

# National Enteric Surveillance Program (NESP)

ANNUAL SUMMARY 2015

PROTECTING CANADIANS FROM ILLNESS



Public Health  
Agency of Canada

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Canada

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

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# NATIONAL ENTERIC SURVEILLANCE PROGRAM (NESP)

## ANNUAL SUMMARY 2015

INCLUDING SEROTYPE AND PHAGE TYPE TABLES FOR 2015, NESP AND NML

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

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## Executive Summary

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

In 2015, a total of 16,104 isolate results were reported to NESP. *Salmonella spp.* was the most common organism identified with a 10% increase in 2015 (7,716 cases) compared to an average of 7,032 cases between 2010 and 2014. As in previous years, in 2015 *Salmonella* Enteritidis, *Salmonella* Typhimurium and *Salmonella* Heidelberg remain the top 3 serotypes of all *Salmonella* reported to NESP, accounting for 57% of all identified serotypes.

Verotoxigenic *Escherichia coli* (VTEC) O157 was identified in 22 isolates in 2015 (1.1 cases per 100,000), the lowest annual number of VTEC isolates since the inception of NESP in 1997. By contrast, an increase in the reports of *E. coli* non-O157 isolates was observed in 2015. Improved diagnostic tests for detecting *E.coli* non-O157 have contributed to a better understanding of the importance of this organism and associated severity of infection. The noted increase is likely therefore a reflection of changes in testing practices by some provincial laboratories. Compared to previous years, the number of isolates identified for *Listeria monocytogenes* (125 isolates, 0.35 cases per 100,000), *Shigella* (739 isolates, 2.1 cases per 100,000), and Hepatitis A (182 isolates 0.5 cases per 100,000) remained stable.

Extra-intestinal isolation site information and travel destination are available for a limited number of isolates reported. In 2015, 5% of all reported enteric pathogens were isolated from an extra-intestinal source, the majority from blood specimens. Among the *Salmonella* isolates, *S. Dublin* (38%) and *S. Heidelberg* (11%) had the highest proportion identified from a blood sample compared other non-typhoidal serotypes. Information on travel destination was available for 2% of enteric pathogens reported to the NESP. The most commonly reported travel destinations were the Caribbean and Central America (including Mexico), accounting for 39% of travel-related cases.

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

In Canada the surveillance of enteric diseases are captured through the National Enteric Surveillance Program (NESP) and the Canadian Notifiable Diseases Surveillance System (CNDSS). NESP is jointly administered by the Public Health Agency of Canada's (PHAC) National Microbiology Laboratory (NML) and the Centre for Foodborne, Environmental and Zoonotic Infectious Diseases (CFEZID). Since 1997 NESP has been providing weekly analysis and reporting on laboratory confirmed cases of enteric illness submitted by the Provincial Public Health Laboratories (PPHL). Monitoring of the aggregated data allows for the rapid evaluation and response to outbreaks of enteric illness. The system provides the first and most timely level of characterization (primarily species and serotype) of data critical to, and integrated with, downstream surveillance programs such as PulseNet Canada<sup>a</sup>. In addition, the data allows for the description of trends of pathogen subtypes and on the incidence of nationally notifiable enteric pathogens.

CNDSS receives data that are collected by local health units, forwarded to provincial/territorial health authorities and collated by the Centre for Communicable Diseases and Infection Control (CCDIC) at PHAC. These data may be more reliable indicators 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 trends are more current and responsive to trends. A comparison of national case counts and incidence rates for enteric diseases is included (Appendix 1).

### Data Collection

Isolates (or specimens) are submitted to provincial public health microbiology laboratories for testing and/or confirmation of the enteric pathogen. On a weekly basis, each provincial public health laboratory summarizes the number of enteric microorganisms isolated from human patients onto a NESP report form. The information details the genus, species and serotype

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

(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. Data are submitted to NML either directly by faxing or emailing the completed NESP report form or by entering the data via the web-based application (webNESP) hosted on the Canadian Network for Public Health Intelligence (CNPHI). The information is submitted as soon as possible and no later than the second day after a weekend or holiday. An exception to this reporting scheme occurs when the isolate must be sent to another laboratory for completion of the identification. In this case, the isolate is reported at the level of typing or identification attained (e.g. *Salmonella* sp.) for the week in which it was sent to the reference laboratory. The NESP record is then updated when the final identification is received from the reference laboratory (e.g. report in week 35 that one “*Salmonella* sp.” reported in week 33 has been confirmed as “*S. Anatum*”). This updated information is submitted with the next weekly NESP report form.

All data sent to NESP are aggregated by province and pathogen and do not contain any patient identifiers, locators, or other confidential information. NESP partners endeavor to include only the number of isolates from new cases identified at the laboratory that week, or updates to previously reported numbers. To avoid duplication, the provincial laboratories attempt to identify multiple, repeat, or follow-up specimens from the same individual, and consider all identical isolates from the same patient that are collected over a 3-month period as a single case.

### **Data Analysis and Dissemination**

Data analysis is conducted weekly by NESP 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 5-year median.

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

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

### **Limitations**

It should be noted that there are some inherent limitations of these data. For some organisms the number of isolates reported to NESP is a subset of laboratory isolations and may not reflect the incidence of disease at the provincial or national level. For example, *Campylobacter* isolates are not routinely forwarded to provincial or central reference laboratories for further testing beyond genus/species characterizations and are therefore greatly under-represented in NESP. By contrast, *Salmonella* and *E. coli* O157 isolates captured by NESP are more representative of the true incidence of disease in Canada, as the number of cases reported to CNDSS and isolates reported to NESP show a high degree of concurrence for both diseases. There may be over-reporting of organisms in NESP due to reporting of multiple specimens from a single patient, but efforts are made to minimize this occurrence. Information regarding extra-intestinal isolation sites and foreign travel are not consistently reported to NESP from all laboratories and therefore any interpretation should be considered with caution.

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

[NML.Enterics@phac-aspc.gc.ca](mailto:NML.Enterics@phac-aspc.gc.ca)

[NESP@phac-aspc.gc.ca](mailto:NESP@phac-aspc.gc.ca)

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

## Laboratory-confirmed Isolate Counts & Incidence Rates

In 2015 provincial laboratories reported the results of 16,104 isolates of enteric pathogens to NESP, a slight decrease from the average number of notifications in the previous 5 years (16,416). The most frequently reported enteric pathogen group was *Salmonella*, followed by enteric viruses (Norovirus, Hepatitis A, Rotavirus and Adenovirus) and enteric parasites (*Giardia*, *Cryptosporidium*, *Entamoeba histolytica/dispar* and *Cyclospora*) (Table 1). A complete list of organisms isolate counts reported to NESP by province and territory in 2015 is shown in Appendix 2.

**Table 1. Number of isolates reported to NESP by major organism group per province or territory, 2015**

GROUP	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	TOTAL	% OF TOTAL ISOLATES REPORTED
<i>Campylobacter</i> <sup>1</sup>	356	301	142	73	130	178	165	80	38	46	.	7	.	1514	9.4%
<i>E. coli</i> <sup>2</sup>	110	99	74	40	161	110	5	4	4	10	8	0	.	625	3.9%
<i>Listeria</i>	13	5	1	3	61	28	4	8	1	1	.	.	.	125	0.8%
<i>Salmonella</i>	1196	1148	273	237	3003	1380	187	170	21	80	5	16	.	7716	47.9%
<i>Shigella</i>	147	87	11	20	238	224	6	5	.	1	.	.	.	739	4.6%
<i>Vibrio</i>	27	31	2	1	15	5	3	1	1	.	.	.	.	86	0.5%
<i>Yersinia</i>	70	61	14	7	154	65	2	2	.	1	7	1	.	384	2.4%
Parasites <sup>1</sup>	257	12	120	151	686	342	113	98	11	28	19	2	.	1847	11.5%
Viruses <sup>1</sup>	227	192	205	103	1008	700	188	179	76	187	1	.	.	3066	19.1%
<b>Total</b>	2403	1936	842	635	5456	3032	673	547	160	354	40	26	0	16104	.

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

<sup>2</sup> *E. coli* includes O157 serotypes (379 cases), non-O157 serotypes (229 cases), and non-typed VTEC (18 cases).

Annual national incidence rates for the groups of enteric pathogens reported to NESP between 2010 and 2015 are shown in Table 2 and Appendix 1. Isolates of *E. coli* O157, *Listeria monocytogenes*, *Salmonella* and *Shigella* are routinely forwarded to provincial microbiology laboratories, while isolates for *Campylobacter*, *Yersinia*, enteric parasites (*Giardia*, *Cryptosporidium*, *Entamoeba histolytica/dispar* and *Cyclospora*) and enteric viruses (Norovirus, Rotavirus and Adenovirus) are not routinely reported to the provincial or central reference laboratories. As such, NESP incidence rates are considered to be reflective of the true incidence rate for those routinely reported pathogens enabling the calculation of provincial and territorial incidence rates as shown in Table 3.

**Table 2. Annual national totals and rates (per 100,000) for enteric pathogens and organism groups reported to NESP, 2010-2015**

GROUP	2010		2011		2012		2013		2014		2015	
	Total	Rate <sup>1</sup>										
<i>E. coli</i> O157 <sup>2</sup>	405	1.19	481	1.40	486	1.39	472	1.34	458	1.28	378	1.05
<i>Listeria</i> <sup>3</sup>	.	.	132	0.38	124	0.36	117	0.33	133	0.37	125	0.35
<i>Salmonella</i>	7254	21.25	6804	19.74	6980	20.01	6270	17.77	7851	22.00	7716	21.44
<i>Shigella</i>	739	2.17	861	2.50	988	2.83	621	1.76	681	1.91	739	2.05
<i>Campylobacter</i>	1837	5.38	1938	5.62	1994	5.72	1866	5.29	1676	4.70	1514	4.21
<i>Vibrio</i>	51	0.15	47	0.14	61	0.17	48	0.14	82	0.23	86	0.24
<i>Yersinia</i>	341	1.00	381	1.11	322	0.92	278	0.79	341	0.96	384	1.06
Parasites	1585	4.64	1190	3.45	1320	3.78	1665	4.72	1811	5.08	1847	5.13
Viruses	4662	13.66	4441	12.88	4523	12.97	4058	11.50	2934	8.22	3066	8.55

<sup>1</sup>Rates calculated using the population estimates for Canada as reported by Statistics Canada.

<sup>2</sup>Only cases of *E. coli* O157 are included in this table; additional details about *E. coli* non-O157 are outlined in the *E. coli* section of this report.

<sup>3</sup>Reporting of *Listeria monocytogenes* to NESP began in July 2010.

**Table 3. Rates<sup>1</sup> (per 100,000) of infection per province/territory for select groups of pathogens routinely reported to NESP, 2015**

GROUP	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU
<i>E. coli</i> O157 <sup>2</sup>	0.81	1.97	1.05	1.31	1.04	0.81	0.66	0.42	2.73	0.19	8.05	.	.
<i>Listeria</i>	0.28	0.12	0.09	0.23	0.44	0.34	0.53	0.85	0.68	0.19	.	.	.
<i>Salmonella</i>	25.43	27.22	23.97	18.25	21.68	16.66	24.80	17.99	15.00	15.15	13.41	36.16	.
<i>Shigella</i>	3.13	2.06	0.97	1.54	1.72	2.70	0.80	0.53	.	0.19	.	.	.

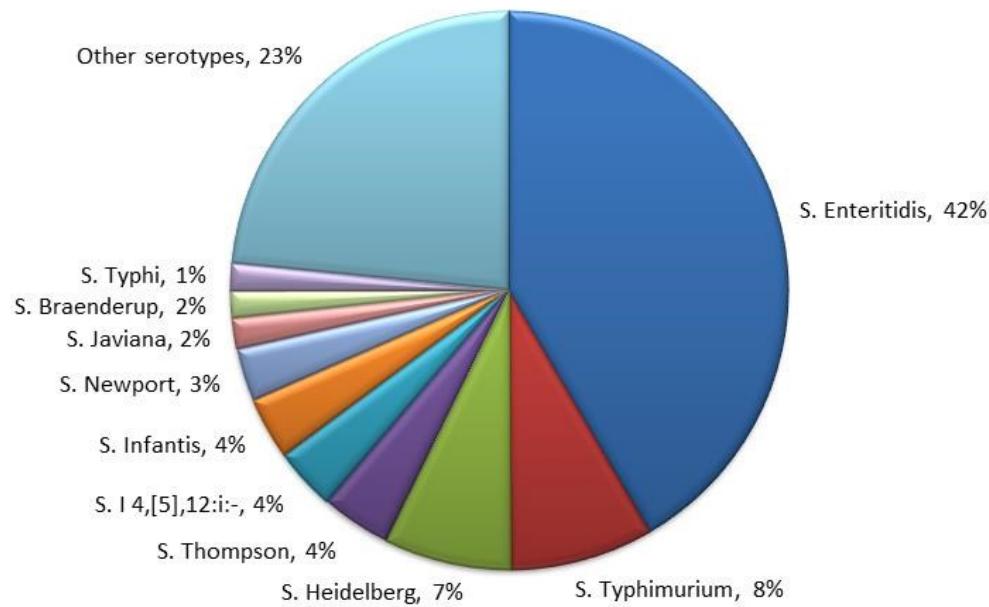
<sup>1</sup>Rates calculated using the population estimates for Canada as reported by Statistics Canada.

<sup>2</sup>Only cases of *E. coli* O157 are included in this table, as *E. coli* non-O157 is not consistently reported by provinces and territories.

## Salmonella

A total of 7,716 *Salmonella* isolate results representing 241 different serotypes were reported to NESP in 2015. *Salmonella Enteritidis* accounted for 42% of all human salmonellosis, and together with the 9 remaining most common serotypes (Figure 1), they account for 77% of all *Salmonella* infections reported to NESP in 2015. National, provincial and territorial case counts for *Salmonella* reported in 2015 are shown in Table 4 and Appendix 2.

**Figure 1. Proportion of *Salmonella* serotypes causing human illness as reported to NESP, 2015 (n=7,716)**

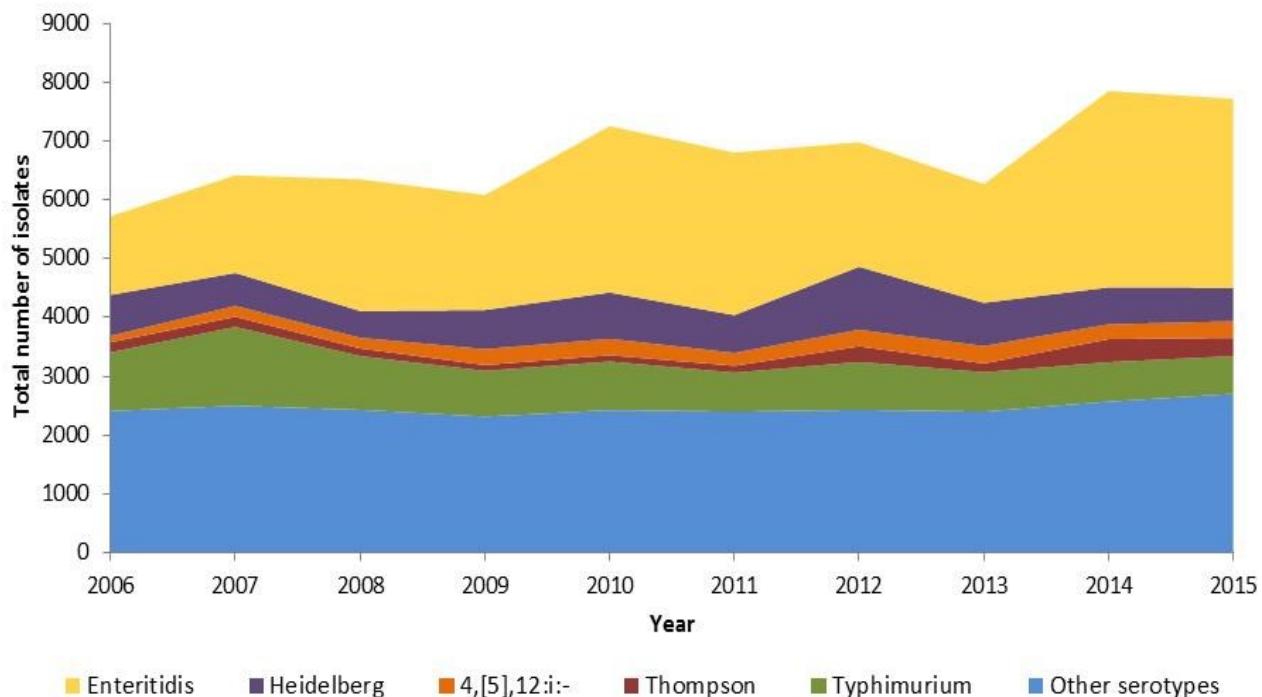


<sup>1</sup> Other serotypes (1,810 isolates) were divided among 231 serotypes and 40 isolates were reported as unspecified *Salmonella* species.

**Table 4. Number of isolates reported to NESP per province and territory of the ten most commonly reported *Salmonella* serotypes, 2015**

Serotype	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YK	NT	NU	TOTAL	% of <i>Salmonella</i> Total
Enteritidis	612	626	133	95	1052	471	73	87	14	37	4	6	.	3210	42
Typhimurium	61	68	29	19	288	153	11	7	.	4	.	2	.	642	8
Heidelberg	61	36	14	8	203	194	28	18	3	7	.	.	.	572	7
Thompson	9	11	1	3	196	80	2	5	3	.	.	.	.	311	4
ssp I 4,[5],12:i:-	37	53	13	1	114	53	5	3	.	1	.	.	.	280	4
Infantis	37	29	6	13	135	47	7	3	1	1	.	.	.	279	4
Newport	37	22	7	17	92	33	14	7	.	6	.	.	.	235	3
Javiana	18	20	2	5	49	30	3	6	.	3	.	.	.	136	2
Braenderup	15	16	5	1	69	15	.	1	.	1	.	.	.	123	2
Typhi	17	27	1	5	62	8	.	.	.	.	.	1	.	121	2
Total	904	908	211	167	2260	1084	143	137	21	60	4	9	0	5908	77

Compared to the average number of *Salmonella* notifications received between 2010 and 2014 (7,032 cases), there was a 10% increase observed in 2015 (7,716 in 2015) (Figure 2). While *S. Enteritidis* has remained the top serotype over this time period, changes were observed in *S. Typhimurium* and *S. Heidelberg* which led them to switch in ranking in 2012 and 2013 (Table 5). New to the top 10 group is *S. Braenderup* which ranked 9<sup>th</sup> in 2015.

**Figure 2. Annual counts between 2006 and 2015 for the top 5 *Salmonella* serotypes reported in 2015 to NESP**

**Table 5. National total counts (overall rank) for the ten most commonly reported *Salmonella* serotypes to NESP in 2015, their ranking in previous years (2010-2014) and other serotypes that dropped from the top 10 serotypes within each year.**

Serotype	2010	2011	2012	2013	2014	2015
Enteritidis	2828 (1)	2763 (1)	2117 (1)	2019 (1)	3337 (1)	3210 (1)
Typhimurium	827 (2)	661 (2)	814 (3)	668 (3)	671 (2)	642 (2)
Heidelberg	787 (3)	641 (3)	1072 (2)	733 (2)	628 (3)	572 (3)
Thompson	107 (7)	118 (8)	265 (5)	149 (6)	392 (4)	310 (4)
ssp I 4,[5],12:i:-	278 (4)	219 (4)	281 (4)	299 (4)	251 (5)	280 (5)
Infantis	106 (8)	185 (7)	184 (6)	116 (8)	164 (7)	279 (6)
Newport	146 (6)	195 (6)	153 (7)	153 (7)	224 (6)	235 (7)
Javiana	90 (12)	77 (12)	87 (12)	113 (9)	133 (9)	136 (8)
Braenderup	73 (15)	78 (11)	98 (10)	57 (18)	71 (14)	123 (9)
Typhi	180 (5)	196 (5)	144 (8)	134 (7)	140 (8)	121 (10)
Hadar	95 (10)	75 (13)	70 (14)	73 (12)	61 (16)	42 (19)
Oranienburg	104 (9)	52 (18)	55 (18)	64 (13)	81 (11)	68 (14)
Paratyphi A	91 (11)	94 (10)	79 (13)	73 (12)	64 (15)	77 (13)
Saintpaul	88 (13)	101 (9)	94 (11)	91 (10)	131 (10)	108 (11)
ssp I 4,[5],12:b:-	90 (12)	62 (15)	108 (9)	59 (17)	40 (20)	48 (18)

PulseNet Canada applies molecular methods, including PFGE, to differentiate *Salmonella* subtypes in real-time and to identify case clusters. For some serotypes PFGE does not provide sufficient discriminatory power to fully differentiate between strains. Therefore, for *S. Enteritidis* and *S. Heidelberg*, phage typing with additional PulseNet Canada molecular data is used for detecting trends and potential clusters. Although phage types are not reported to NESP on a weekly basis, they have been used to identify long-term trends, to inform PulseNet Canada surveillance and outbreak response activities, and for provincial-level activities. Although valuable, phage typing is expected to be phased out in 2017 as more refined genomic methods are implemented. Appendix 3 contains a list of all *Salmonella* phage types reported by the NML in 2015.

## *Salmonella* Enteritidis

In 2015, 3,210 isolates of *S. Enteritidis* were reported to NESP representing approximately 42% of all *Salmonella* isolates. The incidence rate observed in 2015 was 49% higher (8.9 cases per 100,000 population) relative to the 2006-2010 baseline period (6.0 cases per 100,000 population) and slightly lower compared to the annual incidence rate reported in 2014 (9.4 per 100,000 population) (Figure 3).

The 3 most commonly reported phage types (PT) for *S. Enteritidis* continued to be PT 8, PT 13a and PT 13 (Figure 4). In 2015, PT 35 replaced PT 64 as the fourth most commonly reported phage type. These four phage types represent 64% of all *S. Enteritidis* isolates (Figure 5). Decreases in total isolate counts were also observed between 2014 and 2015 for PT 8 (37% decrease) and PT 13 (22% decrease), while PT 13a increased 86% between 2014 and 2015 (Figure 4).

## *Salmonella* Typhimurium

Compared to the baseline period (2006-2010), a 39% decrease in the incidence of *S. Typhimurium* cases was noted in 2015 (2.9 versus 1.8 cases per 100,000 population, respectively). Although *S. Typhimurium* continues to rank among the top 3 most common serotypes causing human salmonellosis in Canada, it represents only 8% of all *Salmonella* isolates reported to NESP in 2015 (Table 5).

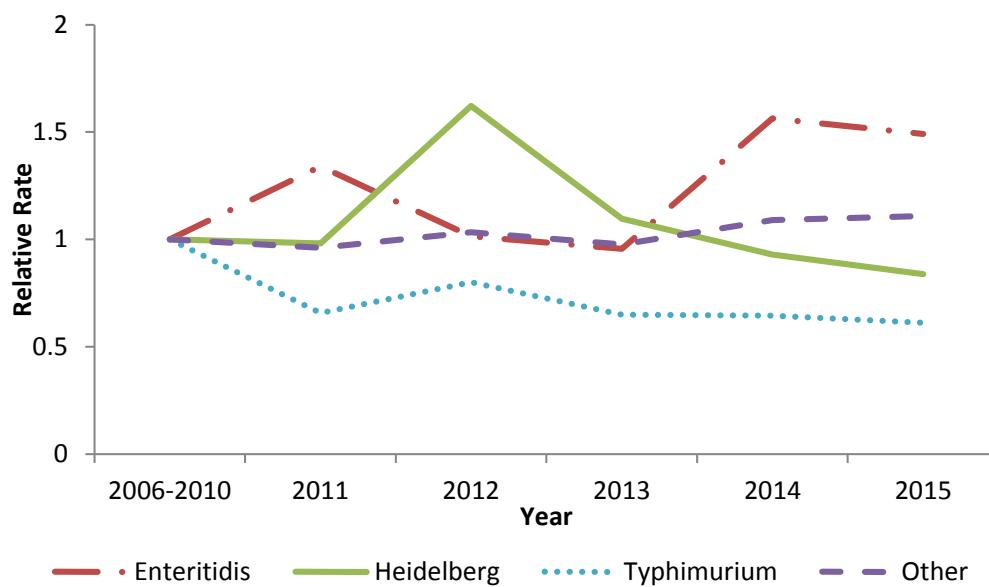
Changes among the top 4 most commonly reported phage types for *S. Typhimurium* was observed in 2015. While the top 4 phage types reported to NESP in 2014 were PT 104 (81 isolates), PT 108 (58 isolates), PT 10 (54 isolates) and PT 104b (43 isolates), in 2015 these changed to PT 193 (97 isolates), PT 108 (94 isolates), PT 104 (51 isolates) and PT 104b (43 isolates). These four phage types represented 47% of all *S. Typhimurium* isolates reported to NESP in 2015 (Figure 5). While the relative frequency of PT 104b remained the same between these two years, a large increase in reporting was observed for PT 193 (185%) and PT 108 (62%) in 2015 compared to 2014 (Figure 4).

## *Salmonella* Heidelberg

*Salmonella* Heidelberg, the third most common serotype in Canada, represented 7% of all human *Salmonella* isolates reported to NESP in 2015. Despite a notable increase in reported isolates in 2012, the 2015 overall incidence (1.6 per 100,000 population) decreased 16% compared to the baseline period (1.9 per 100,000 population between 2006 and 2010) (Figure 3).

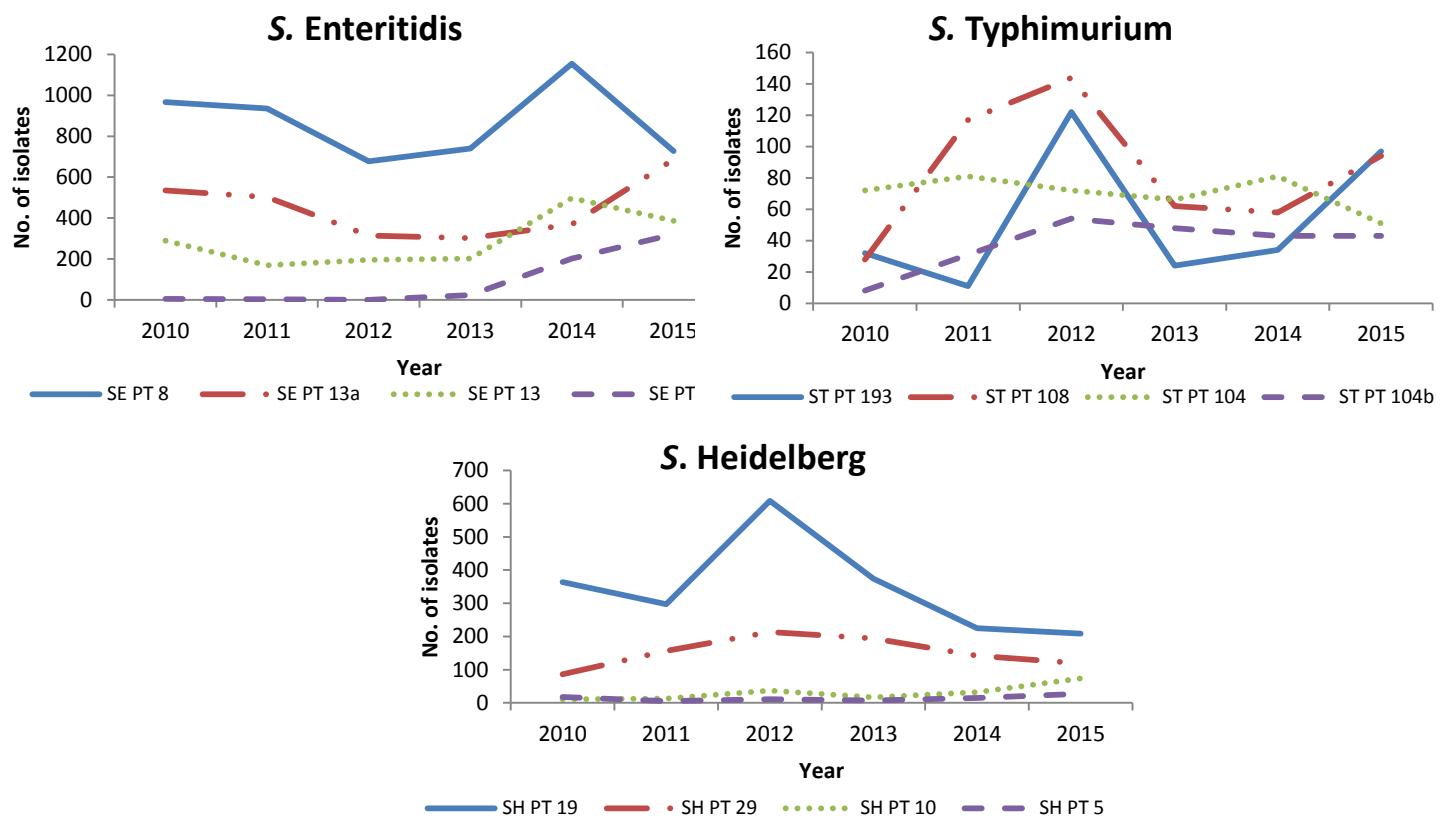
PTs 19, 29, 10 and 5 were the four most commonly identified among *S.* Heidelberg isolates, representing 74% of all isolates reported to NESP (Figure 4 and Figure 5). The frequency for these phage types has remained relatively stable over time, with the exception of PT 10 which increased from 11 isolates in 2010 to 74 isolates in 2015, representing a 131% increase between these years (Figure 4)

**Figure 3. Relative incidence rates<sup>1</sup> of *S. Enteritidis*, *S. Heidelberg*, *S. Typhimurium* and other *Salmonella* serotype reported to NESP by Year, 2011-2015 compared to the 2006-2010 baseline period.**

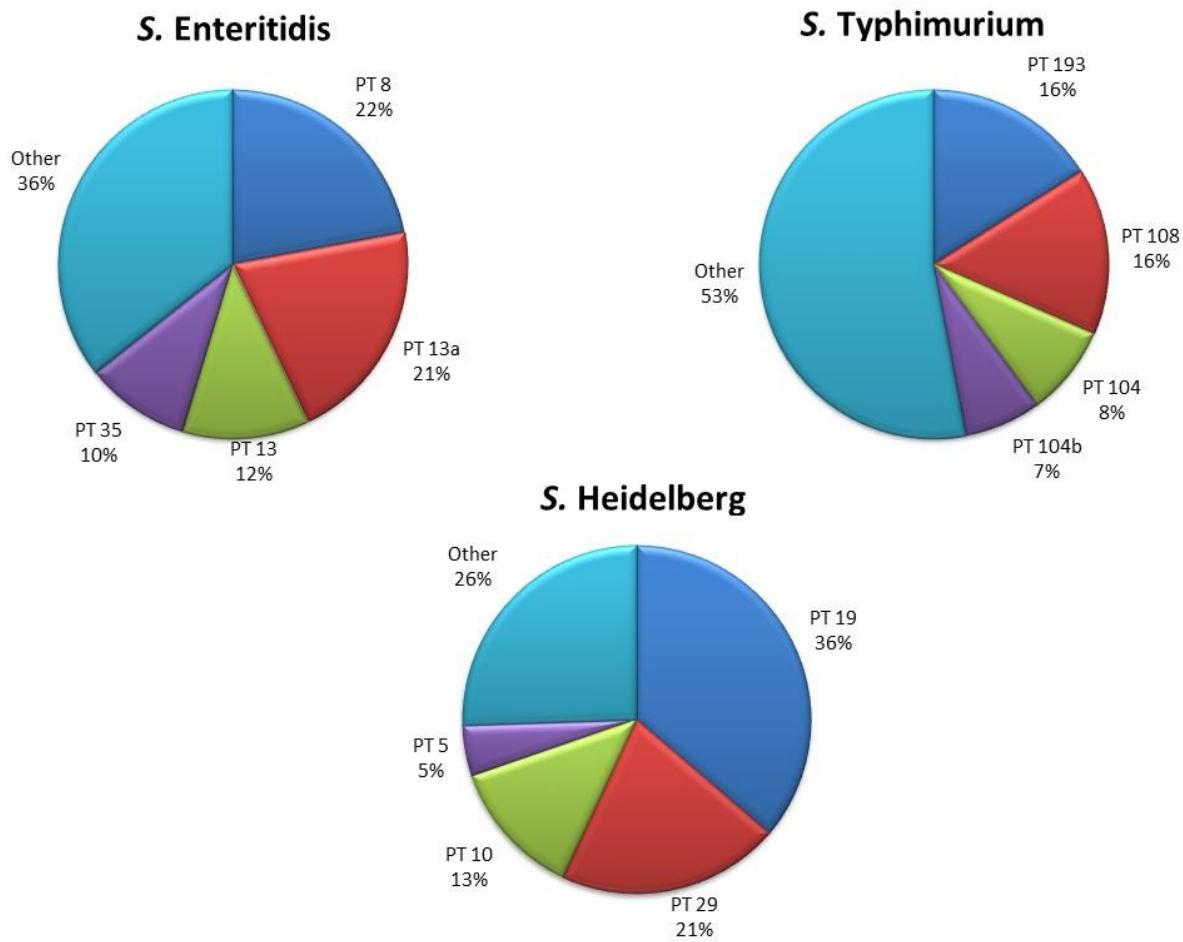


<sup>1</sup> Rates are compared to the 2006-2010 baseline period.

**Figure 4. Total number of isolates for the four most common phage types of *S. Enteritidis* and *S. Typhimurium* and *S. Heidelberg* as reported by the National Microbiology Laboratory, 2010-2015**



**Figure 5. Distribution of phage types for *S. Enteritidis*, *S. Typhimurium* and *S. Heidelberg* in 2015 as reported by the National Microbiology Laboratory<sup>1</sup>**



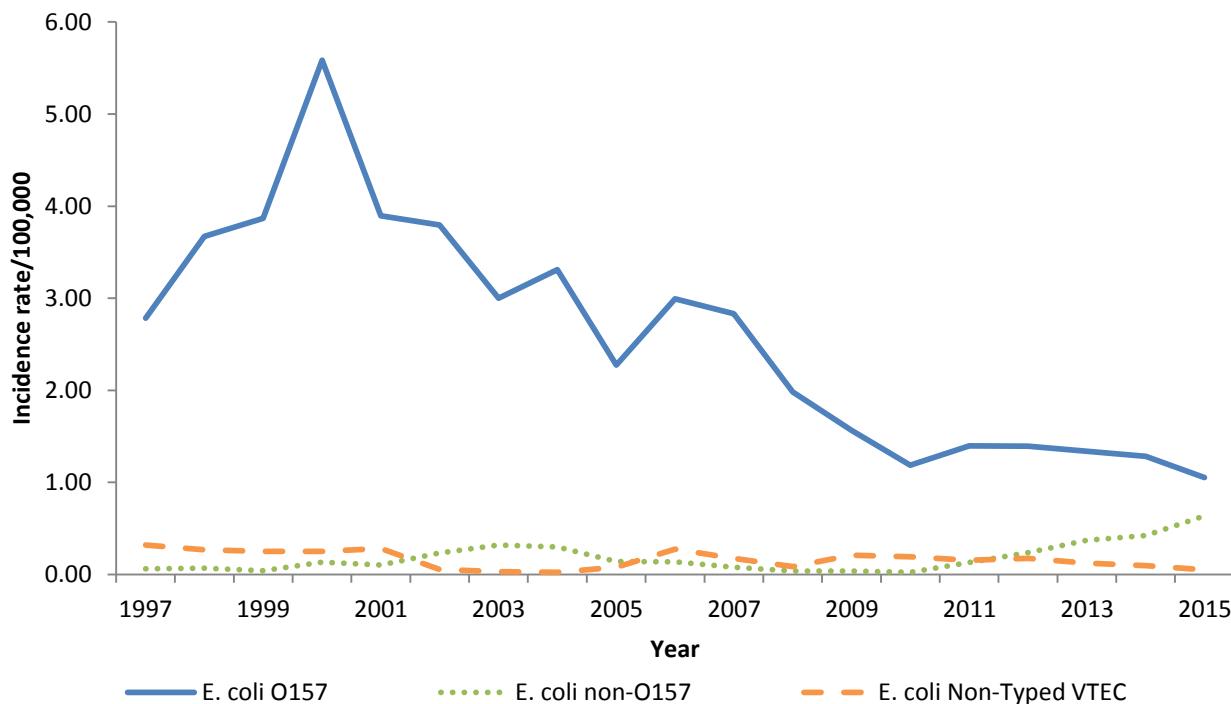
<sup>1</sup> Pie chart totals may exceed 100% due to rounding

## *Escherichia coli*

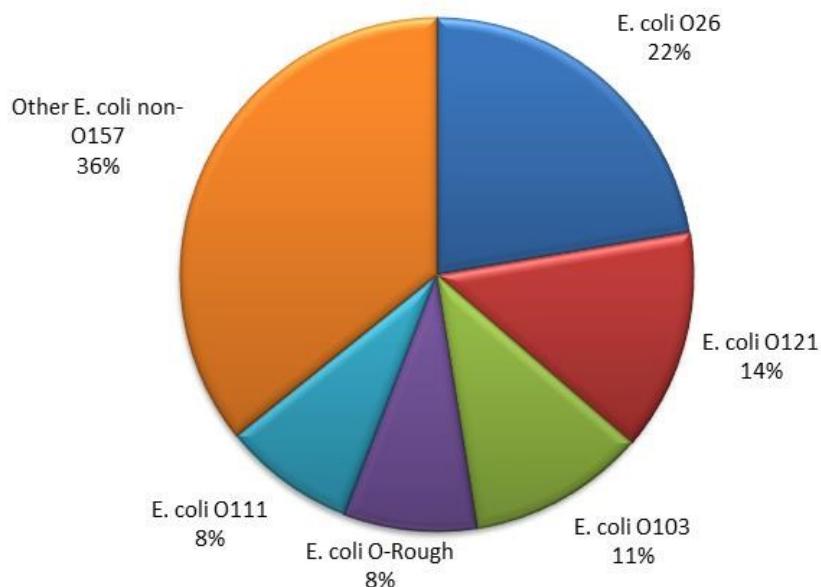
The highest incidence rate of verotoxigenic *E. coli* (VTEC) O157 was observed in 2000 with a total of 5.6 cases per 100,000 population reported to NESP (Figure 6). Since then, there has been a consistent decline with the 2015 incidence rate being the lowest observed to date (1.1 cases per 100,000 population). A continued increase in the incidence of non-O157 isolates has been observed since 2012 (0.6 cases per 100,000 population in 2015, the highest to date) (Figure 6). Of note however, *E. coli* non-O157 are reported less consistently than *E. coli* O157 to NESP by the provincial laboratories and that the observed increase is likely as a result of the recognition of the importance of non-O157 VTEC infections and therefore a reflection of changes in testing practices by some provincial laboratories.

Among the non-O157, in 2015 64% of these isolates were represented by 5 serotypes: *E. coli* O26, *E. coli* O121, *E. coli* O103, *E. coli* O-ROUGH, and *E. coli* O111 (Figure 7). Since 2011, steady increases have been observed in the incidence rates related to these serotypes, particularly for *E. coli* O26 which has increased from 0.01 cases per 100,000 population in 2011 to 0.11 cases per 100,000 population in 2015 (Figure 8). As mentioned above, these increases are likely due, in part, to testing practices by provincial laboratories. All *E. coli* serotypes data reported to NESP is summarized in Appendix 2; serotype information for confirmed non-O157 VTEC isolates sent to the NML in 2015 is provided in Appendix 4.

**Figure 6. Incidence rate of *E. coli* O157 , *E. coli* non-O157, & *E. coli* Non-Typed Serotypes reported to NESP, 1997-2015**

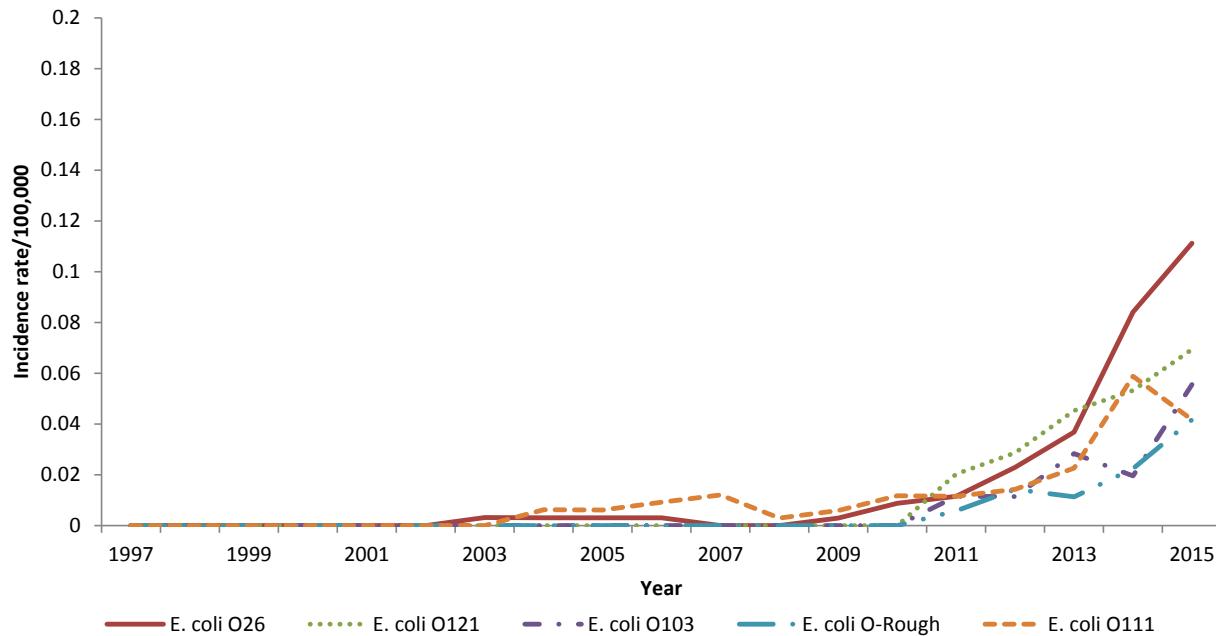


**Figure 7. Distribution of *E. coli* non-O157 serotypes reported to NESP in 2015.<sup>1</sup>**



<sup>1</sup> Pie chart totals may exceed 100% due to rounding

**Figure 8. Incidence rate of the top 5 *E. coli* non-O157 serotypes reported to NESP, 1997-2015**



## *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 to NESP. In 2015, 125 isolates (0.35 cases per 100,000 population) were reported. The majority of these were isolated from blood samples (89%) followed by cerebrospinal fluid (6%) (Table 6). Jurisdiction specific reporting of *Listeria monocytogenes* is presented in Table 1.

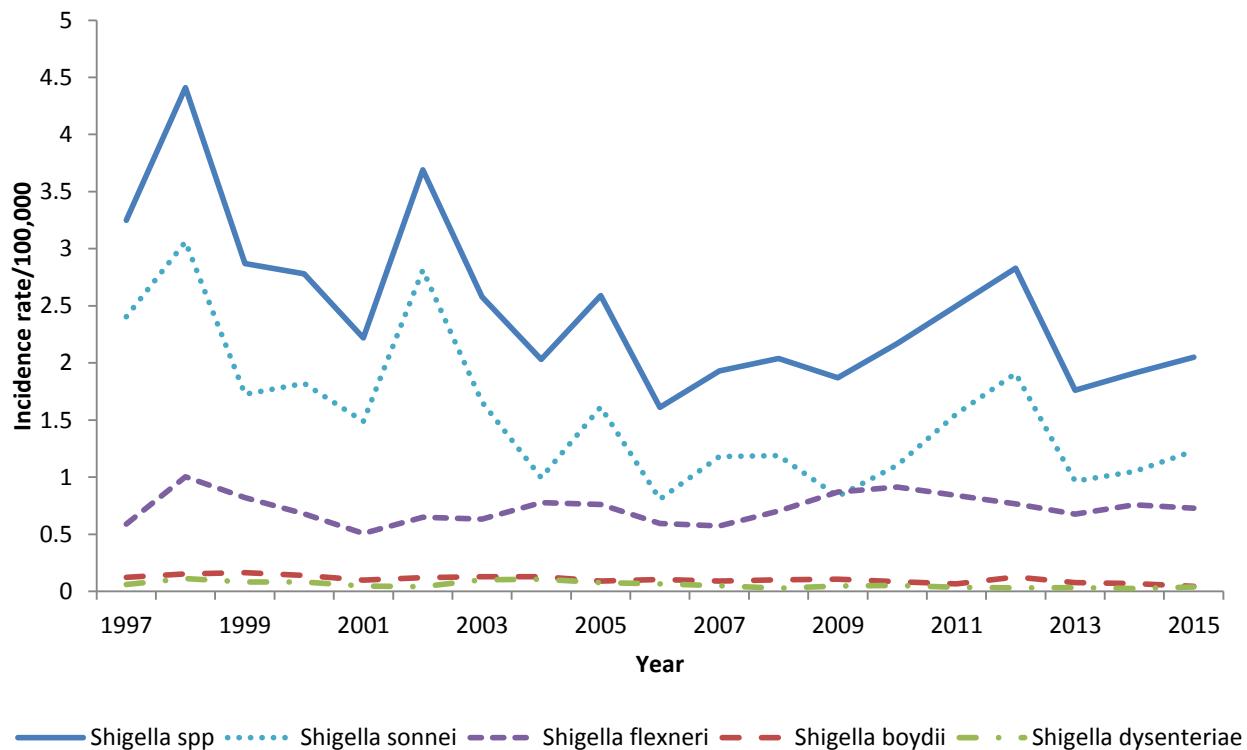
**Table 6. Collection site of *L. monocytogenes* isolates as reported to NESP, 2015**

Site	No. Isolates	Percent (%)
Blood	111	88.8
Cerebrospinal fluid	8	6.4
Other tissue or fluid <sup>1</sup>	6	4.8
Total	125	100.0

<sup>1</sup>Pleural fluid, abscess and lymph node biopsy

## *Shigella*

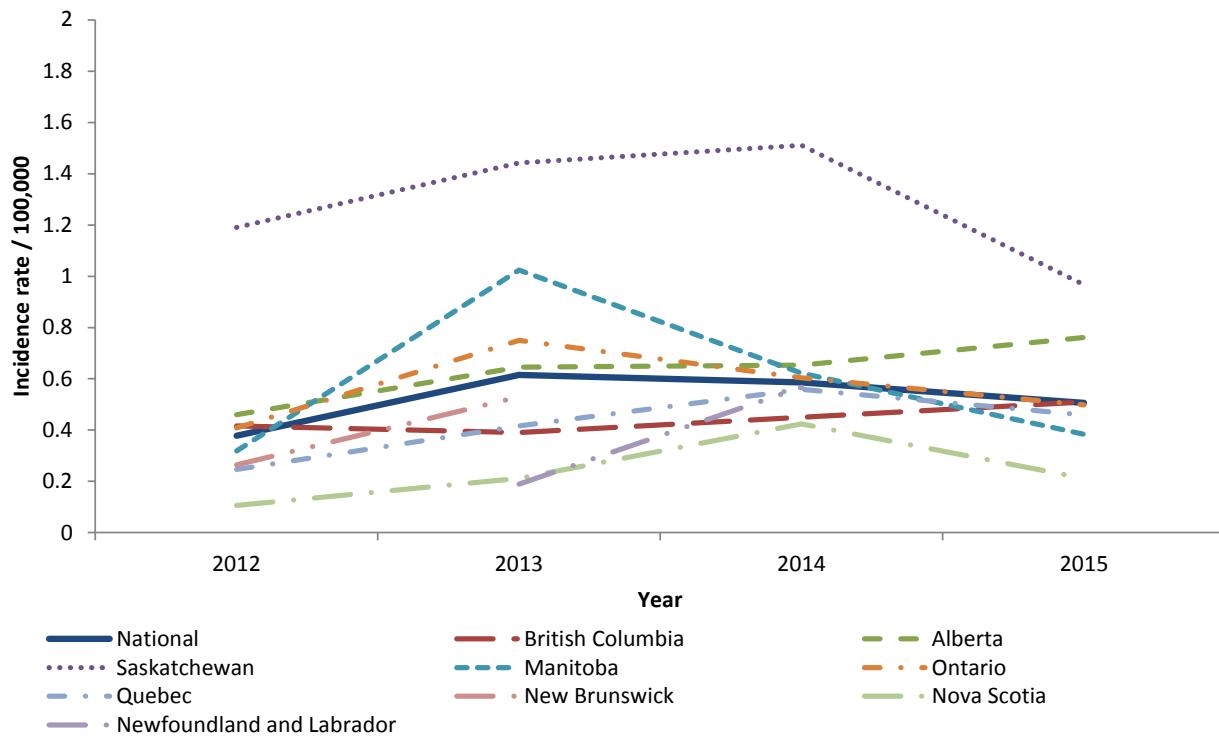
There were 739 *Shigella* isolates reported to NESP in 2015, a rate of 2.1 cases per 100,000 population compared to an average of 2.23 cases per 100,000 reported between 2010 and 2014 (Figure 9). Of the total *Shigella* reported, 60% were *Shigella sonnei* (442 isolates) and 35% *Shigella flexneri* (262 isolates). Incidence trends for *Shigella* are driven by trends observed within *Shigella sonnei* isolates, leading to trends over time showing an overall decrease (Figure 9). However, for the other *Shigella* species, incidence trends over time have remained relatively stable with an incidence of 0.73 cases per 100,000 for *Shigella flexneri* and 0.04 cases per 100,000 for both *Shigella boydii* and *Shigella dysenteriae* observed in 2015 (Figure 9).

**Figure 9. Incidence rate of *Shigella* species reported to NESP, 1997-2015**

## Hepatitis A

NESP was expanded to include Hepatitis A as of July 2012 to provide timely national surveillance for multi-jurisdictional outbreak detection. Overall, Hepatitis A incidence has remained relatively stable with 0.4 cases per 100,000 population reported in 2012 compared to 0.5 cases per 100,000 population in 2015 (Figure 10). At the provincial level, similar trends have been observed with incidence remaining similar in 2015 as that reported in 2012, including those provinces that experienced a slight increase in 2013 (Manitoba, New Brunswick, and Ontario) (Figure 10). Of note, the incidence for Hepatitis A observed in Saskatchewan (Figure 10) is above the national incidence, with a reported incidence in 2015 of 1.0 case per 100,000 compared to 0.5 cases per 100,000, respectively. This has been observed since surveillance began in 2012.

**Figure 10. National and provincial incidence rates of Hepatitis A reported to NESP, 2012-2015.**



## Isolates Collected from Extra-intestinal Isolation Sites

The number of isolates collected from extra-intestinal sites (excluding *L. monocytogenes*) reported to NESP in 2015 is outlined in Table 7. Although information regarding extra-intestinal isolation sites is collected by NESP, these data are not consistently reported to provincial laboratories and therefore are not adequately represented in the NESP report.

**Table 7. Number of isolates collected from extra-intestinal sites as reported to NESP, 2015**

Organism	Blood	Urine	Other <sup>1</sup>	Total/Overall	Percent (%)
<b>Campylobacter</b>	<b>40</b>	<b>0</b>	<b>2</b>	<b>42/1514</b>	<b>2.8</b>
<i>coli</i>	3			3/139	2.2
<i>fetus</i> ssp <i>fetus</i>	12		1	13/40	32.5
<i>jejuni</i>	20			20/1154	1.7
<i>lari</i>	1			1/18	5.6
<i>urealyticus</i>	2			2/3	66.7
Other species <sup>2</sup>	2		1	3/160	1.9
<b><i>Listeria monocytogenes</i></b>	<b>111</b>	<b>0</b>	<b>14</b>	<b>125/125</b>	<b>100.0</b>
<b><i>Salmonella</i> serotype</b>	<b>339</b>	<b>206</b>	<b>34</b>	<b>579/7717</b>	<b>7.5</b>
Agona	2	1		3/63	4.8
Anatum		2		2/33	6.1
Bareilly	1	1		2/28	7.1
Bovismorbificans		3		3/24	12.5
Braenderup	1	1		2/123	1.6
Brandenburg		1	2	3/15	20.0
Bredeney	1	1		2/2	100.0
Choleraesuis	2			2/3	66.7
Derby		2		2/35	5.7
Dublin	10	1		11/26	42.3
Ealing		2		2/6	33.3
Enteritidis	104	49	16	169/3209	5.3
Hadar		4		4/42	9.5
Havana	1	1		2/13	15.4
Heidelberg	61	31	3	95/571	16.6
Infantis	3	14	1	18/279	6.5
Javiana	5	4		9/136	6.6
Kentucky		2		2/32	6.3
Mbandaka	2	3		5/35	14.3
Montevideo		2		2/26	7.7
Muenchen		4		4/91	4.4
Newport	2	4		6/235	2.6
Oranienburg	7	3		10/68	14.7
Panama	2			2/27	7.4
Paratyphi A	31			31/77	40.3
Paratyphi A var Java	1	2		3/57	5.3
Poona	3			3/15	20.0
Reading	3			3/48	6.3
Saintpaul		6	1	7/108	6.5

Organism	Blood	Urine	Other <sup>1</sup>	Total/Overall	Percent (%)
Sandiego	2	1		3/26	11.5
Schwarzengrund	1	3		4/30	13.3
Senftenberg		3	2	5/25	20.0
Stanley	2	1		3/66	4.5
Thompson	10	7	4	21/311	6.8
Typhi	50			50/121	41.3
Typhimurium	7	6	2	15/642	2.3
Virchow	5			5/30	16.7
ssp I 4,[5],12:b:-	2			2/48	4.2
ssp I 4,[5],12:i:-	2	3	1	6/280	2.1
ssp I 9,12:-:-	2			2/15	13.3
ssp I Rough-O:-:-		8		8/16	50.0
ssp IIIb		2		2/3	66.7
Other serovars <sup>3</sup>	14	28	2	44/679	6.5
<b>Shigella species</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>1/739</b>	<b>0.1</b>
<i>flexneri</i>	1			1/262	0.4
<b>Vibrio species</b>	<b>1</b>	<b>0</b>	<b>6</b>	<b>7/85</b>	<b>8.2</b>
<i>alginolyticus</i>			3	3/5	60.0
<i>cholerae</i>	1		2	3/15	20.0
<i>parahaemolyticus</i>			1	1/61	1.6
Total	492	206	56	<b>754/16109</b>	4.7

<sup>1</sup> Other sites include: **Abcess:** *S. Enteritidis* (1), *S. Thompson* (1), *L. monocytogenes* (1); **Abdominal fluid:** *S. Thompson* (1); **Abdominal tissue:** *S. Typhimurium* (1); **Abdominal wound swab:** *S. Enteritidis* (1); **Bartholin's gland:** *S. Thompson* (1); **Bile:** *S. Heidelberg* (1); **Bone:** *S. Brandenburg* (1); **Bronchial washing:** *Vibrio parahaemolyticus* (1); **Buttock:** *S. Enteritidis* (1); **Ear:** *Vibrio alginolyticus* (3), *Vibrio cholera* (1); **Endotracheal secretions:** *S. Heidelberg* (1); **Femur:** *S. Brandenburg* (1); **Gallbladder aspirate:** *S. Paratyphi B* (1); **Ishiorectal secretion:** *S. Weltevreden* (1); **Joint fluid:** *S. Enteritidis* (1); **Liver abscess:** *Entamoeba histolytica/dispar* (1); **Lymph node:** *L. monocytogenes* (1); **Neck fluid:** *S. Enteritidis* (1); **Perianal:** *S. Enteritidis* (2); **Peritoneal fluid:** *L. monocytogenes* (3), *S. Enteritidis* (2), *S. Heidelberg* (1); **Pleural fluid:** *C. rectus* (1), *L. monocytogenes* (1); **Pus:** *S. Saintpaul* (1), *S. Thompson* (1); **Rectal:** ssp I 4,[5],12:i:- (1); **Spinal fluid:** *L. monocytogenes* (8), *Enterovirus* (1); **Sputum:** *S. Senftenberg* (1); **Synovial liquid:** *C. fetus* (1); **Thigh:** *Vibrio cholera* (1); **Tissue:** *S. Enteritidis* (1); **Vertebral spine:** *S. Typhimurium* (1); and **Wound:** *S. Enteritidis* (4), *S. Infantis* (1), *S. Senftenberg* (1).

<sup>2</sup> Other species of *Campylobacter* include those where only a single isolate from an extra-intestinal source was reported: *C. hyointestinalis* (blood), *C. rectus* (pleural fluid) and *C. sp* (blood).

<sup>3</sup> Other *Salmonella* serotypes include those where only a single isolate from an extra-intestinal source was reported: *S. Aberdeen*, *S. Abony*, *S. Adelaide*, *S. Alachua*, *S. Baildon*, *S. Bonariensis*, *S. Chester*, *S. Coeln*, *S. Duesseldorf*, *S. Eastbourne*, *S. Florida*, *S. Gaminara*, *S. Give*, *S. Glostrup*, *S. Hvittingfoss*, *S. Johannesburg*, *S. Kiambu*, *S. Koblenz*, *S. Liverpool*, *S. Lomalinda*, *S. Miami*, *S. Minnesota*, *S. Mkamba*, *S. Muenster*, *S. Paratyphi B*, *S. Rissen*, *S. Uganda*, *S. Weltevreden*, *S. Worthington*, *S. ssp I* (multiple), *S. ssp II*, *S. ssp IIIa* and *S. ssp IIIb* (multiple).

## Travel-Associated Infections

Information on international travel is rarely reported to provincial laboratories and is therefore greatly under-represented in NESP. A total of 284 cases of enteric infection recorded through NESP were reported as travel-related, representing 1.8% of all pathogens reported to NESP in 2015 (Table 8 & Table 9). The Caribbean and Central America (including Mexico) were the most frequently identified regions accounting for 39% of all reported travel among these cases. Four percent of cases traveled to more than one location, while destination information was not provided for 21% of cases with indicated travel history.

Salmonellosis was the most commonly reported travel-related infection, accounting for 36% of all travel-related infections reported to NESP in 2015. Among these travel-related cases, 49% were infected with *S. Enteritidis* with 54% having reported travel to the Caribbean.

Among the travel-related parasitic infections, 64% (58/91) were giardiasis and 31% were infections with *Entamoeba histolitica/dispar* (31%). Although information on travel destination was only available for less than half of the giardiasis travel-related cases, the majority reported traveling to countries in Africa.

There was a single isolate of *Vibrio cholerae* O1 reported to NESP in 2015, this case reported traveling to India during their exposure period.

**Table 8. Number of infections by geographical region as reported to NESP, 2015**

Geographic Region	No. of Cases (%)
Caribbean	51 (20.0)
Asia	49 (17.3)
Central America	54 (19.1)
Africa	41 (14.4)
South America	5 (1.8)
North America	5 (1.8)
Europe	8 (2.8)
Multiple destinations	12 (4.2)
Destination not identified	59 (20.8)
<b>Total</b>	<b>284 (100)</b>

**Table 9. Number of travel-acquired infections reported to NESP by organism, 2015**

Organism	No. of Cases (% of total travel)	% of Pathogen Total	Country or Region (number of cases >1) <sup>1</sup>
<b><i>Campylobacter</i> species</b>	<b>37 (13.0%)</b>	<b>2.4</b>	
<i>coli</i>	3	2.2	India, Pakistan, Multiple destinations
<i>jejuni</i>	23	2.0	Costa Rica, Cuba, Europe, Hong Kong, India, Italy, Mexico (6), Nepal, Peru, Turkey (2), USA, Multiple destinations (3) and Unknown (3)
<i>jejuni/coli</i>	11	28.9	Argentina, Cuba, Dominican Republic (2), India, Mexico, Spain, and Unknown (4)
<b><i>Escherichia coli</i></b>	<b>4 (1.4%)</b>	<b>0.6</b>	
O157:H7	3	1.1	Cuba, Haiti, and USA
O26:H11	1	40.0	USA
<b><i>Salmonella enterica</i> subsp. <i>enterica</i> serotypes</b>	<b>102 (35.9%)</b>	<b>1.3</b>	
Enteritidis	50	1.6	Cuba (15), Dominican Republic (11), Europe, Indonesia, Jamaica, Mexico (19), Spain, Unknown
Infantis	4	1.4	Cuba (2), Hungary, Mexico
Javiana	7	4.8	Cuba (4), Dominican Republic, Mexico, USA
Newport	5	2.1	India, Indonesia, Mexico (2), Unknown
Paratyphi A	2	2.6	India, Pakistan
Paratyphi B var. Java	2	3.5	Indonesia, Mexico
Saintpaul	2	1.9	Costa Rica, Mexico
ssp I 4,[5],12:i:-	4	1.4	Cuba, Jamaica, Multiple destinations and Thailand
Thompson	3	0.9	Africa, Jamaica, Mexico
Typhi	9	7.4	Bangladesh, India (3), Pakistan (4), Uganda
Typhimurium	5	0.8	Cuba, Ecuador, Mexico, Multiple destinations, South Africa
Other serotypes <sup>2</sup>	9	0.2	Africa, Cuba, India, Mexico (2), Multiple destinations (2), Unknown, Panama
<b><i>Shigella</i> species</b>	<b>14 (4.9%)</b>	<b>1.9</b>	
<i>dysenteriae</i>	1	7.1	Bangladesh
<i>flexneri</i>	1	0.4	Honduras
<i>sonnei</i>	12	2.7	Costa Rica, Cuba, Dominican Republic (2), England, Israel, Jamaica, Mexico, Morocco, Nicaragua, Somalia, Unknown

Organism	No. of Cases (% of total travel)	% of Pathogen Total	Country or Region (number of cases >1) <sup>1</sup>
<b>Vibrio species</b>	<b>2 (0.7%)</b>	<b>2.3</b>	
<i>cholerae</i> O1 bio E1 Tor	1	100	India
<i>parahaemolyticus</i>	1	1.6	Multiple destinations
<b>Yersinia species</b>	<b>1 (0.4%)</b>	<b>0.3</b>	
<i>enterocolitica</i>	1	0.3	Unknown
<b>Parasites</b>	<b>91 (32.0%)</b>	<b>4.9</b>	
<i>Cryptosporidium</i>	3	0.8	Dominican Republic, Multiple destinations (2)
<i>Cyclospora</i>	1	1.9	Mexico
<i>Entamoeba histolytica/dispar</i>	28	4.8	Burundi, Congo (3), Eritrea (3), India, Iraq (2), Poland, Sri Lanka, Sudan, Uganda, Unknown
<i>Entamoeba polecki</i>	1	100	USA
<i>Giardia</i>	58	6.9	Burundi (2), Congo (5), Costa Rica, Cuba, Eritrea (6), Ethiopia, Iran, Iraq, Syria (2), Tanzania (3), Thailand, Uganda, Unknown (32), Multiple destinations
<b>Viruses</b>	<b>33 (11.6%)</b>	<b>1.1</b>	
Hepatitis A	33	18.1	Afghanistan, Africa, Algeria, Bangladesh, Chad (3), Colombia (2), Guatemala, India (7), Lebanon (2), Mali, Mexico (7), Nicaragua, Pakistan (2), Philippines, Sudan, Unknown
<b>Total</b>	<b>284</b>	<b>1.8</b>	

<sup>1</sup> Where more than one case reported travel to a country or region, the number of travelers is indicated in brackets.

<sup>2</sup> Other serotypes includes the *Salmonella* serotypes that were reported as travel-associated by a single case: S. Blockley, S. Braenderup, S. Eastbourne, S. Kentucky, S. Mississippi, S. Panama, S. Reading, S. ssp I 9,12:-:1,5, and S. Telelkebir

**Appendix 1. Comparison of national totals, incidence per 100 000 and proportion captured between the Canadian Notifiable Disease Surveillance System (CNDSS) and the NESP for enteric, food and waterborne diseases, 2015**

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>7</sup> )
	N	Rate per 100,000	N	Rate per 100,000	
<b>2015</b>					
Botulism	12	0.03	-	-	N/A
Campylobacteriosis <sup>1</sup>	9080	25.33	1514	-	16.7
Cholera	3	0.01	3	0.01	100.0
Cryptosporidiosis <sup>1</sup>	872	2.43	379	-	43.5
Cyclosporiasis <sup>1</sup>	333	0.93	54	-	16.2
Giardiasis <sup>1</sup>	3736	10.42	830	-	22.2
Hepatitis A	183	0.51	182	0.51	99.5
Invasive Listeriosis	145	0.40	125	0.35	86.2
Norovirus <sup>1,2,3</sup>	408	8.53	2312	-	N/A
Paralytic Shellfish Poisoning <sup>4</sup>	0	0.00	-	-	N/A
Salmonellosis	7731	21.57	7596	21.11	98.3
Shigellosis	904	2.52	739	2.05	81.7
Typhoid <sup>5</sup>	121	0.34	121	0.33	100.0
Verotoxigenic <i>Escherichia coli</i> Infection	634	1.77	626	1.73	98.7

<sup>1</sup> *Campylobacter*, parasites (*Cryptosporidium*, *Cyclospora* and *Giardia*) and Norovirus are not routinely reported to provincial or central reference laboratories and are greatly under-represented in NESP; therefore no rate was calculated for NESP.

<sup>2</sup> BC, MB, NB, NS, NT, ON, PE, QC, SK and YT did not report on Norovirus in 2015. The populations of these provinces/territories have been removed for rate calculation.

<sup>3</sup> For Norovirus some provinces/territories report only on aggregated outbreak related data; these data are not included here.

<sup>4</sup> AB, MB, NT, QC, and SK did not report on Paralytic Shellfish Poisoning in 2015. The population of these provinces and territory has been removed for rate calculation.

<sup>5</sup> Typhoid includes lab confirmation of *Salmonella* Typhi; *Salmonella* Paratyphi A, B and C are reported under salmonellosis.

<sup>7</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.

**Appendix 2. Species and serotype data reported to NESP by province and territory, 2015**

NESP 2015	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YK <sup>3</sup>	NT	NU	TOTAL
<b>Campylobacter</b>														
<i>C. coli</i>	25	16	10	12	24	41	6	2	2	1				139
<i>C. concisus</i>		1												1
<i>C. curvus</i>							1							1
<i>C. fetus</i> ssp. <i>fetus</i>					8	31		1						40
<i>C. hyoilectinalis</i>		2				13								15
<i>C. insulaenigrae</i>		1												1
<i>C. jejuni</i>	312	278	126	57	83	73	111	41	35	34		7		1157
<i>C. jejuni/coli</i>								33		5				38
<i>C. lari</i>	4		1		3	8		1	1					18
<i>C. rectus</i>						1								1
<i>C. sp</i>				4			47	1		5				57
<i>C. upsaliensis</i>	15	3	5		12	7	1	1		1				45
<i>C. urealyticus</i>						3								3
<b>Total Campylobacter</b>	<b>356</b>	<b>301</b>	<b>142</b>	<b>73</b>	<b>130</b>	<b>178</b>	<b>165</b>	<b>80</b>	<b>38</b>	<b>46</b>	<b>0</b>	<b>7</b>	<b>0</b>	<b>1516</b>
<b>Escherichia coli</b>														
<i>E. coli</i> O2:H undetermined			1											1
<i>E. coli</i> O5:H Nonmotile	1						1							2
<i>E. coli</i> O5:H Nonmotile VTEC		1												1
<i>E. coli</i> O8:H undetermined					1									1
<i>E. coli</i> O8:H49	1													1
<i>E. coli</i> O13:H undetermined							1							1
<i>E. coli</i> O16:H undetermined							1							1
<i>E. coli</i> O25:H4							1							1
<i>E. coli</i> O26	1			1										2
<i>E. coli</i> O26:H Untypable VTEC	1	1												2
<i>E. coli</i> O26:H undetermined			1											1
<i>E. coli</i> O26:H11	7		10		4	4								25
<i>E. coli</i> O26:H11 VTEC		3												3
<i>E. coli</i> O26:H32			1											1
<i>E. coli</i> O26:H Nonmotile	4		1			1								6
<i>E. coli</i> O42:H45	1													1
<i>E. coli</i> O45:H2						1								1
<i>E. coli</i> O49:H7			1											1
<i>E. coli</i> O51:H49						1								1
<i>E. coli</i> O52:H undetermined					1									1
<i>E. coli</i> O62:H2							1							1
<i>E. coli</i> O63:H6			1											1
<i>E. coli</i> O71:H11			1											1
<i>E. coli</i> O71:H Nonmotile			1											1
<i>E. coli</i> O73:H18	1													1
<i>E. coli</i> O73:H45							1							1
<i>E. coli</i> O76:H Nonmotile			1											1

<sup>3</sup> In the Yukon, bacterial case counts (including *Campylobacter*, *E. coli*, *Salmonella* and *Shigella*) are frequently reported through British Columbia, and are therefore not representative of the incidence of disease in the territory.



NESP 2015	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YK <sup>3</sup>	NT	NU	TOTAL
<i>E. coli</i> O172:H Nonmotile	1													1
<i>E. coli</i> O174:H21	1													1
<i>E. coli</i> O177:H11			1											1
<i>E. coli</i> O177:H Nonmotile	1		1											2
<i>E. coli</i> O181:H Undetermined	1													1
<i>E. coli</i> O186:H2	1		1											2
<i>E. coli</i> O186:H Nonmotile VTEC		1												1
<i>E. coli</i> O-Rough:H2						1								1
<i>E. coli</i> O-Rough:H7	1													1
<i>E. coli</i> O-Rough:H8	1										1			2
<i>E. coli</i> O-Rough:H12	1													1
<i>E. coli</i> O-Rough:H18			1											1
<i>E. coli</i> O-Rough:H21	1													1
<i>E. coli</i> O-Rough:H25						1								1
<i>E. coli</i> O-Rough:H Nonmotile	3		3											6
<i>E. coli</i> O-Rough:H undetermined			1											1
<i>E. coli</i> Non-O157 VTEC	5			15		21				9				50
<i>E. coli</i> Non-Typed VTEC	9			5		1					2			17
<i>E. coli</i>				1										1
<b>Total <i>E. coli</i></b>	<b>110</b>	<b>99</b>	<b>74</b>	<b>40</b>	<b>161</b>	<b>110</b>	<b>5</b>	<b>4</b>	<b>4</b>	<b>10</b>	<b>8</b>	<b>0</b>	<b>0</b>	<b>625</b>
<b><i>Listeria</i></b>														
<i>L. monocytogenes</i>	13	5	1	3	61	28	4	8	1	1				125
<b><i>Salmonella</i></b>														
S. Aba								1						1
S. Abaetetuba						2								2
S. Aberdeen					3	2								5
S. Abony							1							1
S. Adelaide	1	1			2	1								5
S. Agbeni		1			1									2
S. Ago					1	2								3
S. Agona	11	14	2	4	24	7		1						63
S. Alachua	2			1	3	1								7
S. Albany					3									3
S. Altona					1									1
S. Anatum	9	4	3	1	11	4		1						33
S. Apeyeme					1									1
S. Arechavaleta					3									3
S. Argentueil					1									1
S. Augustenborg	1													1
S. Bahrenfeld					1									1
S. Baildon		2			3									5
S. Bareilly	4	4			11	7	1	1						28
S. Barranquilla						1								1
S. Benin					1									1
S. Berta				1	3	3				1				8
S. Blockley		1			6	1	1							9



NESP 2015	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YK <sup>3</sup>	NT	NU	TOTAL
S. Infantis	37	29	6	13	135	47	7	3	1	1				279
S. Irumu	1				1									2
S. Isangi	2				3									5
S. Itami										1				1
S. Javiana	18	20	2	5	49	30	3	6		3				136
S. Johannesburg	1				1									2
S. Kedougou	1													1
S. Kentucky	7	3	2		13	6	1							32
S. Kiambu	1	3	1		15									20
S. Kingabwa					1									1
S. Kintambo					1									1
S. Kisarawe			1	2										3
S. Koblenz						1								1
S. Kottbus					3	1								4
S. Krefeld				1	1									2
S. Lagos	1													1
S. Larochelle	1				1									2
S. Lexington					1									1
S. Litchfield	4	2			6	2								14
S. Liverpool	1				1	1								3
S. Livingstone		1												1
S. Lomalinda			1		1						2			4
S. London	2				1	1								4
S. Manhattan	1	2	1	1	7	3								15
S. Mbandaka	2	8		1	16	6	2							35
S. Meleagridis	2					1								3
S. Menston		1												1
S. Miami	1	1	1		2	3								8
S. Michigan	1													1
S. Minnesota	1	2			1	1								5
S. Mississippi	1			1	7	2		1						12
S. Mkamba						1								1
S. Monschau						1								1
S. Montevideo		2	1	1	14	6				2				26
S. Muenchen	5	3	4	2	35	33	3	1		4		1		91
S. Muenster				1	8	1								10
S. Nessziona					7			1						8
S. Newport	37	22	7	17	92	33	14	7		6				235
S. Nigeria	1													1
S. Nima			1											1
S. Norwich	1				8		2							11
S. Ohio		1	1		6	2								10
S. Oranienburg	11	10	2	2	27	13	1	2						68
S. Orientalis					1									1
S. Oslo	2	1		1	5									9
S. Othmarschen					1									1
S. Oxford					1									1
S. Panama	6	4	1	1	9	4	1		1					27





<b>NESP 2015</b>	<b>BC</b>	<b>AB</b>	<b>SK</b>	<b>MB</b>	<b>ON</b>	<b>QC</b>	<b>NB</b>	<b>NS</b>	<b>PE</b>	<b>NL</b>	<b>YK<sup>3</sup></b>	<b>NT</b>	<b>NU</b>	<b>TOTAL</b>
S. ssp IIIb 47:k:z35		1												1
S. ssp IIIb 47:z10:1,5,7	2													2
S. ssp IIIb 47:z10:z35					1									1
S. ssp IIIb 48:c:z		1												1
S. ssp IIIb 48:i:z:[z72]		1												1
S. ssp IIIb 48:r:z					1									1
S. ssp IIIb 50:k:z					1									1
S. ssp IIIb 50:k:z:[z50],[z57],		1												1
S. ssp IIIb 50:k:z:z86					1									1
S. ssp IIIb 50:l,v:-	1													1
S. ssp IIIb 60:z52:z		1												1
S. ssp IIIb 61:c:z35					1									1
S. ssp IIIb 61:i:z53		1												1
S. ssp IIIb 61:l,v:1,5,7	1													1
S. ssp IIIb 61:l,v:1,5,7:[z57]		4												4
S. ssp IIIb 61:r:z53:[z47],[z50]					1									1
S. ssp IIIb 65:k:z53						1								1
S. ssp IIIb Rough-O:k:-:z84		1												1
S. ssp IIIb Rough-O:r:e,n,x,z15	1													1
S. ssp IV 40:z4,z23:-		1												1
S. ssp IV 44:z4,z23:-					3									3
S. ssp IV 48:g,z51:-	1	1			2	1								5
S. ssp IV 48:z4,z32:-	1				1									2
S. ssp IV 50:g,z51:-			1		2									3
S. ssp IV 50:z4,z23:-	1				1									2
S. ssp IV Rough-O:z4,z32:-					1									1
S. ssp VI 48:z10:1,5					1									1
S. sp				4	7		2	1		5				19
<b>Total <i>Salmonella</i></b>	<b>1196</b>	<b>1148</b>	<b>273</b>	<b>237</b>	<b>3003</b>	<b>1380</b>	<b>187</b>	<b>170</b>	<b>21</b>	<b>80</b>	<b>5</b>	<b>16</b>	<b>0</b>	<b>7716</b>

Shigella

NESP 2015	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YK <sup>3</sup>	NT	NU	TOTAL
<i>Shigella flexneri</i> 1	1													1
<i>Shigella flexneri</i> 1a						2								2
<i>Shigella flexneri</i> 1b		4			19	9								32
<i>Shigella flexneri</i> 2	12													12
<i>Shigella flexneri</i> 2a	7	10			14	14								45
<i>Shigella flexneri</i> 2b					1	1								2
<i>Shigella flexneri</i> 3	5													5
<i>Shigella flexneri</i> 3a	3	2			30	53								88
<i>Shigella flexneri</i> 3b	4	2			7	2								15
<i>Shigella flexneri</i> 4	5	2				1								8
<i>Shigella flexneri</i> 4a		1			3	1								5
<i>Shigella flexneri</i> 4c					1									1
<i>Shigella flexneri</i> 6	3	3			5	1								12
<i>Shigella flexneri</i> Prov. SH-104	3				2	4								9
<i>Shigella flexneri</i> var. X						3								3
<i>Shigella flexneri</i> var. Y		3			2			1						6
<i>Shigella sonnei</i>	90	57	9	7	143	128	5	3						442
<i>Shigella</i> sp.	3					1				1				5
<b>Total <i>Shigella</i></b>	<b>147</b>	<b>87</b>	<b>11</b>	<b>20</b>	<b>238</b>	<b>224</b>	<b>6</b>	<b>5</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>739</b>
<b>Vibrio</b>														
<i>Vibrio alginolyticus</i>		2			2			1						5
<i>Vibrio cholerae</i> O1						1								1
<i>Vibrio cholerae</i> O1 Ogawa					1									1
<i>Vibrio cholerae</i> O1 bio E1 Tor					1									1
<i>Vibrio cholerae</i> non-O1/O139	1	4			1	4								10
<i>Vibrio cholerae</i> non-O1/O139/O75/O14			1				1							2
<i>Vibrio fluvialis</i>	1				1									2
<i>Vibrio parahaemolyticus</i>	25	25	1	1	7		2		1					62
<i>Vibrio vulnificus</i>					2									2
<b>Total <i>Vibrio</i></b>	<b>27</b>	<b>31</b>	<b>2</b>	<b>1</b>	<b>15</b>	<b>5</b>	<b>3</b>	<b>1</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>86</b>
<b>Yersinia</b>														
<i>Yersinia bercovieri</i>		1												1
<i>Yersinia enterocolitica</i>	51	47	11	4	154	58	2	2			7	1		337
<i>Yersinia frederiksenii</i>	16	2	1											19
<i>Yersinia intermedia</i>	1	9	2											12
<i>Yersinia kristensenii</i>	1													1
<i>Yersinia pseudotuberculosis</i>	1	1												2
<i>Yersinia rohdei</i>		1												1
<i>Yersinia</i> sp					3		7			1				11
<b>Total <i>Yersinia</i></b>	<b>70</b>	<b>61</b>	<b>14</b>	<b>7</b>	<b>154</b>	<b>65</b>	<b>2</b>	<b>2</b>	<b>0</b>	<b>1</b>	<b>7</b>	<b>1</b>	<b>0</b>	<b>384</b>
<b>Parasites</b>														
<i>Cryptosporidium</i>	17	6	12	36	229	22	18	19	12	7	1			379
<i>Cyclospora</i>	5	1		4	34	9		1						54
<i>Entamoeba histolytica/dispar</i>	182	4	23	22	127	208	1	6			8			581
<i>Entamoeba polecki</i>									0					0

NESP 2015	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YK <sup>3</sup>	NT	NU	TOTAL
Giardia	53	1	85	89	296	103	94	72	6	21	10	2		832
<b>Total Parasites</b>	<b>257</b>	<b>12</b>	<b>120</b>	<b>151</b>	<b>686</b>	<b>342</b>	<b>113</b>	<b>98</b>	<b>18</b>	<b>28</b>	<b>19</b>	<b>2</b>	<b>0</b>	<b>1846</b>
<b>Viruses</b>														
Adenovirus	24	2		19	80			3		1				129
Astrovirus		2			5									7
Enterovirus				8						4				12
Hepatitis A	24	32	11	5	69	38	1	2						182
Norovirus	157	137	120	45	701	660	101	165	68	155	1			2310
Rotavirus	22	19	74	26	153	2	86	9	8	27				426
<b>Total Viruses</b>	<b>227</b>	<b>192</b>	<b>205</b>	<b>103</b>	<b>1008</b>	<b>700</b>	<b>188</b>	<b>179</b>	<b>76</b>	<b>187</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>3064</b>

### **Appendix 3. Phage types of isolates submitted to the NML, 2015**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
	14c		2									2
	31		1	1	3	1						6
	33	5										5
	34					1						1
	38				1							1
	91					1						1
	ATEC-22		1									1
	ATEC-29						1					1
	Untypable					1						1
	<b>Subtotal</b>	<b>6</b>	<b>7</b>	<b>1</b>	<b>5</b>	<b>27</b>	<b>19</b>	<b>0</b>	<b>1</b>	<b>1</b>	<b>0</b>	<b>67</b>
<i>E. coli</i> O157:H Undetermined	14a							1				1
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
<i>E. coli</i> O157:H Untypable	ATEC-23		1									1
	<b>Subtotal</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
<i>E. coli</i> O Rough:H7	K1 Negative					2						2
	K1 Positive	1									1	2
	<b>Subtotal</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>2</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>4</b>
<i>E. coli</i> O Rough:H Nonmotile	K1 Negative	2		2		5		1			2	12
	K1 Positive					1						1
	<b>Subtotal</b>	<b>2</b>	<b>0</b>	<b>2</b>	<b>0</b>	<b>6</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>2</b>	<b>13</b>
<i>E. coli</i> O Untypable:H Nonmotile	K1 Negative										1	1
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>1</b>
<b>Salmonella</b>												
S. Berta	N/A (Resembles Enteritidis 13a)										1	1
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>1</b>
S. Brandenburg	N/A						1					1
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
S. Dublin	N/A	1										1
	<b>Subtotal</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
S. Enteritidis	1	22	47	2	4	118	42	8	8	1	8	260
	1b	4	9	1		9	1					24
	2	4	2		1	17	5		3			32
	3					1	1					2
	3a					1						1
	3b	1										1
	4	3	2		1	24	6		1		1	38
	4a	3	3			4						10
	4b					2	3					5
	6	4	1	1		5	2					13
	6a	6	1			6	2		2			17
	6d					1						1
	7					5	6					11
	7a	1				1						2
	8	112	95	33	24	257	134	30	33	5	4	727
	11b		3	1	2							6
	13	114	59	15	14	71	91	10	6	3	4	387



Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
ATEN-68	1									1		2
ATEN-69							1					1
ATEN-70						1						1
ATEN-71	1					1		1				3
ATEN-72	1											1
ATEN-73							1			1		2
ATEN-74		1										1
ATEN-75		1										1
ATEN-76		1										1
ATEN-77						1						1
ATEN-78		2					1					3
ATEN-79					1							1
ATEN-80						1						1
ATEN-81	1											1
ATEN-82						1						1
ATEN-83		1										1
ATEN-84							1					1
ATEN-86			1			1						2
ATEN-87						1						1
ATEN-88	1											1
ATEN-89							1					1
ATEN-90	1					2						3
ATEN-91						1						1
Nonviable Culture						5						5
Untypable	1	1				10	1					13
<b>Subtotal</b>	<b>682</b>	<b>633</b>	<b>135</b>	<b>95</b>	<b>1059</b>	<b>475</b>	<b>80</b>	<b>89</b>	<b>13</b>	<b>35</b>	<b>3296</b>	
S. Hadar	2				3		1			2		6
	4				1							1
	5		2	1	2	1	3					9
	10					1						1
	11	1			2				1			4
	13	1										1
	33				1							1
	36	1										1
	43		1			2						3
	47		2									2
	Untypable	1	2	2								5
<b>Subtotal</b>	<b>4</b>	<b>7</b>	<b>7</b>	<b>5</b>	<b>5</b>	<b>3</b>	<b>0</b>	<b>3</b>	<b>0</b>	<b>0</b>	<b>34</b>	
S. Heidelberg	1					1						1
	2				2	1		2				5
	4					1	3					4
	5	2	6			11	6		2			27
	6a					3	1					4
	9					2	3					5
	10	2	7	2		23	36		1	1	2	74
	11a						1					1
	16					1	1					2
	17	4		1		1	3					9
	18	2	1		1	2						6

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
	19	13	9	4	1	80	81	8	8	1	4	209
	19a	1				1	2	9	2			15
	19b	1										1
	21	1										1
	25					1						1
	26	1		1		2	3	2	1			10
	29	29	10		6	31	35	6	2			119
	32					1						1
	32b					1						1
	36						1					1
	40		1			1	2					4
	41					4	3	1				8
	51						2					2
	52		1						1			2
	53					9						9
	54	2	1	2			2			1		8
	58					4	4					8
	ATHE-01	1										1
	ATHE-02					1			1			2
	ATHE-07						1					1
	ATHE-09				1		1					2
	ATHE-12					1						1
	ATHE-18	1										1
	ATHE-28				1							1
	ATHE-37				1							1
	ATHE-38							1				1
	ATHE-40		1									1
	ATHE-41						5					5
	ATHE-42	2										2
	ATHE-43	1										1
	ATHE-44	1										1
	ATHE-45	1										1
	ATHE-46						1					1
	ATHE-47	1										1
	ATHE-49						2					2
	ATHE-50								1			1
	ATHE-51					6						6
	ATHE-52					1						1
	ATHE-53		1									1
	ATHE-54						1					1
	ATHE-55	1										1
	Untypable					1				1		2
	<b>Subtotal</b>	<b>67</b>	<b>38</b>	<b>14</b>	<b>10</b>	<b>195</b>	<b>197</b>	<b>27</b>	<b>19</b>	<b>3</b>	<b>7</b>	<b>577</b>
S. Infantis		1				12	2	1			1	16
	3	3	1	1	5	7	2	1	1			21
	4	1	3	1	1	16	8	1				31
	7	13	18	4	3	68	20	2	2	1		131
	8	5	4		1	4	1					15
	11					1						1



Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
	ATNP-35		1									1
	ATNP-36				2							2
	ATNP-37				4							4
	ATNP-38		1									1
	ATNP-39						1					1
	ATNP-40					1						1
	Atypical					1						1
	Untypable				1							1
	<b>Subtotal</b>	<b>34</b>	<b>23</b>	<b>7</b>	<b>17</b>	<b>100</b>	<b>34</b>	<b>14</b>	<b>8</b>	<b>0</b>	<b>7</b>	<b>244</b>
S. Oranienburg	1	3	1		1	2			1			8
	2		2	1								3
	6	1	1			4	3		1			10
	8		2			3	8	1				14
	11		1			3						4
	13					1						1
	15		2	1		3						6
	ATOR-20					2						2
	ATOR-21					1	1					2
	ATOR-22				1							1
	ATOR-23		1									1
	<b>Subtotal</b>	<b>4</b>	<b>10</b>	<b>2</b>	<b>2</b>	<b>19</b>	<b>12</b>	<b>1</b>	<b>2</b>	<b>0</b>	<b>0</b>	<b>52</b>
S. Panama	A	1	1		1		1					4
	G	2	1			1	1	1		1		7
	H		1			1	1					3
	ATPA-07						1					1
	ATPA-08					1						1
	Untypable		1			1						2
	<b>Subtotal</b>	<b>3</b>	<b>4</b>	<b>0</b>	<b>1</b>	<b>4</b>	<b>4</b>	<b>1</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>18</b>
S. Paratyphi B	Dundee	1										1
	ATPB-01				1							1
	ATPB-03							1				1
	ATPB-07						1	2				3
	ATPB-14					1	1					2
	ATPB-17				2							2
	<b>Subtotal</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>3</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>10</b>
S. Paratyphi B var. Java	Battersea			1								1
	Dundee	1		1		1						3
	Dundee var 1	1				1						2
	Dundee var. 2		1									1
	Worksop	1	3									4
	3b var 2	1										1
	ATPB-03		1			1						2
	ATPB-07	1	3			1	3					8
	ATPB-13						1					1
	ATPB-14	1										1
	ATPB-15					1	1					2
	ATPB-18	1										1
	ATPB-20		1									1
	Untypable	3	2			2						7

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
	<b>Subtotal</b>	<b>10</b>	<b>11</b>	<b>2</b>	<b>0</b>	<b>5</b>	<b>7</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>35</b>
S. Thompson	1	2	4		1	164	30	3	5	2	1	212
	2		1		1		6					8
	3	1				5						6
	5					3						3
	8					2	1					3
	14		3			6						9
	18	1	1			1						3
	25					7						7
	26						1					1
	27	1	1	1		7	2			1		13
	ATTH-01					1						1
	ATTH-03					1						1
	ATTH-04						2					2
	ATTH-10					2						2
	ATTH-13					1	1					2
	ATTH-14					1			1			2
	ATTH-15					2						2
	ATTH-16					1						1
	ATTH-17					4						4
	Nonviable Culture					1						1
	Untypeable					1						1
	<b>Subtotal</b>	<b>5</b>	<b>10</b>	<b>1</b>	<b>2</b>	<b>210</b>	<b>43</b>	<b>3</b>	<b>6</b>	<b>3</b>	<b>1</b>	<b>284</b>
S. Typhi	28		2			3						5
	35	1										1
	A	2			2	5						9
	B2					2	1					3
	C4		1									1
	D1		1			3						4
	DVS	4	2			1						7
	E1	1	6	1	4	16						28
	E9 var		1			9	1					11
	E9 var.	1	1			4	1					7
	E9 var.	1										1
	E14	1				1						2
	M1		1			2	2					5
	O	1										1
	UVS	3	10		2	5	2					22
	UVS I+IV	2	1			4	1					8
	Nonviable Culture					1						1
	Untypeable	1	3			6						10
	<b>Subtotal</b>	<b>18</b>	<b>29</b>	<b>1</b>	<b>8</b>	<b>62</b>	<b>8</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>126</b>
S. Typhimurium	1				1	5	1					7
	2		1	1		1	1	1				5
	3					2						2
	4			1								1
	7					1						1
	9					1						1

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
	10			1	4	26	3					34
	12				1	5	3					9
	12a						1					1
	15a					2						2
	20						1					1
	21					2						2
	22		1			1	1					3
	35		1			1	2	1		1		6
	39						1					1
	40			1								1
	41		4	1		5						10
	46				1							1
	66						1	1				2
	66a						2	1				3
	69						1					1
	81						1					1
	99						2					2
	104	2	23	8	1	9	7		1			51
	104a					13	3	3	2			21
	104b		1	2	1	31	8					43
	106						1					1
	107					3	1					4
	108	2	9	4		45	33	1				94
	109						1					1
	110b						2					2
	116				1							1
	120		2			3	2					7
	125					1						1
	132					3	2	1	1			7
	135		1	1		5		1	1			9
	136					2						2
	153		1									1
	160					1						1
	170a					1						1
	177		1				1					2
	179		1			3						4
	186					1	4	1				6
	191	1										1
	193	2	9	1	2	29	50	2	2			97
	193a					1						1
	195	1								1	2	
	ATTM-04	2			1							3
	ATTM-12			1								1
	ATTM-14				1							1
	ATTM-15						1					1
	ATTM-57			1								1
	ATTM-58					2						2
	ATTM-78					1						1
	ATTM-96				1							1

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
ATTM-104				1								1
ATTM-109	1	5		1	7	1				2		17
ATTM-120						1						1
ATTM-124						1						1
ATTM-125				1								1
ATTM-126						2						2
ATTM-128	4	1			6							11
ATTM-129									1			1
ATTM-130							2					2
ATTM-141							1					1
ATTM-143						1						1
ATTM-147							1					1
ATTM-150						3						3
ATTM-157						1						1
ATTM-158						1						1
ATTM-159		1										1
ATTM-160							1					1
ATTM-162		1				1						2
ATTM-163						1						1
ATTM-164		1										1
ATTM-166						1						1
ATTM-168						1						1
ATTM-169						1						1
ATTM-170						1						1
ATTM-172				1								1
ATTM-174		1										1
ATTM-176						1						1
ATTM-177							1					1
ATTM-178					1							1
ATTM-179							1					1
ATTM-180		1										1
ATTM-181						1						1
ATTM-185							1					1
ATTM-186						2						2
ATTM-187						1						1
ATTM-189						1						1
ATTM-190						1						1
ATTM-191						2						2
ATTM-192						1	1					2
ATTM-195							1					1
ATTM-196						1						1
ATTM-197						1						1
ATTM-198						1						1
ATTM-202							1					1
ATTM-203		1										1
ATTM-205						1						1
ATTM-206							1					1
U274		1	1			1						3
U276						1						1



Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
	ATTM-165					4	1					5
	ATTM-167					1						1
	ATTM-171					2						2
	ATTM-173		1						1			2
	ATTM-175						1			2		3
	ATTM-182						2					2
	ATTM-183						1					1
	ATTM-184		1									1
	ATTM-188					2						2
	ATTM-193				1							1
	ATTM-194		1									1
	ATTM-199						1					1
	ATTM-200						1					1
	ATTM-201				1							1
	ATTM-207						1					1
	U291	1	2	2	1	6	4	1				17
	U302						1					1
	U302 var					1						1
	U311	1				1						2
	U324		1									1
	UT1		2			3						5
	UT2	1				2	4	1				8
	UT6						1					1
	UT7					1						1
	Untypable		1									1
	<b>Subtotal</b>	<b>13</b>	<b>53</b>	<b>13</b>	<b>14</b>	<b>112</b>	<b>53</b>	<b>5</b>	<b>4</b>	<b>0</b>	<b>5</b>	<b>272</b>
S. ssp I 4,[5],12,[27]:H Nonmotile	N/A	1										1
	<b>Subtotal</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
S. ssp I 9,12,Vi:H Nonmotile	Untypable	1	1			2						4
	<b>Subtotal</b>	<b>1</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>2</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>4</b>
S. ssp I 9,12:H Nonmotile	Untypable		1									1
	<b>Subtotal</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
S. ssp I O Rough:-:1,5	12					1						1
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
S. ssp I O Rough:H Nonmotile	10		1									1
	24					1						1
	Untypable		1									1
	<b>Subtotal</b>	<b>0</b>	<b>2</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>3</b>
S. ssp IIb 61:l,v:1,5,7:[z57]	N/A	1										1
	<b>Subtotal</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
<b>Shigella</b>												
Shigella boydii 1	9					1						1
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
Shigella boydii 2	6	1	1			2	1					5
	<b>Subtotal</b>	<b>1</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>2</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>5</b>
Shigella boydii 4	13					1						1

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	Total
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
<i>Shigella boydii</i> 13	ATSB-05		1									1
	<b>Subtotal</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
<i>Shigella boydii</i> 14	13						1					1
	ATSB-06					1						1
	<b>Subtotal</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>2</b>
<i>Shigella boydii</i> 20	3		1									1
	<b>Subtotal</b>	<b>0</b>	<b>1</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>1</b>
<i>Shigella sonnei</i>	1		33	6		90		6	2			137
	1a					2						2
	4					1						1
	7		1	2		1						4
	9		2			5						7
	10					1						1
	11					1						1
	14			1					1			2
	15		1			2						3
	19		1	1		1						3
	ATSS-01					1						1
	ATSS-03					1						1
	ATSS-04		2			2						4
	ATSS-13					1						1
	ATSS-15		1			6						7
	ATSS-18		3									3
	ATSS-20					1						1
	ATSS-21		11			4						15
	ATSS-26					1						1
	ATSS-27		1									1
	ATSS-28					1						1
	ATSS-29					1						1
	ATSS-30					2						2
	ATSS-31					1						1
	Nonviable Culture		1			2						3
	<b>Subtotal</b>	<b>0</b>	<b>57</b>	<b>10</b>	<b>0</b>	<b>128</b>	<b>0</b>	<b>6</b>	<b>3</b>	<b>0</b>	<b>0</b>	<b>204</b>
<b>Total</b>		<b>921</b>	<b>1072</b>	<b>244</b>	<b>201</b>	<b>2505</b>	<b>1100</b>	<b>165</b>	<b>147</b>	<b>24</b>	<b>69</b>	<b>6448</b>

#### **Appendix 4. Non-O157 serotypes of shiga toxin-producing *E. coli* tested by the NML, 2015**



Serotype	BC	AB	SK	MB	ON	QC	NB	NS	PE	NL	YT	NT	NU	Total
<i>E. coli</i> O162:H17										1				1
<i>E. coli</i> O162:H33			1											1
<i>E. coli</i> O165:H25				1										1
<i>E. coli</i> O165:H Nonmotile				1										1
<i>E. coli</i> O169:H41					10									10
<i>E. coli</i> O171:H2		1												1
<i>E. coli</i> O172:H Nonmotile	1													1
<i>E. coli</i> O174:H21	1													1
<i>E. coli</i> O175:H28					1									1
<i>E. coli</i> O177:H11			1											1
<i>E. coli</i> O177:H Nonmotile	1		1											2
<i>E. coli</i> O181:H Undetermined	1													1
<i>E. coli</i> O184:H7					1									1
<i>E. coli</i> O186:H2	1		1											2
<i>E. coli</i> O186:H Nonmotile		2												2
<i>E. coli</i> O Rough:H2					1									1
<i>E. coli</i> O Rough:H7	1				2					1				4
<i>E. coli</i> O Rough:H8	1													1
<i>E. coli</i> O Rough:H11		2		1										3
<i>E. coli</i> O Rough:H12	2													2
<i>E. coli</i> O Rough:H14		1												1
<i>E. coli</i> O Rough:H18			1											1
<i>E. coli</i> O Rough:H19				1	1									2
<i>E. coli</i> O Rough:H21	1				1									2
<i>E. coli</i> O Rough:H25						1								1
<i>E. coli</i> O Rough:H41					6									6
<i>E. coli</i> O Rough:H45						1								1
<i>E. coli</i> O Rough:H Nonmotile	3		3		7		1			2				16
<i>E. coli</i> O Rough:H Undetermined		1	1		1					1				4
<i>E. coli</i> O Untypable:H Nonmotile										1				1
<i>E. coli</i> Inactive			3	4	1	3								11
<i>E. coli</i> No serotype assigned		2		2					1					5
<b>Total</b>	<b>64</b>	<b>31</b>	<b>71</b>	<b>27</b>	<b>84</b>	<b>27</b>	<b>2</b>	<b>0</b>	<b>5</b>	<b>28</b>	<b>0</b>	<b>0</b>	<b>0</b>	<b>339</b>