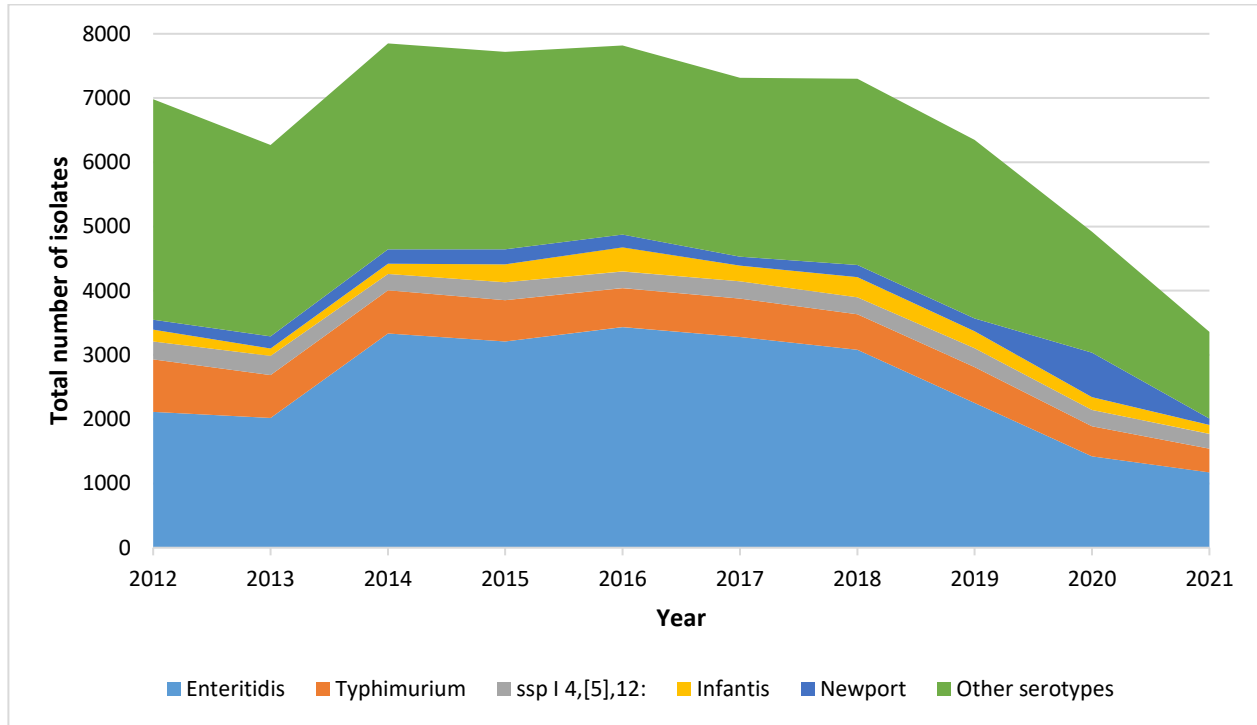
Compared to the average number of *Salmonella* notifications received between 2016 and 2020 (6,740 cases), there was a 50.1% decrease observed in 2021 (3,360 cases). The national incidence rate of *Salmonella* (8.79 cases per 100,000 population) also continued to decrease in comparison to the previous 5 years, likely due to the impacts of COVID-19 and the continued impact of the CFIA regulation<sup>f</sup> implemented in April 2019 to address *Salmonella* in frozen raw 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 2021, five provinces reported incidence rates of *Salmonella* higher than the national reported incidence rate: British Columbia (10.46 cases per 100,000 population), Alberta (9.81 cases per 100,000 population), New Brunswick (12.02 cases per 100,000 population), Nova Scotia (10.80 cases per 100,000 population), and Newfoundland and Labrador (12.49 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 high discriminatory genomic subtype data for outbreak detection and response.

<sup>f</sup> *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 2012 and 2021 for the top five *Salmonella* serotypes reported to NESP in 2021**



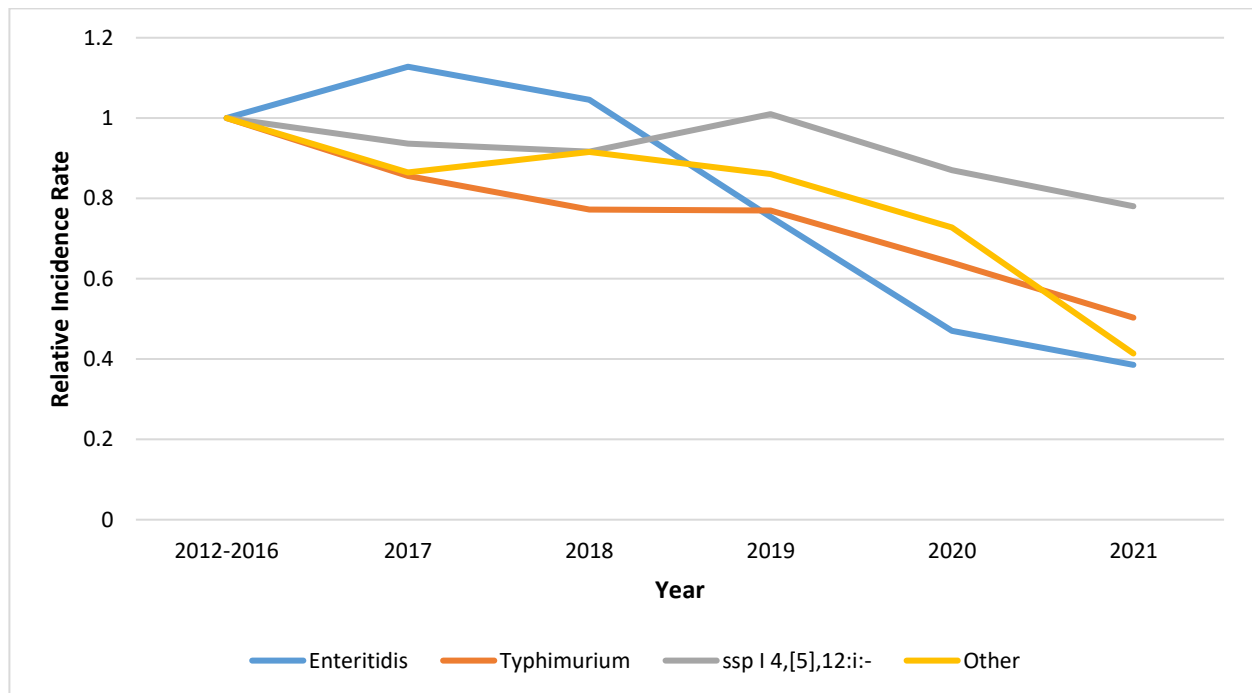
**Table 5. National total counts (overall rank) for the ten most commonly reported *Salmonella* serotypes to NESP, 2016-2021**

Serotypes	2016	2017	2018	2019	2020	2021	Average no. of isolates (2016-2020)
Enteritidis	3,433	3,278	3,083	2,254	1,422	1,172	2,694
Typhimurium	607	602	551	557	468	370	557
ssp I 4,[5],12:i:-	259	265	263	294	256	231	267
Infantis	378	244	313	264	198	138	279
Newport	198	143	192	200	693	99	285
Heidelberg	580	444	390	267	207	97	378
Thompson	290	135	148	98	126	95	159
Typhi	136	181	198	232	113	57	172
Muenchen	61	89	53	80	55	56	68
Oranienburg	61	53	113	104	71	55	80
Javiana	114	111	118	143	50	49	107
Braenderup	81	145	127	102	81	42	107
Paratyphi A	62	62	56	116	43	37	68
Montevideo	30	32	45	36	71	31	43
Agona	120	103	125	101	35	24	97

## Salmonella Enteritidis

In 2021, 1,172 isolates of *S. Enteritidis*, 34.9% of all *Salmonella* submissions, were reported to NESP. The incidence rate observed in 2021 was 61.4% lower (3.07 cases per 100,000 population) relative to the 2012-2016 baseline period (7.95 cases per 100,000 population). A general decrease in incidence can be seen from 2017-2020 as well, suggesting that the rate observed in 2021 is part of an ongoing trend unrelated to the impacts of COVID-19 (Figure 3) and was also likely a continuation of impacts of new CFIA poultry product regulations<sup>9</sup>.

**Figure 3. Relative incidence rates<sup>1</sup> (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, 2017-2021 compared to the 2012-2016 baseline period**



<sup>1</sup> Rates are compared to the 2012-2016 baseline period.

<sup>9</sup>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>

### *Salmonella* Typhimurium

Compared to the 2012-2016 baseline period, a 49.7% decrease in the incidence of *S. Typhimurium* cases was noted in 2021 (1.92 versus 0.97 cases per 100,000 population, respectively). From 2017-2021, 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 11.0% of all *Salmonella* isolates reported to NESP in 2021 (Figure 1 and Table 5).

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

*Salmonella* ssp I 4,[5],12:i:-, for the second time since NESP was launched in 1997 (first time being 2019), was the third most common serotype in Canada, representing 6.9% of all human *Salmonella* isolates reported to NESP in 2021. The 2021 overall incidence (0.60 cases per 100,000 population) was 22.0% lower than the 2012-2016 baseline period (0.77 cases per 100,000 population).

## *Escherichia coli*

Unless otherwise indicated, it is assumed that all the isolates reported to NESP from the provinces and territories are Shiga toxin-producing *Escherichia coli* (STEC). The 2021 rate of O157 (0.68 cases per 100,000 population) is similar to the 2020 rate of O157, but lower than the relatively stable rates seen between 2010 and 2019, which is likely due to the impacts of COVID-19 during 2020-2021 (Figure 4). In 2021, three provinces reported incidence rates of *E. coli* O157 higher than the national reported incidence rate: Alberta (1.51 cases per 100,000 population), Manitoba (0.93 cases per 100,000 population), and Prince Edward Island (1.21 cases per 100,000 population) (Table 3). The incidence rate of non-O157 STEC increased slightly in 2021 (0.98 cases per 100,000 population) from 2020 (0.84 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 2021 represent the fifth consecutive year where the proportion of non-O157 STEC reported has exceeded the proportion of O157 isolates. It should be noted that non-O157 STEC are suspected to be reported less consistently than *E. coli* O157 to NESP. Therefore, any changes observed over time may also be a reflection in testing practices by some provincial public health laboratories. Further, 8.4% of *E. coli* isolates reported to NESP were identified using culture-independent diagnostic tests (CIDT), which are PCR-based tests used for the identification of organisms without an isolate cultured. According to national guidance<sup>h</sup>, reflex cultures are to be obtained from CIDT positive samples. Reflex culture of a CIDT positive sample may obtain an isolate for further sub-typing, which would be updated in NESP.

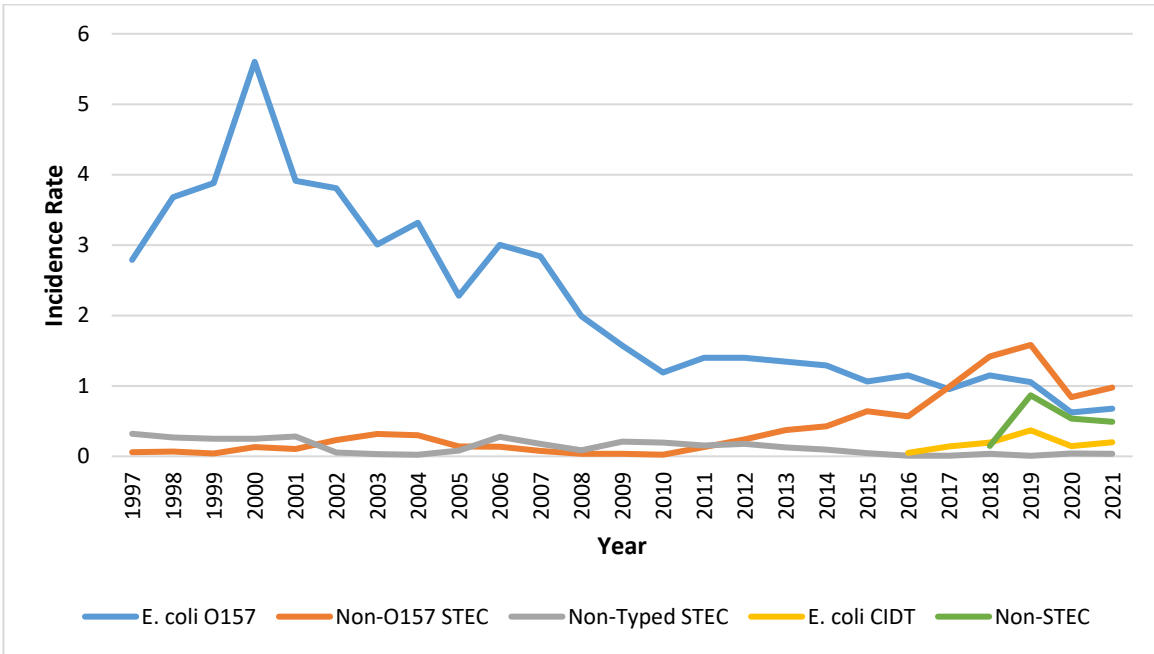
Among non-O157 STEC isolates serotyped in 2021, 60% of these were represented by five serotypes: *E. coli* O26, *E. coli* O103, *E. coli* O121, *E. coli* O111, and *E. coli* O186 (Figure 5). In 2021, 16.8% of non-O157 STEC did not have additional serotype information. In 2017, a request was submitted 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.

All of the top 5 serotypes from the broader list of the non-O157 STEC isolates where a serotype result was available showed an increased rate per 100,000 population in 2021 compared to 2020. However, with the exception of *E. coli* O121, all of the top five serotypes among serotyped *E. coli* isolates showed a decreased rate in 2021 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 2.

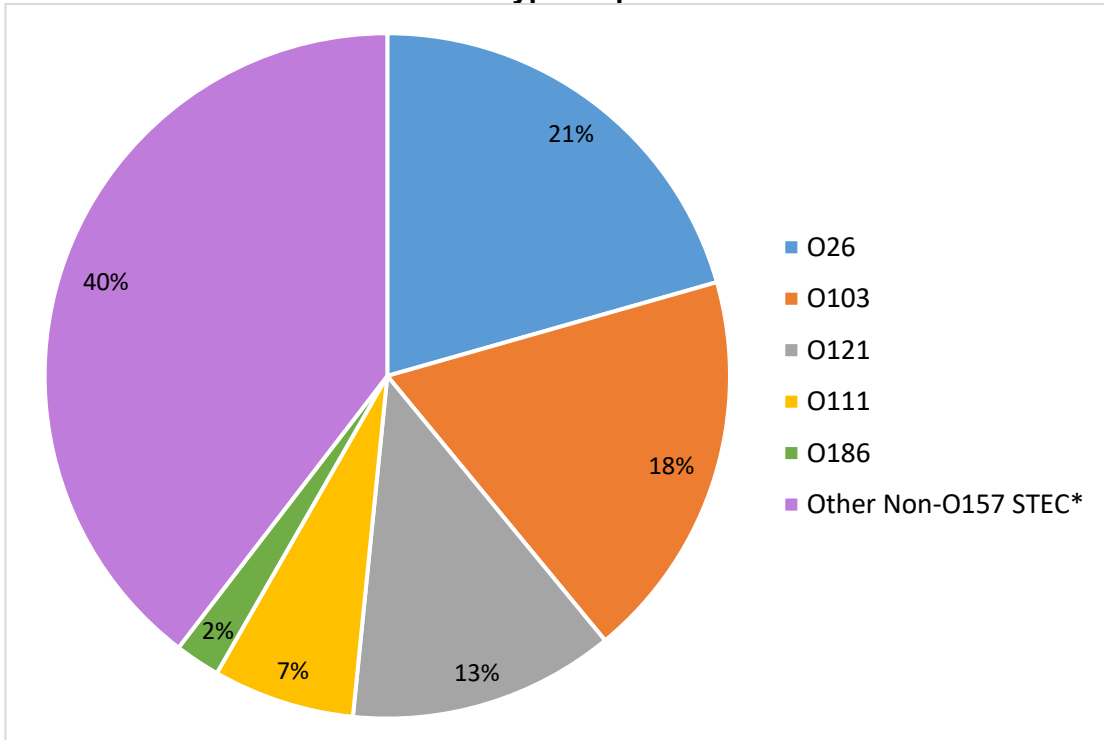
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<sup>h</sup>Public Health Agency of Canada. CPHLN recommendations for the laboratory detection of Shiga toxin-producing *Escherichia coli* (O157 and non-O157). *Can Commun Dis Rep* 2018;44(11):304-7. <https://doi.org/10.14745/ccdr.v44i11a06>

**Figure 4. Incidence rates (per 100,000 population) of *E. coli* O157, non-O157 STEC, & other non-typed *E. coli* reported to NESP, 1997-2021**



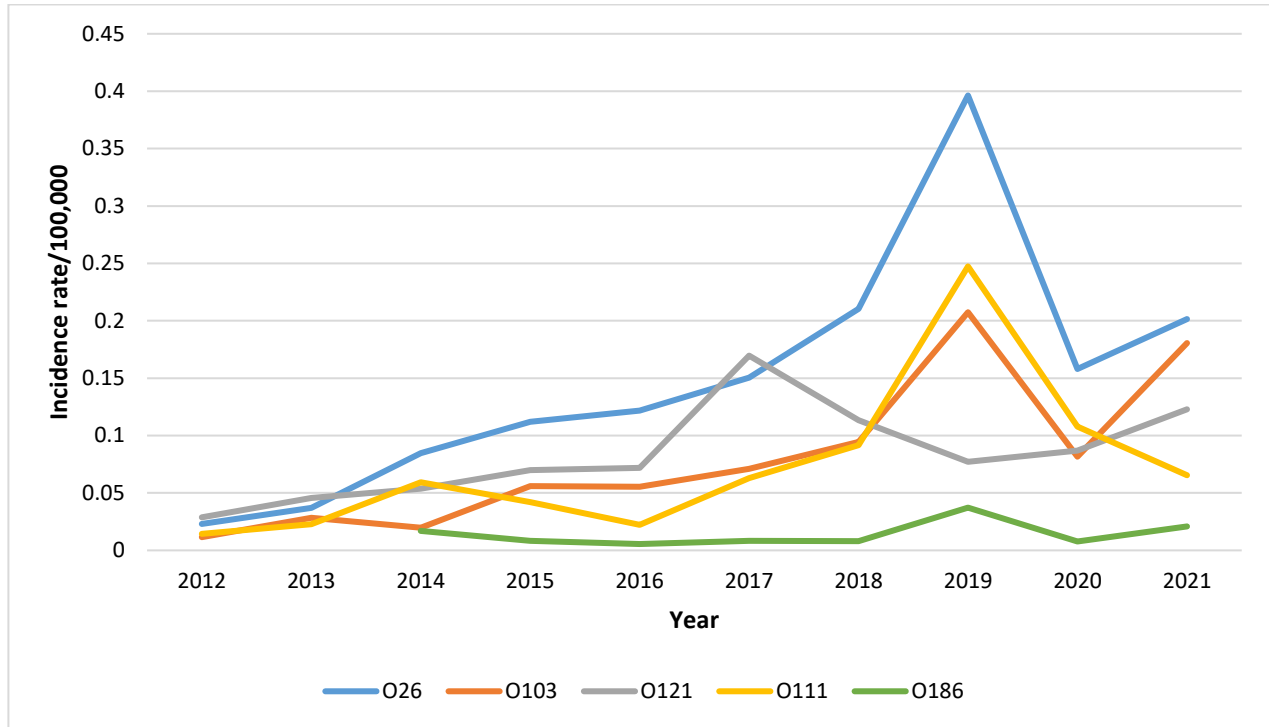
**Figure 5. Distribution of non-O157 STEC serotypes reported to NESP in 2021**



\*Other serotypes (148 isolates) were divided among 34 serotypes and 63 isolates were reported as unspecified non-O157 STEC.



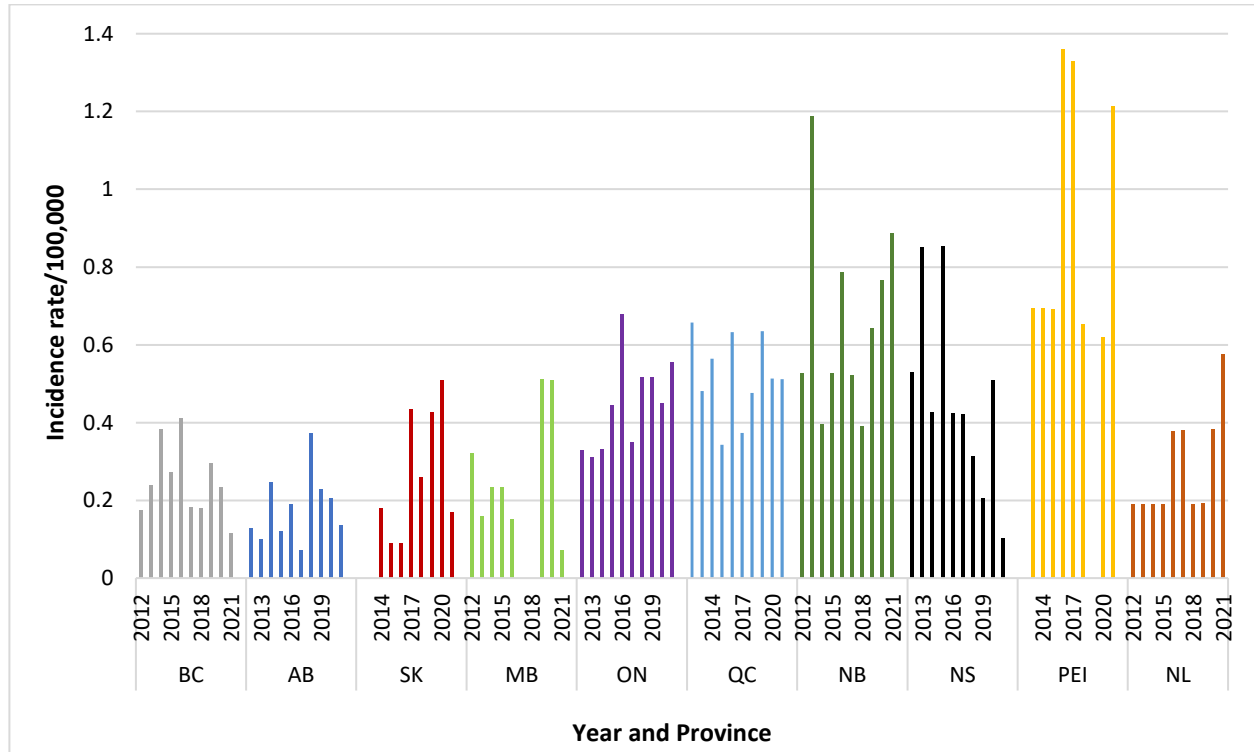
**Figure 6. Incidence rate (per 100,000 population) of the top five serotyped non-O157 STEC serotypes reported to NESP, 2012-2021**



## 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. A similar number of isolates for invasive listeriosis were reported in 2021 (154) compared to 2020 (158). This remains lower compared to 2019 (174). The national incidence rate of *Listeria monocytogenes* remained similar in 2021 (0.40 cases per 100,000 population) to 2020 (0.42 cases per 100,000 population) and 2019 (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 triple that of other provinces. In 2021, five provinces reported incidence rates of *Listeria monocytogenes* higher than the national reported incidence rate: Ontario (0.55 cases per 100,000 population), Québec (0.51 cases per 100,000 population), New Brunswick (0.89 cases per 100,000 population), Prince Edward Island (1.21 cases per 100,000 population), and Newfoundland and Labrador (0.58 cases per 100,000 population) (Table 3).

**Figure 7. Incidence rate (per 100,000 population) of invasive listeriosis reported to NESP by province, 2012-2021<sup>i</sup>**



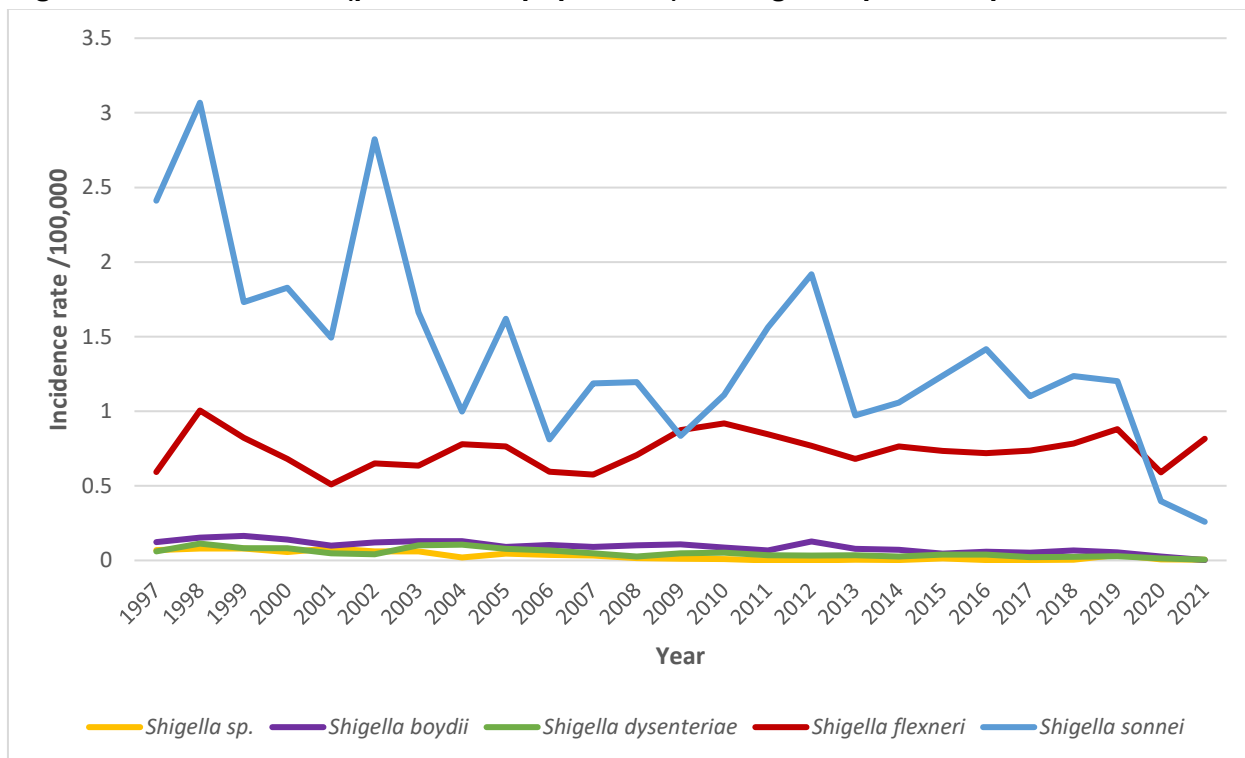
<sup>i</sup> There were no cases of invasive listeriosis reported in 2021 by Yukon, Northwest Territories, and Nunavut.

## Shigella

There were 416 isolates of *Shigella* reported in 2021, representing a rate of 1.09 cases per 100,000 population which is similar to the 2020 rate of 1.03 cases per 100,000 population. This rate is lower than the average of 2.11 cases per 100,000 population reported between 2015 and 2019 (Figure 8). In 2021, the only province reporting an incidence rate of *Shigella* higher than the national reported incidence rate was British Columbia with 3.98 cases per 100,000 population.

Isolates of *Shigella sonnei* and *Shigella flexneri* comprised 24% and 75% of total notifications respectively. Overall trends for *Shigella* have historically been driven by the incidence of *S. sonnei* (0.26 cases per 100,000 population). However, the rate of *S. flexneri* (0.82 cases per 100,000) surpassed that of *S. sonnei* in 2020 and remained higher in 2021 (Figure 8). Among the other *Shigella* species, incidence trends over time have remained relatively unchanged with an incidence of 0.003 cases per 100,000 population for *Shigella boydii* and 0.01 cases per 100,000 population for *Shigella dysenteriae* observed in 2021 (Figure 8). Rates of most species of *Shigella* remained lower in 2021 compared to 2019, likely due to the impacts of COVID-19 (Figure 8). However, this is not true for *Shigella flexneri* which appears to have returned to levels reported pre-COVID-19.

**Figure 8. Incidence rate (per 100,000 population) of *Shigella* species reported to NESP, 1997-2021**

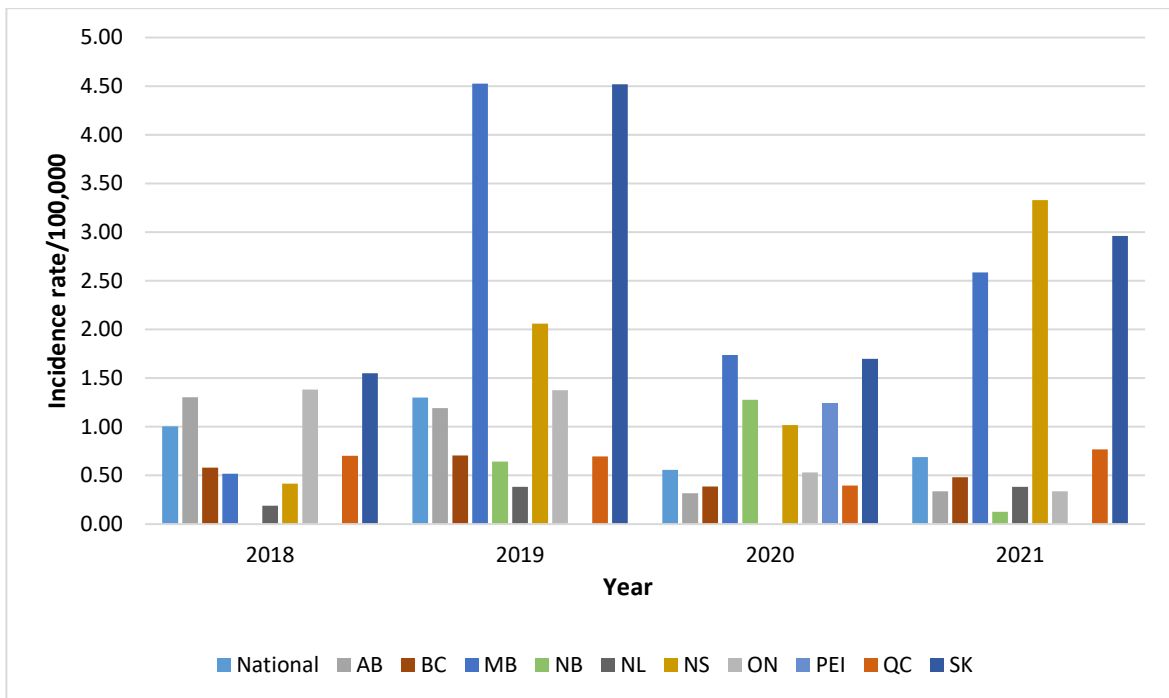
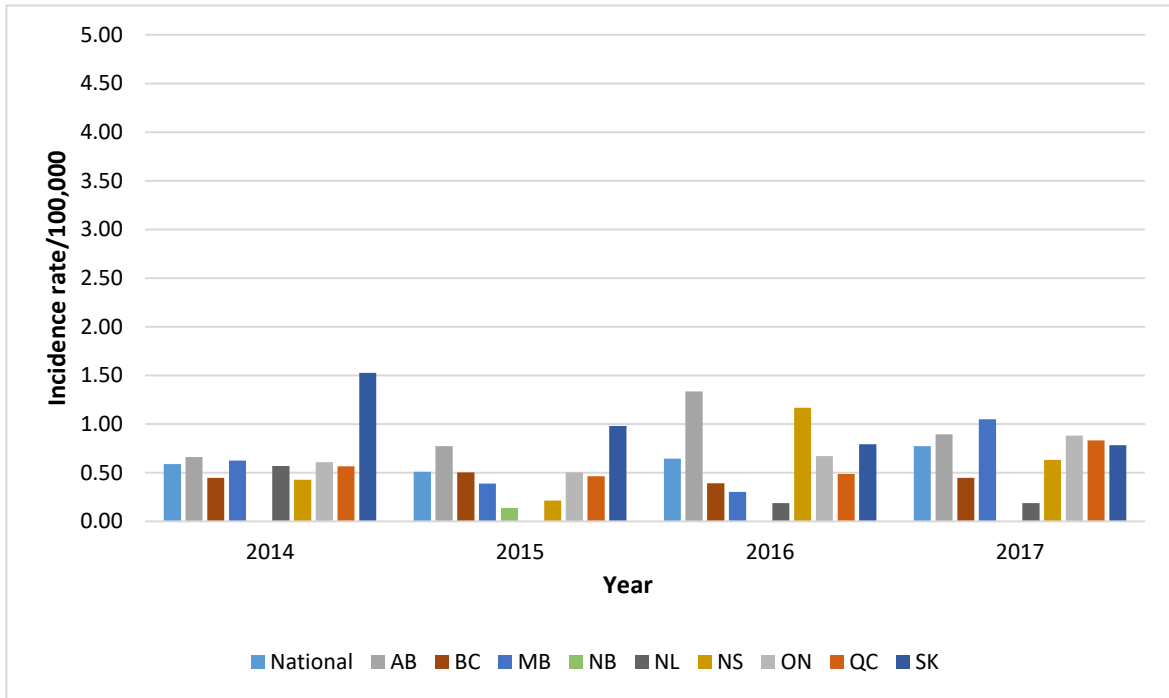


## Hepatitis A

The national incidence rate for Hepatitis A in 2021 was higher than in 2020 (0.69 cases per 100,000 population in 2021 compared to 0.56 in 2020). However, this is still lower than the 2019 rate (1.30 cases per 100,000 population), likely due to the impacts of COVID-19 (Figure 9). In 2021, three provinces reported incidence rates of Hepatitis A higher than the national reported incidence rate: Manitoba (2.59 cases per 100,000 population), Saskatchewan (2.96 cases per 100,000 population), and Nova Scotia (3.33 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 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 the case meets a confirmed case definition or not. If local public health determines it is not a case (e.g., due to recent immunization), this information may not always be relayed back to the laboratory, and therefore, Hepatitis A data reported through NESP are not corrected in this scenario and may cause over-reporting. 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/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, 2014-2021**



**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, 2020<sup>1,2</sup>**

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 <sup>10</sup> )
	N	Rate per 100,000 population <sup>3</sup>	N	Rate per 100,000 population	
2020					
Botulism	7	0.02	-	-	N/A
Campylobacteriosis <sup>4</sup>	7,332	20	1,289	-	17.6
Cholera <sup>5</sup>	1	0.003	0	0	0.0
Cryptosporidiosis <sup>4</sup>	917	2.5	278	-	30.3
Cyclosporiasis <sup>4</sup>	486	1.3	68	-	14.0
Giardiasis <sup>4</sup>	2,394	6.5	488	-	20.4
Hepatitis A	157	0.4	212	0.56	135.0 <sup>10</sup>
Invasive Listeriosis	148	0.4	158	0.42	106.8 <sup>10</sup>
Norovirus <sup>4,6,7</sup>	158	3.5	622	-	N/A
Paralytic Shellfish Poisoning <sup>8</sup>	0	0	-	-	N/A
Salmonellosis	4,493	12.3	4,806	12.64	107.0 <sup>10</sup>
Shigellosis	431	1.2	393	1.03	91.2
Typhoid <sup>9</sup>	79	0.2	113	0.30	143.0 <sup>10</sup>
Shiga toxinogenic <i>Escherichia coli</i> Infection	617	1.7	557 <sup>11</sup>	1.47	90.3

<sup>1</sup>CNDSS data for 2021 was not available at the time this summary was produced.

<sup>2</sup>Data for the year 2020 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.

<sup>3</sup>2020 data from MB is not available for botulism, campylobacteriosis, cholera, cryptosporidiosis, cyclosporiasis, giardiasis, hepatitis A, listeriosis, salmonellosis, shigellosis, typhoid, and verotoxigenic *Escherichia coli* infection. The population of this province has been removed for rate calculation.

<sup>4</sup>*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.

<sup>5</sup>Includes *Vibrio cholerae* serotype O1 or O139.

<sup>6</sup>BC, MB, NB, NL, NS, NT, ON, QC and SK did not report on norovirus in 2020 to CNDSS. The populations of these provinces and territory have been removed for rate calculation.

<sup>7</sup>For Norovirus some provinces/territories report only on aggregated outbreak related data; these data are not included here.

<sup>8</sup>AB, MB, NT, QC and SK did not report on paralytic shellfish poisoning in 2020. The populations of these provinces and territory have been removed for rate calculation.

<sup>9</sup>Typhoid includes lab confirmation of *Salmonella* Typhi; *Salmonella* Paratyphi A, B and C are reported under salmonellosis.

<sup>10</sup>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.

<sup>11</sup> Unless otherwise indicated, it is assumed that all the samples reported to NESP from the provinces and territories are Shiga toxinogenic *Escherichia coli* (STEC). This value does not include any non-typed *E. coli*.











	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL
<i>Salmonella</i> Leeuwarden	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> Limete	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> Litchfield	1	2	0	1	6	3	0	0	0	0	0	0	0	13
<i>Salmonella</i> Livingstone	0	1	0	0	15	0	0	0	0	0	0	0	0	16
<i>Salmonella</i> Lomalinda	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Lome	0	1	1	0	2	2	1	0	0	0	0	0	0	7
<i>Salmonella</i> Mahina	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Manhattan	0	0	0	2	8	1	0	0	0	0	0	0	0	11
<i>Salmonella</i> Mbandaka	0	5	0	0	5	3	0	1	0	0	0	0	0	14
<i>Salmonella</i> Menston	0	0	0	0	9	0	0	0	0	0	0	0	0	9
<i>Salmonella</i> Miami	0	0	0	0	3	1	0	0	0	0	0	0	0	4
<i>Salmonella</i> Michigan	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Minnesota	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Mississippi	0	0	0	0	1	0	0	3	1	0	0	0	0	5
<i>Salmonella</i> Montevideo	1	1	1	1	4	20	2	1	0	0	0	0	0	31
<i>Salmonella</i> Morotai	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Muenchen	3	4	1	0	29	12	1	4	0	2	0	0	0	56
<i>Salmonella</i> Muenster	2	1	0	0	2	0	0	0	0	0	0	0	0	5
<i>Salmonella</i> Newport	12	17	5	3	45	13	0	2	0	2	0	0	0	99
<i>Salmonella</i> Nigeria	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> Nima	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> Ohio	1	0	0	0	7	2	0	0	0	0	0	0	0	10
<i>Salmonella</i> Oranienburg	8	4	1	1	17	20	3	1	0	0	0	0	0	55
<i>Salmonella</i> Orion	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Oslo	0	0	0	0	2	1	0	1	0	0	0	0	0	4
<i>Salmonella</i> Panama	0	3	0	0	5	1	1	0	0	0	0	0	0	10
<i>Salmonella</i> Paratyphi A	6	2	0	0	10	1	0	0	0	0	0	0	0	19
<i>Salmonella</i> Paratyphi B	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Paratyphi B var. Java	12	9	0	0	5	9	1	1	0	0	0	0	0	37
<i>Salmonella</i> Plymouth	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> Pomona	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Poona	1	3	1	0	6	3	0	0	0	0	0	0	0	14
<i>Salmonella</i> Reading	10	13	5	4	17	1	0	0	0	0	0	0	0	50
<i>Salmonella</i> Rissen	0	1	0	0	2	0	0	0	0	0	0	0	0	3
<i>Salmonella</i> Rubislaw	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Saintpaul	2	2	1	1	16	7	0	1	0	0	0	0	0	30
<i>Salmonella</i> Sandiego	3	0	0	0	3	0	0	0	0	0	0	0	0	6
<i>Salmonella</i> Sandiego/Chester	0	0	0	0	0	2	0	0	0	0	0	0	0	2
<i>Salmonella</i> Scarborough	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> Schwarzengrund	1	6	0	1	2	5	2	0	0	0	0	0	0	17





	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL
<i>Salmonella</i> ssp I 9,12:-:1,5	3	0	0	0	0	0	0	0	0	0	0	0	0	3
<i>Salmonella</i> ssp I Rough-O:H undetermined	0	0	0	0	2	0	0	0	0	0	0	0	0	2
<i>Salmonella</i> ssp I Rough-O:HNM	3	0	0	1	8	0	0	0	0	0	0	0	0	12
<i>Salmonella</i> ssp I Rough-O:d:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp I Rough-O:d:1,2	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp I Rough-O:d:1,7	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp I Rough-O:g,m,p:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp I Rough-O:g,m:-	1	0	0	0	2	0	0	0	0	0	0	0	0	3
<i>Salmonella</i> ssp I Rough-O:g,p:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp I Rough-O:i:1,2	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp I Rough-O:i:1,5	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp I Rough-O:l,w:-	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp II 16:m,t:-	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp II 43:g,z62:e,n,x	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIa 41:z4,z23:-	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIa 48:z4,z24:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb	0	0	0	1	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 16:z10:e,n,x,z15	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 38:l,v:z35	0	0	0	0	0	2	0	0	0	0	0	0	0	2
<i>Salmonella</i> ssp IIIb 38:z10:e,n,x,z15	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 47:k:z35	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 48:i:z[z72]	0	1	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 48:z4,z24:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 50:k:z	0	1	0	0	1	0	0	0	0	0	0	0	0	2
<i>Salmonella</i> ssp IIIb 50:k:z:[z50],[z57]	0	0	0	0	0	2	0	0	0	0	0	0	0	2
<i>Salmonella</i> ssp IIIb 6,14:z10:z	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 60:r:z	0	0	0	0	0	1	1	0	0	0	0	0	0	2
<i>Salmonella</i> ssp IIIb 60:z52:z53	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 61:k:1,5,7	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 61:l,v:1,5,7	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IIIb 61:r:z	2	1	0	0	0	0	0	0	0	0	0	0	0	3
<i>Salmonella</i> ssp IV 40:z4,z23:-	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IV 45:g,z51:-	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IV 48:g,z51:-	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Salmonella</i> ssp IV 48:z4,z32:-	0	0	0	0	2	0	0	0	0	0	0	0	0	2
<i>Salmonella</i> ssp IV 50:g,z51:-	0	3	0	0	2	0	0	0	0	0	0	0	0	5
<i>Salmonella</i> ssp IV 50:z4,z23:-	0	0	0	0	2	0	0	0	0	0	0	0	0	2
<b>Total Salmonella</b>	544	436	97	81	1,246	675	95	107	12	65	2	0	0	3,360



	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL
<i>Yersinia</i> sp	0	0	0	0	0	1	1	0	0	0	0	0	0	2
<b>Total <i>Yersinia</i></b>	129	34	5	4	103	17	2	0	1	1	2	0	0	298
<b>Parasites</b>														
<i>Cryptosporidium</i>	9	2	16	15	209	0	21	6	7	22	0	0	0	307
<i>Cyclospora</i>	1	0	0	1	27	0	0	0	0	3	0	0	0	32
<i>Entamoeba histolytica/dispar</i>	94	3	0	2	63	0	0	0	0	0	4	0	0	166
<i>Giardia</i>	51	0	47	35	66	0	66	56	4	52	10	0	0	387
<b>Total Parasites</b>	155	5	63	53	365	0	87	62	11	77	14	0	0	892
<b>Viruses</b>														
Adenovirus	1	77	0	10	20	0	0	0	0	15	0	0	1	124
Astrovirus	2	1	0	1	0	0	0	0	0	10	0	0	0	14
Hepatitis A	25	15	35	36	50	66	1	33	0	2	0	0	0	263
Norovirus	30	205	70	18	53	0	8	10	14	33	1	0	1	443
Rotavirus	7	13	7	9	23	0	14	0	3	6	0	0	0	82
Sapovirus	3	9	0	0	0	0	0	0	0	0	0	0	0	12
<b>Total Virus</b>	68	320	112	74	146	66	23	43	17	66	1	0	2	938

<sup>1</sup>Cases visiting a different province or territory are captured in the total count for the province or territory where the case was detected.

\*These isolates were reported to NESP labelled as STEC. Unless otherwise indicated, it is assumed that all other *E. coli* reported to NESP are STEC.

### Appendix 3: NESP support for outbreak investigations

NESP data supported 4 out of 5 National Outbreak Investigation Coordinating Committees (OICCs). More information about the OICCs that NESP supported can be seen below in Table 6.

**Table 6. Multi-jurisdictional Outbreak Investigations in 2021**

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
[2021-006] [OICC: <i>Salmonella</i> Enteritidis in NL and NS] [January, 2021 – April, 2021]	Eggs	70	2020-10-28	2021-03-25 (isolation date of last case; onset not available)	NL 27 NS 43
[2021-107] [OICC: Cluster of Hepatitis A in QC and NS] [July, 2021 – October, 2021]	Frozen mango	3	2021-03-18	2021-06-13	QC 2 NS 1
[2021-149] [OICC: <i>Salmonella</i> Oranienburg in QC and ON] [August, 2021 – November, 2021]	Unconfirmed	13	2021-06-26	2021-09-09 (isolation date of last case)	ON 3 QC 10
[2021-180] [OICC: <i>Salmonella</i> Enteritidis in BC, AB, SK, MB & ON] [October, 2021 – March, 2022]	Frozen corn	118	2021-09-06	2022-01-27 (isolation date of last case)	BC 44 AB 55 SK 4 MB 13 ON 2

#### Appendix 4: Impacts of COVID-19 - Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019 for select pathogens

In March of 2020, the COVID-19 pandemic was declared<sup>j</sup> 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<sup>k</sup> 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. Similar to the 2020 NESP Annual Summary, interpretation of the data and findings in the 2021 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 1-7 compare 2021 NESP data with the pre-pandemic period five-year (2015-2019) average for select pathogens. Data from NESP are plotted along with the COVID-19 national case numbers as a proxy for the stage of the pandemic and the related public health measures, however this should not be interpreted as implying any direct link between these illnesses.

The impact that the public health measures for COVID-19 had on the pathogens reported through NESP in 2021 was variable. For all *Salmonella* serotypes (Figure 1), the 2021 NESP counts remain lower than the historical average throughout the year. The same trend was observed in all *Salmonella* serotypes excluding *S. Enteritidis* (Figure 2) and *S. Enteritidis* only (Figure 3). In all three figures, there is more pronounced disparity between the 2021 NESP data and the 2015-2019 historical data in the first half of the year compared to the last half of the time period. Possible explanation of these findings include more stringent public health measures and public health adaptations that were in place during the spring of 2021, but were generally de-escalated in the summer and autumn. The 2021 NESP counts for all three *Salmonella* figures

<sup>j</sup> <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)

<sup>k</sup> <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).

were lower than the 2020 NESP counts seen in the 2020 NESP Annual Report. These differences may be partially explained by the absence of COVID-19 public health measures prior to March 2020, and an outbreak of *S. Newport* that occurred in the summer of 2020.

Focusing on certain *Salmonella* serotypes and groupings, the magnitude of the difference between the 2021 NESP data and the pre-pandemic historical average in the first half of the year is greater for *Salmonella* Enteritidis (Figure 3) compared to all other *Salmonella* serotypes excluding *S. Enteritidis* (Figure 2). In the second half of 2021, this disparity decreased as relatively fewer *S. Enteritidis* isolates were reported to NESP. 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 frozen raw breaded chicken products.

Regarding *E. coli* O157 (Figure 4) and non-O157 STEC (Figure 5), 2021 case counts appear generally comparable to the pre-pandemic historical average. Throughout the summer months (i.e. weeks 28-38), cases of non-O157 STEC surpasses the pre-pandemic historical average, whereas cases of *E. coli* O157 remain lower than the historical average over the same time period. The divergence of trends in *E. coli* O157 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 2021 (Figure 6) are comparable to trends observed in 2020 (data not shown) 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.

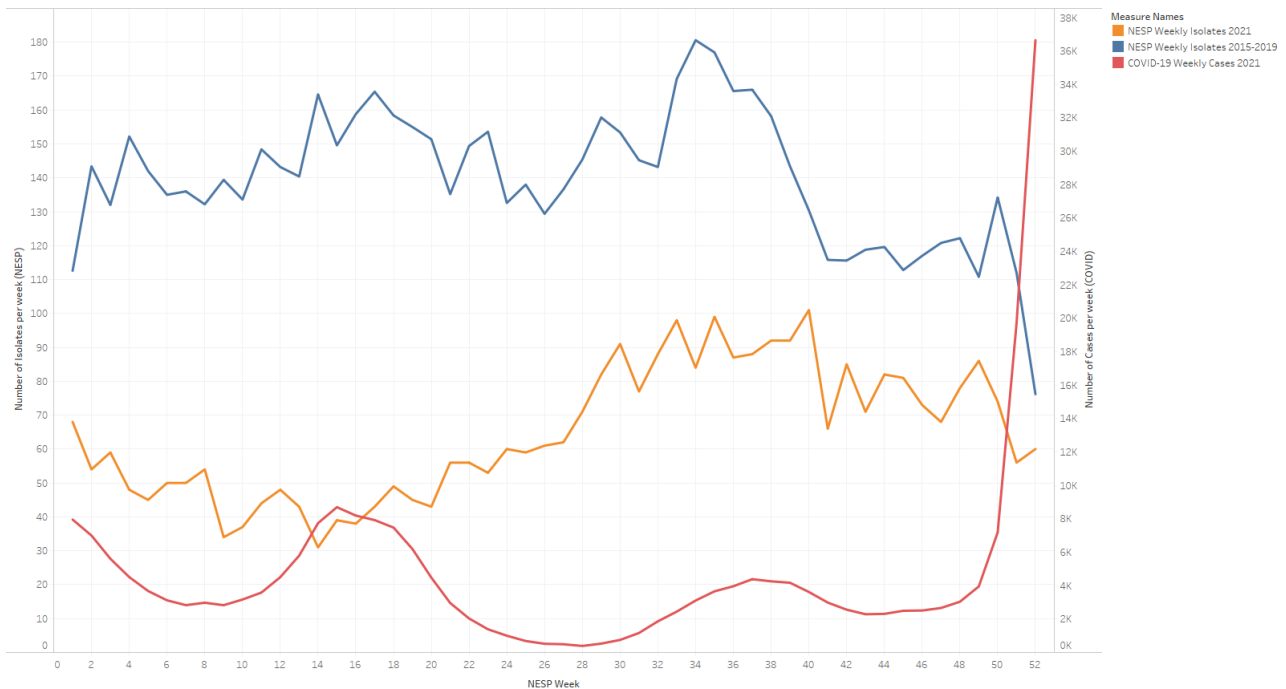
For *Shigella*, cases reported in 2021 generally remain lower than the pre-pandemic historical average (Figure 7) similar to trends in *Shigella* reported in 2020 (data not shown). Shigellosis is frequently travel-related and this microorganism is often transmitted through person-to-person contact, and thus the impact of COVID-19 public health measures in place likely played a role in the lower level of *Shigella* observed in 2021.



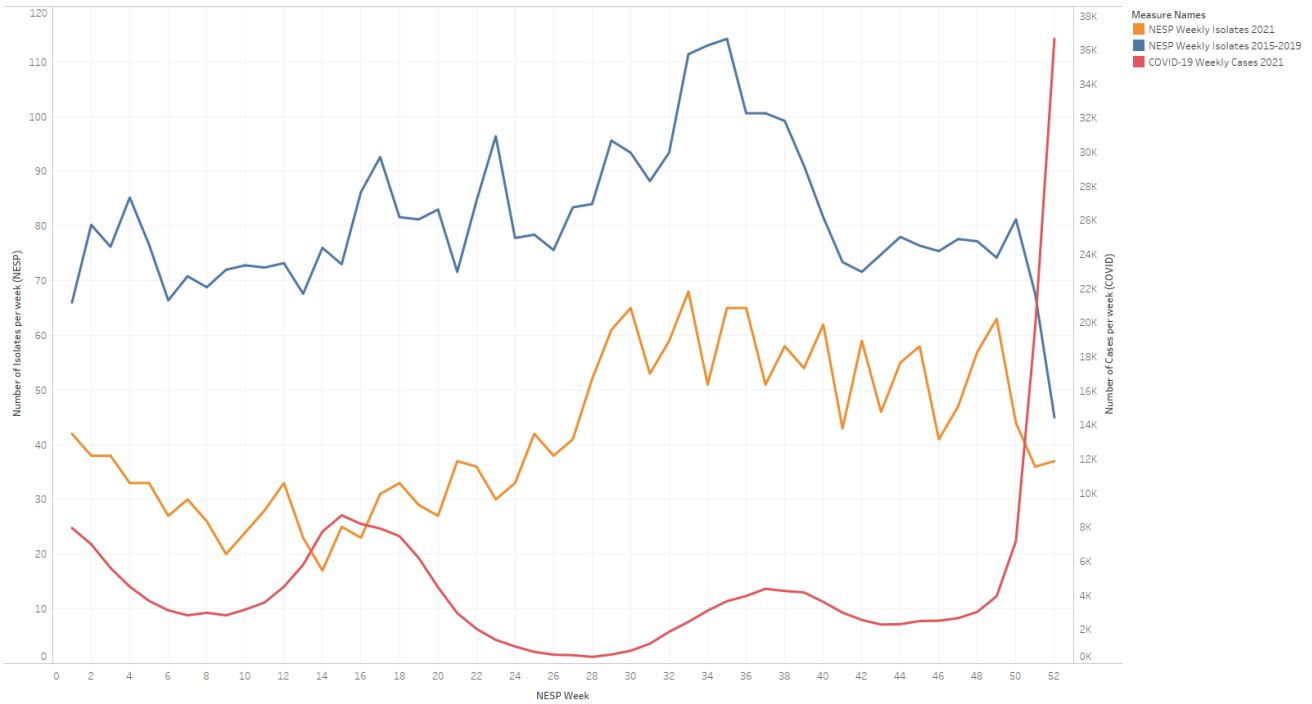
In general, compared to pre-pandemic counts, larger decreases were seen in 2021 for pathogens that typically are more often associated with travel, are typically milder symptom-wise or less invasive, or are more frequently transmitted via person-to-person contact. The main exception to this finding relates 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 2021 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). 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 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. Additional analyses are underway to further explore the impact of COVID-19 on the occurrence of enteric diseases in Canada as collected and reported by NESP.

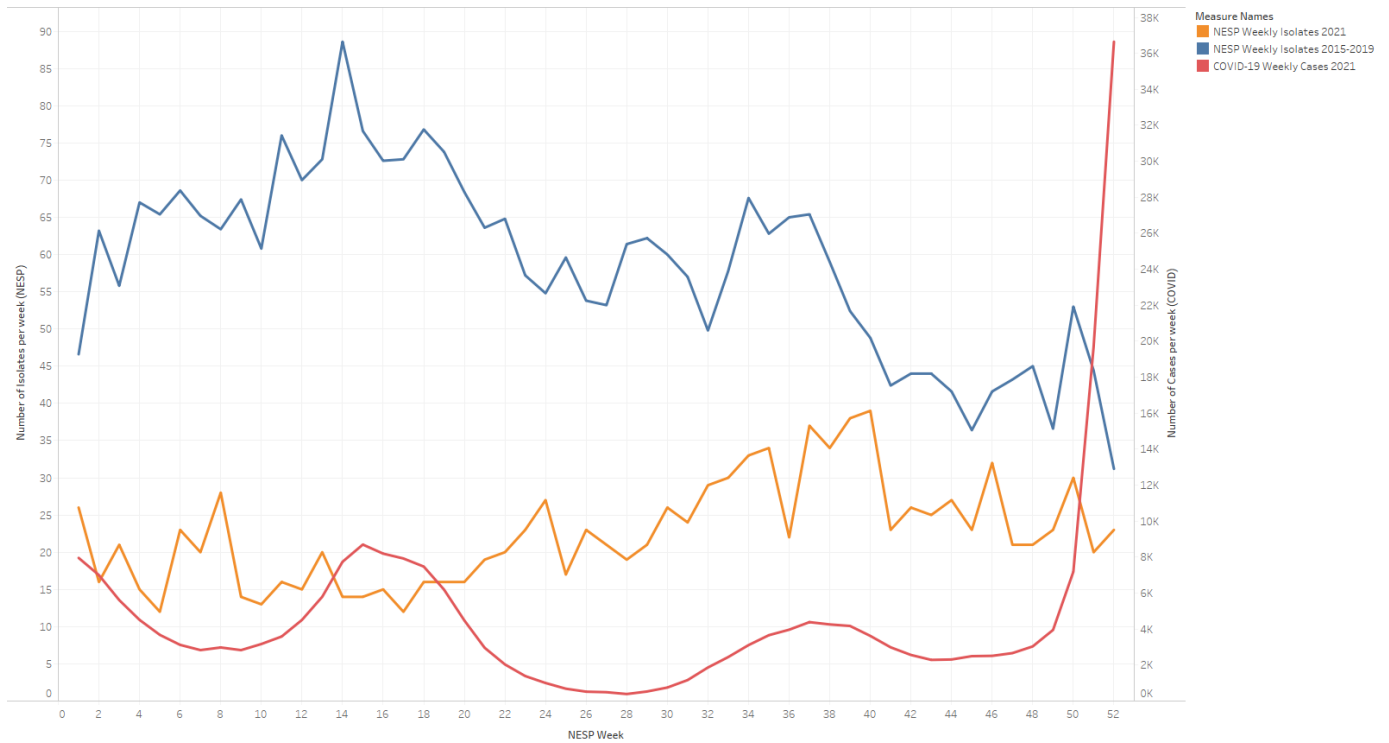
**Figure 1: Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019, all *Salmonella* serotypes, overlaid with 2021 Canadian case counts of COVID-19.**



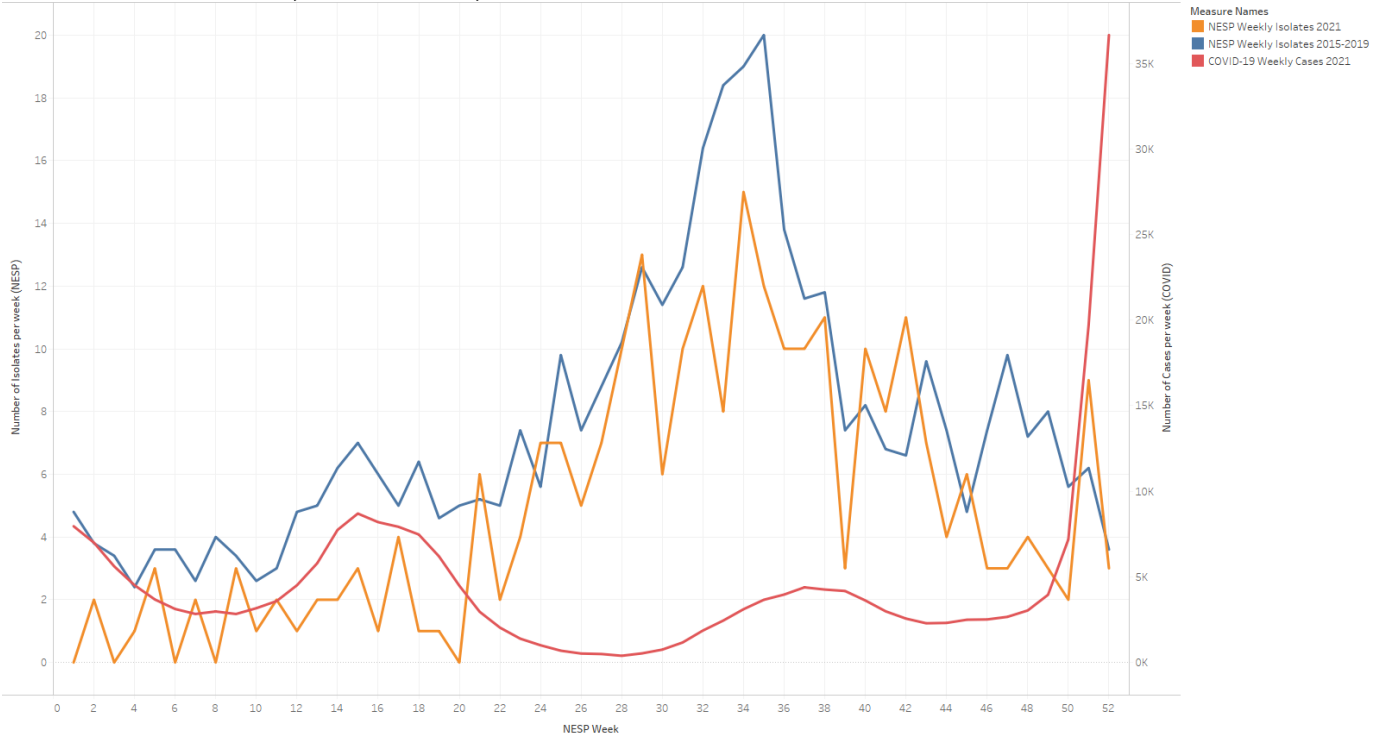
**Figure 2: Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019, all *Salmonella* serotypes excluding *S. Enteritidis*, overlaid with 2021 Canadian case counts of COVID-19.**



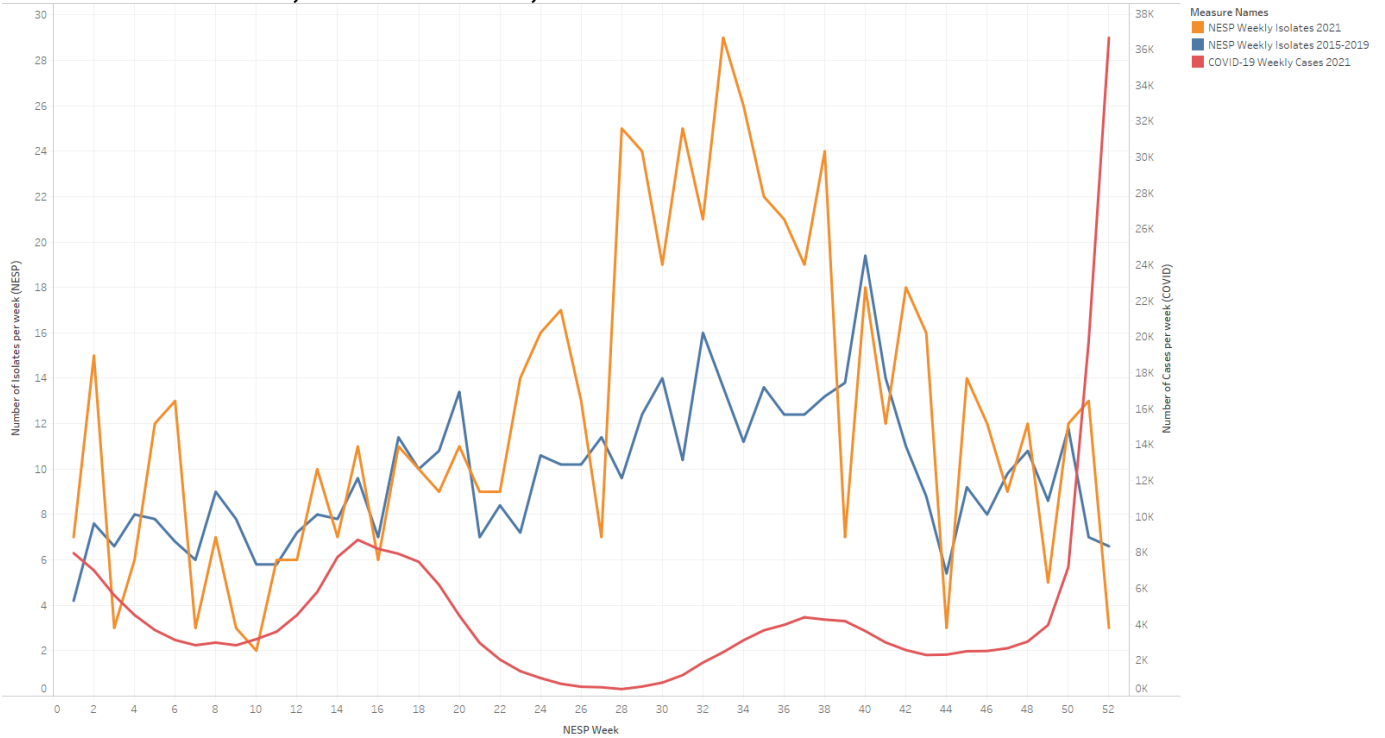
**Figure 3: Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019, *S. Enteritidis*, overlaid with 2021 Canadian case counts of COVID-19.**



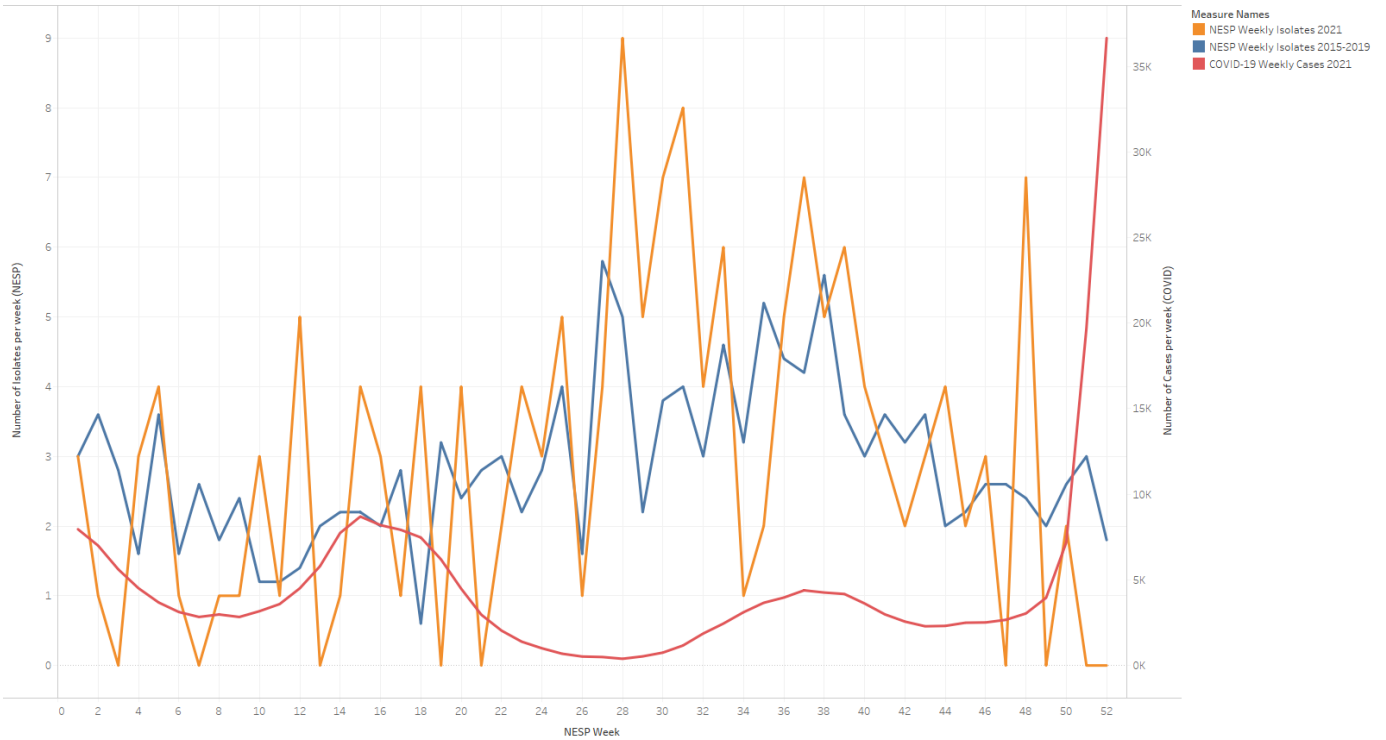
**Figure 4: Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019, *E. coli* O157, overlaid with 2021 Canadian case counts of COVID-19.**



**Figure 5: Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019, non-O157 STEC, overlaid with 2021 Canadian case counts of COVID-19.**



**Figure 6: Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019, *Listeria monocytogenes*, overlaid with 2021 Canadian case counts of COVID-19.**



**Figure 7: Comparison of NESP weekly isolate counts for 2021 and the average weekly isolate counts for 2015-2019, *Shigella*, overlaid with 2021 Canadian case counts of COVID-19.**

