National Enteric Surveillance Program (NESP)

ANNUAL SUMMARY 2010

Including Serotype and Phage Type Tables for 2010, NESP and NML

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

and

Provincial Public Health Microbiology Laboratories

Public Health Agency of Canada | Agence de la santé publique du Canada

Canada

Acknowledgments

NESP Coordination Team:

Matthew Gilmour, Chief, Enteric Diseases Section, NML
Lori Lozinski, Clerk, Enteric Diseases Section, NML
Frank Pollari, Manager, Enteric Disease Surveillance and Population Studies Division, CFEZID
Andrea Nesbitt, Epidemiologist, Enteric Disease Surveillance and Population Studies Division, CFEZID
Regan Murray, Epidemiologist, Enteric Disease Surveillance and Population Studies Division, CFEZID
Vanessa Morton, Epidemiologist, Enteric Disease Surveillance and Population Studies Division, CFEZID

NML Data:

Helen Tabor, Head, Identification & Serotyping Unit
Rafiq Ahmed, Head, Phage typing Unit
Celine Nadon, Head, PulseNet Canada

Provincial/Territorial Microbiology Laboratory Partners:

BC Centre for Disease Control Public Health Microbiology & Reference Laboratory
Alberta Provincial Microbiology Laboratory (ProvLab)
Saskatchewan Disease Control Laboratory
Cadham Provincial Microbiology Laboratory (Manitoba)
Public Health Ontario
Institut national de santé publique du Québec (INSPQ)
New Brunswick Public Health Laboratories
Nova Scotia Public Health Laboratories
Prince Edward Island Public Health Laboratories
Newfoundland and Labrador Public Health Laboratory

Provincial/Territorial Epidemiology Partners:

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

Executive Summary

The National Enteric Surveillance Program (NESP) is designed to provide weekly analysis and reporting for laboratory-confirmed isolations of enteric pathogens in Canada, including bacterial, viral and parasitic pathogens. This is an annual summary of data submitted to NESP by provincial/territorial microbiology laboratories in 2010.

Salmonella was the most common pathogen reported to NESP in 2010.The total number of *Salmonella* isolates increased almost 20% over 2009. Within *Salmonella*, *S*. Enteritidis was the most frequently reported serovar. The number of *S*. Enteritidis isolates was the highest ever recorded, accounting for 39% of all *Salmonella* isolates reported to NESP in 2010. In contrast, the number of *E. coli* O157 isolates reported was the lowest ever. The number of isolates of *E. coli* O157 reported in 2010 is half the number reported in 2006. This is a statistically significant decrease.

Listeria monocytogenes was added to the list of pathogens included in NESP on July 4th, 2010. During the six months from July to December 2010, 97 isolates of invasive *L. monocytogenes* were reported nationally. This is more than what would have been expected based on data collected from other sources for previous years, which indicated that 100 to 140 cases would be expected nationally per year. However, a full year of data collection is required before making any conclusions.

This report also summarizes the unusual isolation sites and travel-acquired infections reported through NESP. The majority of enteric pathogens are isolated from faecal matter, with the exception of *L. monocytogenes*. However, a considerable number of bacterial pathogens were isolated from extra-intestinal sites, the most common sites reported being blood and urine. Although travel history is largely under-reported in NESP, 191 enteric infections were identified as associated with international travel. Parasitic infections were the most common, with *Giardia* representing 27% of travel-acquired infections. Mexico and the Caribbean were the most frequent destinations identified by travellers.

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Introduction

The National Enteric Surveillance Program (NESP) is designed to provide timely analysis and reporting for laboratory-confirmed isolations of enteric pathogens in Canada, including bacterial, viral and parasitic pathogens. In collaboration with related programs like PulseNet Canada, NESP supports the real-time detection and response to emerging and priority diseases, and is integrated with international efforts to monitor and limit the spread of pathogenic micro-organisms.

NESP is based on the collection of weekly aggregate laboratory data from across Canada as submitted by the provincial public health microbiology laboratories to the Public Health Agency of Canada (PHAC). Data are submitted to the National Microbiology Laboratory (NML) either directly or using the web-based Canadian Network for Public Health Intelligence (CNPHI). Laboratories submit genus, species, and serotype information on enteric microorganisms isolated from human patients. Compilation and analysis of these weekly data is then conducted jointly between the NML and the Centre for Food-borne, Environmental and Zoonotic Infectious Diseases (CFEZID) to produce a weekly report. The reports alert PHAC and NESP provincial/territorial partners to significant emerging trends in food-borne disease. PulseNet Canada[1] then utilizes these data in conjunction with laboratory DNA fingerprinting testing to detect outbreaks at the earliest possible stage, and to serve as a primary data sharing and communication link between all provincial public health microbiology laboratories, the Canadian Food Inspection Agency, Health Canada, and PHAC. Notably, these two complementary laboratory surveillance networks lead the information sharing and coordinated assessment of laboratory evidence during multi-jurisdictional epidemiologic investigations of some bacterial pathogens, as prescribed in the *Food-borne Illness Outbreak Response Protocol* (FIORP)[2]. To also support communication of laboratory surveillance findings, the on-line WebNESP application of CNPHI allows partners to perform real-time data analysis, trending and display of their data.

This annual report is a summary of the weekly data from all provincial public health microbiology laboratories, and provides longer term trends on the incidence of enteric pathogens in Canada. For some organisms the number of isolates reported to NESP is only **a subset of laboratory isolations within the province and may not reflect the incidence of disease either provincially or nationally.** However, within each disease group, the data may indicate event-related changes in reported trends.

[1] PulseNet Canada, National Microbiology Laboratory, Public Health Agency of Canada: http://www.nml-lnm.gc.ca/Pulsenet/index-eng.htm

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

The Canadian Notifiable Diseases Surveillance System (CNDSS) receives data that are collected on a mandatory basis by local health units, forwarded to provincial/territorial health authorities, and collated by the Surveillance and Risk Assessment Division, Centre for Communicable Diseases and Infection Control, PHAC. These data may be more reliable for total number of illnesses. These surveillance systems are complementary in providing both epidemiological and laboratory results; however discrepancies between them do exist.

Data Collection and Analysis:

Provincial public health laboratories receive isolates (or specimens) and submission forms. Laboratory personnel at each provincial laboratory perform appropriate tests to confirm the identification or subtyping of the agent. Weekly results are summarized onto a NESP report form. The 'report week' for NESP is Sunday to Saturday and is based on the date the laboratory test was completed. All data sent to NESP are aggregate and anonymous. NESP partners endeavour to include only the number of isolates from new cases identified at the laboratory that week or updates to previously reported numbers. The provincial laboratory will attempt to identify multiple, repeat or follow-up specimens from the same individual and will consider all identical isolates from the same patient that are collected over a 3-month period as a single case. The completed NESP report form is faxed or e-mailed to the NML 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.

There were two major changes to NESP data collection in 2010:

1. *Listeria monocytogenes* was added to the list of organisms included in NESP. This change was adopted by all provinces, and reporting began on July 4, 2010. There were three main reasons for this addition: 1) *L. monocytogenes* was initially suggested for inclusion as a result of a NESP organism ranking exercise in 2009, which ranked it high on the criteria necessary for inclusion in NESP; 2) The report of the Independent Investigator into the 2008 Listeriosis Outbreak (aka: the Weatherill report) recommended improved surveillance for enteric pathogens including *L. monocytogenes*; and 3) Invasive listeriosis was reinstated to the list of National Notifiable Diseases in 2009.
2. Ontario began reporting all enteric viruses (including norovirus, rotavirus and adenovirus) in January 2010. This brings it in line with most other provinces.

With respect to data analysis, NESP uses an algorithm to determine whether case counts are significantly higher than expected. The cumulative Poisson probability between the reported case count and the 5-year median value is used to determine statistical significance.

The NESP Weekly Report is sent to all provincial laboratories, at least one epidemiologist or Medical Officer of Health in each province, and multiple stakeholders at the federal level. The reports may be shared with other public health professionals within their respective provinces or organizations, but are not for public distribution. There is no required response by public health professionals to the events or statistical elevations noted in the reports.

Limitations:

It should be noted that there are some inherent limitations of these data. Not all specimens/isolates are referred from the regional and local laboratories to the provincial public health laboratories and therefore the provincial reports and NESP data may be an under-representation of the true incidence of disease in Canada. 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. However, *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. In some cases, there may be over-reporting of organisms in NESP due to reporting of multiple specimens from a single patient, but efforts are made to keep this to a minimum. Information regarding extra-intestinal isolation sites, foreign travel, and outbreaks and case clusters are not routinely or consistently reported to NESP from all laboratories and therefore any interpretation should be considered with caution. Outbreaks and clusters reported to NESP do not represent all enteric illness outbreaks identified nationally nor is the case count representative of the actual final number of cases that may have been associated with the outbreaks and clusters reported to NESP. Therefore, details regarding outbreaks and case clusters are not included in this report; these are more accurately tracked within PulseNet Canada or through other systems.

Isolates Reported by Major Organism Group

NESP collects information on several bacterial, viral and parasitic enteric pathogens. The most frequent enteric pathogens reported in 2010 were *Salmonella* spp. followed by the enteric viruses and *Campylobacter* spp. (Figure 1). As mentioned previously, this does not reflect national incidence rates but testing and reporting practices within the provincial laboratories.

A total of 17 041 enteric pathogens were reported to NESP in 2010. This represents a 19% increase in total number of organism reported over 2009; some of which can be accounted for by new viral testing in Ontario. The number of cases reported per provinces for each major organism group is shown in Table 1. A complete list of all organisms reported per province is located in Appendix 1.

Figure 1. Proportion of isolates reported to NESP attributed to each major organism group

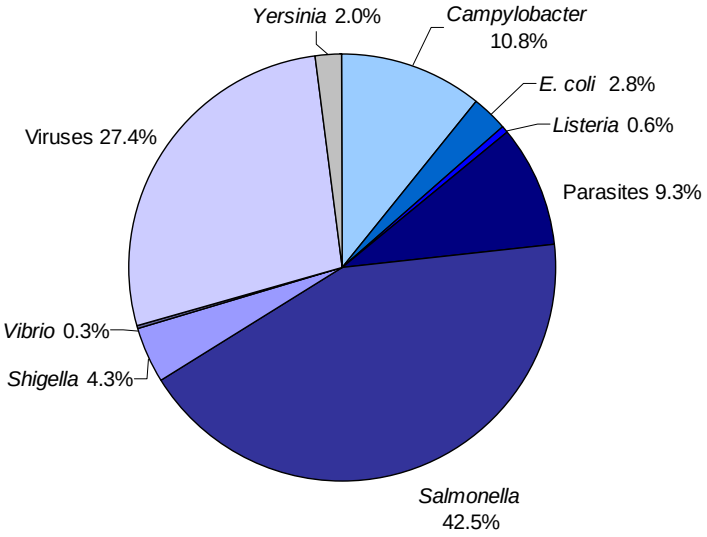


Table 1. Number of isolates reported by major organism groups per Province/Territory

Group	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YK	NT	NU	Total
*Campylobacter**	507	307	155	133	297	131	138	32	90	36	4	2	5	1837
E. coli[‡]	96	62	9	75	157	58	11	2	7	-	-	-	1	478
Listeria[†]	8	4	1	2	38	37	3	-	4	-	-	-	-	97
Parasites*	232	35	132	147	476	292	110	12	106	43	-	-	-	1585
Salmonella	1145	1054	195	252	2955	1219	145	34	169	51	6	6	20	7251
Shigella	187	121	11	49	246	100	7	3	11	2	2	-	-	739
Vibrio	17	13	1	2	4	-	4	6	2	-	-	-	2	51
Viruses*	535	311	650	180	1413	966	169	36	228	172	-	1	1	4662
Yersinia	63	41	23	9	184	17	3	-	1	-	-	-	-	341
Total	**2790**	**1948**	**1177**	**849**	**5770**	**2820**	**590**	**125**	**618**	**304**	**12**	**9**	**29**	**17041**

**Campylobacter,* Parasitic (*Giardia, Cryptosporidium, Entamoeba histolytica/dispar* and *Cyclospora*) and viral infections (Norovirus, Rotavirus and Adenovirus) are not routinely reported to the provincial or central reference laboratories and are greatly under-represented in NESP.
[‡]*E. coli* includes O157 serotype (404 cases) and non-O157 or non-typed serotypes (74 cases).
[†]*L. monocytogenes* reporting began on July 4, 2010

National incidence rates of the major organism groups calculated based on the number of isolates reported to NESP are shown in Table 2. Small increases in the incidence rates of several major organism groups were noted in 2010. This is likely due to an overall increase in the number of isolates reported to NESP. Due to the nature of NESP and the reporting practices used, the number of isolates reported for some pathogens are considered to be an underestimate of the true number of isolates; this is especially true for *Campylobacter*, parasites and enteric viruses. As a result, incidence rates are difficult to interpret and changes in these rates may not be due to actual changes in disease rates.

Isolates of organisms such as *E. coli* O157, *Salmonella* and *Shigella* are routinely forwarded to provincial microbiology laboratories, and as such NESP incidence rates are considered to be reflective of true incidence rates for these pathogens. The national incidence rate of both *Salmonella* and *Shigella* increased in 2010 compared to 2009, whereas *E. coli* O157 has been declining over the last five years (Figure 2). The provincial incidence rates for select organisms are shown in Table 3.

Table 2. Annual national totals and rates (per 100,000) for major organism groups as reported to NESP from 2005 to 2010[†]

Group	2005		2006		2007		2008		2009		2010	
*Campylobacter**	1409	4.37	1958	6.01	1959	5.95	1614	4.84	1751	5.19	1837	5.39
E. coli O157[‡]	736	2.28	978	3.00	934	2.84	661	1.98	529	1.57	404	1.18
Parasites*	1742	5.40	1705	5.23	1678	5.10	1783	5.35	1570	4.66	1585	4.65
Salmonella	6096	18.91	5724	17.57	6419	19.49	6351	19.06	6084	18.04	7251	21.26
Shigella	837	2.60	526	1.61	636	1.93	680	2.04	631	1.87	739	2.17
Vibrio	30	0.09	43	0.13	37	0.11	39	0.12	47	0.14	51	0.15
Viruses*	2277	7.06	4057	12.45	4657	14.14	3248	9.75	3184	9.44	4662	13.67
Yersinia	553	1.71	578	1.77	488	1.48	414	1.24	382	1.13	341	1.00
Total	13680		15569		16808		14790		14178		16870	

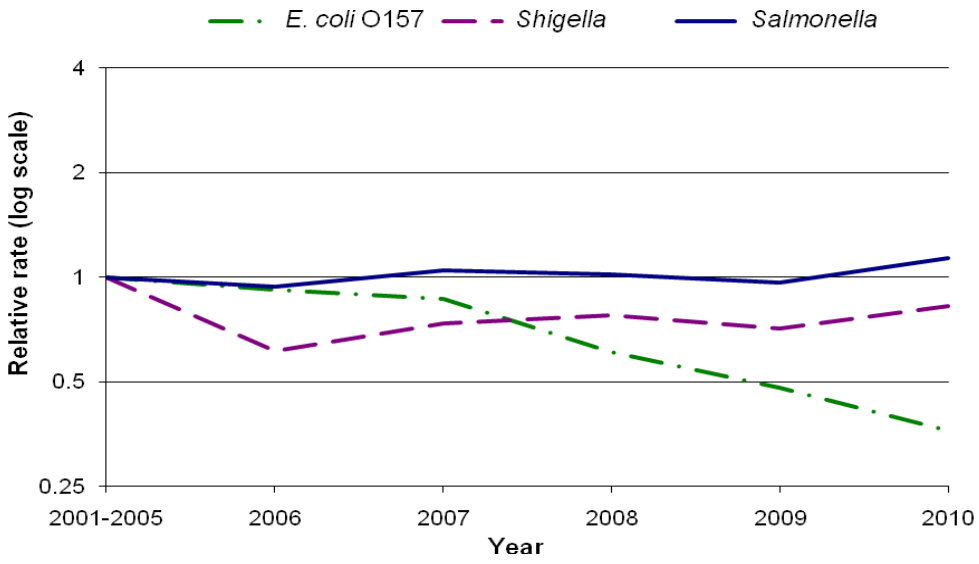
[†]Rates calculated using the population estimates for Canada as of July 1 for years 2005 to 2010 as reported by Statistics Canada.
**Campylobacter,* Parasitic (*Giardia, Cryptosporidium, Entamoeba histolytica/dispar* and *Cyclospora*) and viral infections (Norovirus, Rotavirus and Adenovirus) are not routinely reported to the provincial or central reference laboratories and are greatly under-represented in NESP.
[‡]Only cases of *E. coli* O157 are included in this table, since *E. coli* non-O157 is not consistently reported by provinces.

Table 3. Rates (per 100,000) per province/territory for select major organism groups - NESP 2010[†]

Group	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YK	NT	NU	Nat'l
E. coli O157[‡]	0.93	1.67	0.86	4.45	1.19	0.73	1.46	1.41	0.74	-	-	-	3.01	1.18
Salmonella	25.27	28.33	18.65	20.40	22.37	15.42	19.29	23.90	17.93	10.01	17.38	13.71	60.20	21.26
Shigella	4.13	3.25	1.05	3.97	1.86	1.26	0.93	2.11	1.17	0.39	5.79	-	-	2.17
Vibrio	0.38	0.35	0.10	0.16	0.03	-	0.53	4.22	0.21	-	-	-	6.02	0.15
Yersinia	1.39	1.10	2.20	0.73	1.39	0.21	0.40	-	0.11	-	-	-	-	1.00

[†]Rates calculated using updated postcensal population estimates for Canada, the provinces and the territories as of July 1, 2010 from Statistics Canada.
[‡]Only cases of *E. coli* O157 are included in this table, since *E. coli* non-O157 are not consistently reported by provinces

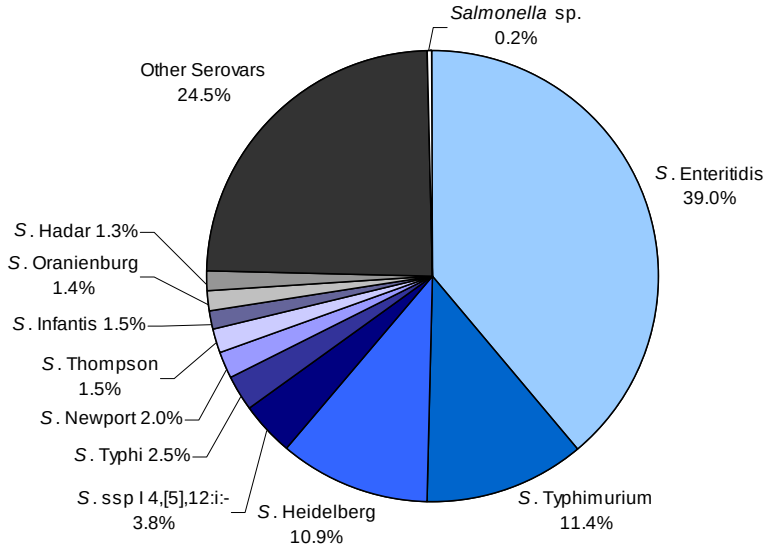
Figure 2. Relative incidence rates of lab-confirmed cases of *Salmonella, Shigella* and *E. coli* O157, by year (compared to the 2001 - 2005 baseline period)



Salmonella

A total of 7251 *Salmonella* isolates and 224 serovars were reported to NESP in 2010, which represents a nearly 20% increase over the number of *Salmonella* isolates reported in 2009. The top 10 *Salmonella* serovars accounted for 75.3% of the total *Salmonella* infections reported (Figure 3). Total numbers of isolates identified in each province of the top 10 *Salmonella* serovars are listed in Table 4, while a full list of *Salmonella* serovars reported to NESP in 2010 is presented in Appendix 1.

Figure 3. Percentage of *Salmonella* serovars as reported to NESP in 2010



*Other serovars (1780 isolates) were divided among 214 serovars and 14 isolates were reported as unspecified *Salmonella* species.

Table 4. Isolates reported per province of the top ten *Salmonella* serovars

Serovar	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YK	NT	NU	Total
Enteritidis	556	420	61	99	1035	439	69	21	83	27	3	2	12	2827
Typhimurium	100	131	55	15	347	139	14	-	17	4	1	1	3	827
Heidelberg	64	128	11	21	276	238	28	5	13	3	-	-	-	787
ssp I 4,[5],12:i:-	46	65	15	25	55	61	8	-	2	-	-	-	1	278
Typhi	34	20	2	8	96	18	-	1	1	-	-	-	-	180
Newport	19	16	4	7	79	17	1	-	2	1	-	-	-	146
Thompson	5	14	5	2	57	19	1	1	2	1	-	-	-	107
Infantis	14	15	1	-	56	11	2	-	5	2	-	-	-	106
Oranienburg	4	6	1	2	81	8	1	-	1	-	-	-	-	104
Hadar	15	4	6	4	55	8	1	-	2	-	-	-	-	95
Top Ten Total	**857**	**819**	**161**	**183**	**2137**	**958**	**125**	**28**	**128**	**38**	**4**	**3**	**16**	**5457**

The ranking among the top three serovars remained unchanged from the previous six years, with *S.* Enteritidis being the most frequently reported, followed by *S*. Typhimurium and *S.* Heidelberg (Table 5). There was only one notable change among the top ten *Salmonella* serovars; *S*. Oranienburg was included in the top ten for the first time since 2007. The number of *S*. Oranienburg reported in 2010 was almost double the number reported in 2009, due to a large outbreak in Ontario.

In 2010, several multi-provincial increases in specific *Salmonella* serovars were noted in NESP. These increases were often highlighted as the topic of the week in the weekly NESP report and frequently corresponded to ongoing outbreaks or initiated an investigation. One example in 2010 was the national increase in cases of *S*. Chester noted in NESP. This was due to a multi-provincial outbreak of *S*. Chester (33 cases) which occurred between June and August 2010. Cases were identified in British Columbia, Ontario, Alberta and Saskatchewan. Head cheese was implicated as the source of these infections.

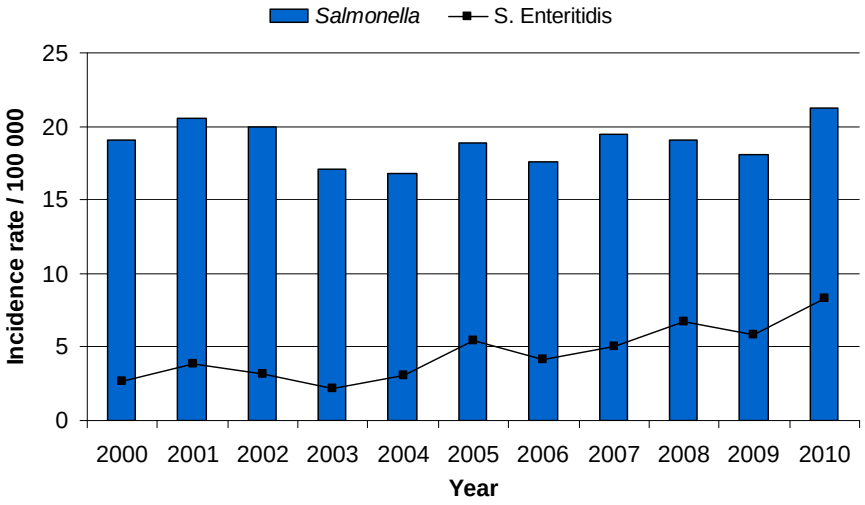
Table 5. National totals (overall rank) for the top ten *Salmonella* serovars as reported to NESP between 2005 and 2010

Species	2005	2006	2007	2008	2009	2010
Enteritidis	1750 (1)	1338 (1)	1661 (1)	2239 (1)	1955 (1)	2827 (1)
Typhimurium	1058 (2)	998 (2)	1341 (2)	914 (2)	777 (2)	827 (2)
Heidelberg	712 (3)	696 (3)	560 (3)	456 (3)	665 (3)	787 (3)
ssp I 4,[5],12:i:-	103	109 (9)	184 (4)	180 (6)	271 (4)	278 (4)
Typhi	123 (8)	177 (4)	158 (6)	192 (4)	164 (5)	180 (5)
Newport	145 (6)	145 (7)	142 (9)	185 (5)	133 (6)	146 (6)
Thompson	235 (4)	171 (5)	173 (5)	130 (7)	99	107 (7)
Infantis	131 (7)	81	131 (10)	119 (8)	110 (8)	106 (8)
Oranienburg	47	67	145 (7)	45	53	104 (9)
Hadar	168 (5)	107 (10)	144 (8)	113 (9)	100 (10)	95 (10)
Saintpaul	115 (9)	166 (6)	123	92	130 (7)	88
Paratyphi A	108 (10)	132 (8)	94	109 (10)	92	91
Javiana	47	49	49	66	102 (9)	90

Continued Prevalence of *S.* Enteritidis

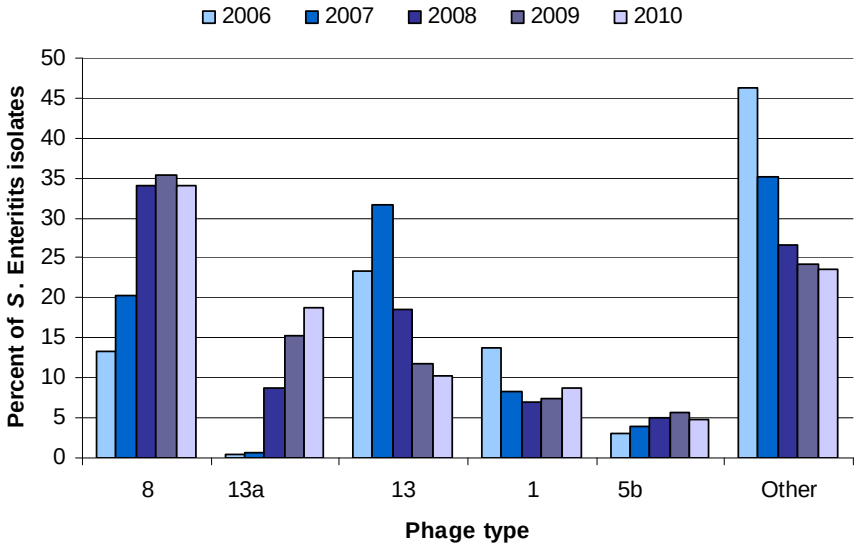
In 2010 a record high of 2827 *S.* Enteritidis isolations were reported to NESP. It was the most prevalent cause of human salmonellosis in Canada representing approximately 39% of all human *Salmonella* isolates reported in 2010. The proportion of salmonellosis cases attributed to *S*. Enteritidis has been steadily increasing over time, from 14% in 2000 to 39% in 2010 (Figure 4). This continual increase in the rate of *S.* Enteritidis infections in numerous provinces has prompted several investigations. Although it has been difficult to establish epidemiological linkages between contaminated products and human disease, poultry and eggs have been implicated as sources.

Figure 4. Incidence rate of *Salmonella* spp. and *S.* Enteritidis as reported to NESP from 2000 to 2010



Phage typing is commonly used to detect changing trends in *S*. Enteritidis. The last five years has seen the emergence of phage type 13a and an increase in phage type 8 (Figure 5). A complete list of all phage types reported by NML is listed in Appendix 2.

Figure 5. Proportion of *S*. Enteritidis isolates reported for the five most common phage types of *S*. Enteritidis (2006 to 2010)



E. coli

One trend observed in NESP is the decline in cases of *E. coli* O157 VTEC (Figure 6). The incidence rate has decreased from 3.00 cases per 100 000 in 2006 to 1.18 cases per 100 000 in 2010. This decline in the number of *E. coli* O157 isolates reported from 2006 to 2010 was found to be statistically significant (p-value <0.0001). However, the national incidence rate of *E. coli* non-O157 reported to NESP has shown little change over the past ten years. It should be noted that *E. coli* non-O157 are reported less consistently than *E. coli* O157 to NESP by the provinces and the specific serotype of E. coli non-O157 isolates is not often reported. The limited *E. coli* serotype data available through NESP are presented in Appendix 1. Serotype information is also available for non-O157, shiga toxin-producing isolates sent to the NML in 2010 (Table 6).

Figure 6. Cases of *E. coli* O157 and *E. coli* non-O157 (includes untyped organisms) serotypes reported to NESP from 2001 to 2010

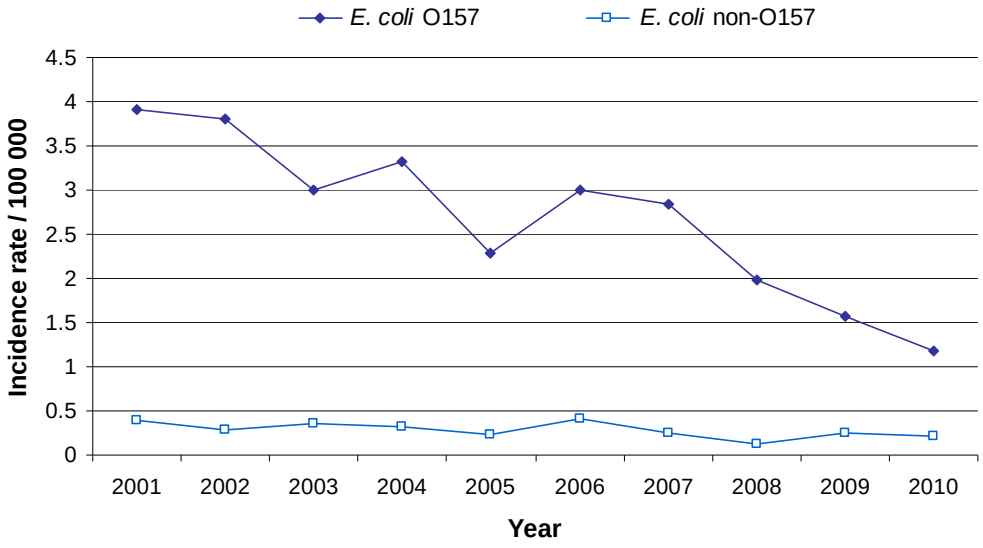


Table 6. Non-O157 serotypes of Shiga toxin-producing *E. coli* tested by the National Microbiology Laboratory*

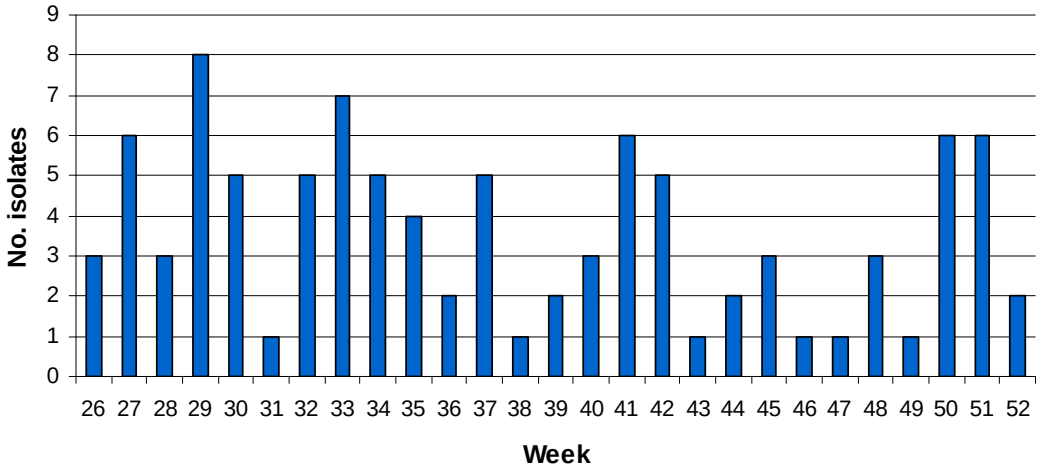
Serotype	Total
O1:K1:H7	1
O26:H11	7
O26:H Nonmotile	1
O52:H45	1
O84:H Rough	1
O103:H2	1
O103:H25	1
O111:H Nonmotile	3
O118:H16	1
O118:H Untypeable	1
O121:H19	7
O153:H16	1
O165:H Nonmotile	1
O177:H Nonmotile	1
O184:H9	1
O184:H Nonmotile	1
O Untypeable:H10	1
O Untypeable:H Rough	1
Total	**32**

*Inclusive of only those isolates where both serotype and toxin testing data were available. These data are not representative of national incidence, as not all human-clinical Shiga toxin-producing *E. coli* are sent to the NML for these reference service tests.

Listeria monocytogenes

In July 2010, the list of organisms included in NESP was expanded to include *L. monocytogenes*. This addition was designed to provide increased national surveillance of invasive listeriosis. During the six months *L. monocytogenes* was included in NESP (July to December 2010), 97 isolates of invasive *L. monocytogenes* were reported (Figure 7). A median of 3 isolates were reported nationally per week. This is more than expected based on listeriosis case data provided by provincial ministries of health for previous years, which indicate 100 to 140 cases would be expected nationally per year. However, a full year of data collection is required before making any conclusions. The breakdown of the total isolates reported by each province/territory is shown in Table 1.

Figure 7. Isolates of invasive *L. monocytogenes* reported to NESP per week in 2010



L. monocytogenes was included in NESP beginning in July 2010; however, all laboratory isolates of *L. monocytogenes* were characterized by PFGE and uploaded to the PulseNet Canada database throughout the entire year (Table 7). While data from PulseNet Canada may not represent the total number of cases, they do provide an indication of the occurrence of disease for the months during 2010 not captured by NESP. Serotype information is available for some of the isolates sent to NML in 2010 (Table 8).

Table 7. Uploads of *L. monocytogenes* PFGE patterns to the PulseNet Canada database in 2010.

Month	Number of Uploads
January	5
February	12
March	13
April	1
May	10
June	15
July	16
August	19
September	12
October	24
November	11
December	16
Total	**154**

Table 8. Serotypes of *L. monocytogenes* isolates sent to the National Microbiology Lab in 2010.

Serotype	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
1/2a	7	2	1	1	17	-	-	-	3	-	**31**
1/2b	1	1	1	1	8	-	-	-	-	-	**12**
1/2c	1	-	-	-	-	-	-	-	-	-	**1**
4a	-	-	-	-	1	-	-	-	-	-	**1**
4b	7	1	1	1	32	-	4	-	5	-	**51**
4c	-	-	-	-	2	-	-	-	-	-	**2**
Untypable	**-**	**-**	**-**	**-**	2	**-**	**-**	**-**	**-**	**-**	**2**
Total *Listeria*	**16**	**4**	**3**	**3**	**62**	-	**4**	**-**	**8**	**-**	**100**

According to the case definition for invasive listeriosis, only isolates obtained from a normally sterile site or placental/fetal tissues should be reported to NESP. Therefore, unlike the other enteric organisms included in NESP, all *L. monocytogenes* isolates are from extra-intestinal sites. The isolation sites of *L. monocytogenes* reported to NESP are shown in Table 9. Blood and CSF were the most common isolation sites reported.

Table 9. Collection site of *L. monocytogenes* isolates as reported to NESP

Site	Total	Percent (%)
Blood	72	74.2
Cerebral Spinal Fluid (CSF)	10	10.3
Knee Fluid	1	1.0
Placenta	1	1.0
Unknown	13	13.4
Total	**97**	100

Isolates Collected from Extra-intestinal Isolation Sites

The number of isolates collected from extra-intestinal sites (i.e. non-faecal specimens) reported to NESP in 2010 is shown in Table 10. Although information regarding extra-intestinal isolation sites is collected by NESP, these data are not consistently reported to provincial or central reference labs. Isolation of an organism from a sterile site may reflect more severe illness and an increased likelihood to seek treatment and be tested. Isolation sites for *L. monocytogenes* are shown separately in Table 9, due to the nature of the illness.

The organisms that had the highest percentage of cases isolated from an extra-intestinal site were *S*. Paratyphi A, *S*. Typhi, and *C. fetus* ssp*. fetus* all of which were most frequently isolated from blood. *Vibrio alginolyticus* also had a high percentage of extra-intestinal cases but a very low number of total cases.

Table 10. Total isolates collected from extra-intestinal isolation sites as reported to NESP in 2010

Organism	Blood	Urine	Other *	Total/ Overall	Percent (%)
Campylobacter	**18**	**1**	**1**	**20/1837**	**1.1**
C. fetus spp *fetus*	8			8/34	**23.5**
C. jejuni	9		1	10/1343	**0.7**
Other species	1	1			
Salmonella	**279**	**133**	**22**	**434/7251**	**6.0**
S. Paratyphi A	30	-	1	31/91	34.1
S. Typhi	56	1	-	57/180	31.7
S. Chester	4	4	-	8/42	19.0
S. Poona	5	1	1	7/41	17.1
S. Heidelberg	73	17	4	94/787	11.9
S. Virchow	4	-	-	4/43	9.3
S. Brandenburg	3	-	1	4/45	8.9
S. Agona	2	3	-	5/78	6.4
S. Paratyphi B var. Java	3	1	-	4/67	6.0
S. Oranienburg	5	1	-	6/104	5.8
S. Infantis	-	5	1	6/106	5.7
S. Hadar	1	4	-	5/95	5.3
S. Muenchen	1	1	-	2/38	5.3
S. Montevideo	1	-	1	2/40	5.0
S. ssp I 4,[5],12:i:-	4	9	-	13/278	4.7
S. Newport	1	4	-	5/146	3.4
S. Saintpaul	1	1	1	3/88	3.4
S. Javiana	1	1	1	3/90	3.3
S. Enteritidis	47	35	8	90/2827	3.2
S. Typhimurium	16	8	1	25/827	3.0
S. Thompson	1	2	-	3/107	2.8
S. Braenderup	-	2	-	2/73	2.7
S. ssp I 4,[5],12:b:-	1	1	-	2/90	2.2
Other serovars	19	32	2		
Shigella	**2**	**1**	**1**	**4/737**	**0.5**
S. sonnei	2	1	1	4/377	1.1
Vibrio	**-**	**-**	**2**	**2/51**	**3.9**
V. alginolyticus	-	-	1	1/2	50.0
V. parahaemolyticus	-	-	1	1/37	2.7
Yersinia	**1**	**-**	**1**	**2/341**	**0.6**
Y. enterocolitica	1	-	1	2/303	0.7
Total	**300**	**135**	**27**	**462**	

*Other sites include: Abdominal aspirate: *S.* Heidelberg (1); Abscess/Wound: *S.* Brandenburg (1), *S.* Enteritidis (3), *S.* Meleagridis (1), *S.* Montevideo (1), *S.* Paratyphi A (1), *S.* Poona (1), *S.* Typhimurium (1), *Shigella sonnei* (1); Amputation site: *S.* Meleagridis (1); Bile: *S.* Heidelberg (1); Biopsy: *S.* Enteritidis (1); Bronchoalveolar lavage: *S.* Saintpaul (1); Ear: *V. alginolyticus* (1); Gall Bladder: *S.* Infantis (1); Pelvis: *S.* Enteritidis (1); Peritoneal Fluid: *C. jejuni* (1), *Y. enterocolitica* (1); Pleural Fluid: *S.* Enteritidis (1); Pleural Tissue: *S.* Heidelberg (1); Shin Culture: *V. parahaemolyticus* (1); Sputum: *S.* Enteritidis (1), *S.* Javiana (1); Tissue: *S.* Enteritidis (1); Vagina: *S.* Heidelberg (1);

Travel-Acquired Infections

Although foreign travel is one of the main risk factors for gastro-intestinal illness, this information is rarely captured or reported and is therefore greatly under-represented in NESP.

A total of 191 cases of enteric infection recorded through NESP were reported in foreign travelers or new immigrants arriving in Canada (Table 11 & Table 12). Asia was the most common region identified (46 cases). However, the popular winter sun destinations of Mexico and the Caribbean combined represent 34% (65 cases) of the travel-acquired infections reported.

Table 11. Number of infections by region/country of origin as reported to NESP

Geographic Region	No. of Cases (%)
Asia	46 (24%)
Mexico	37 (19%)
Caribbean (excluding Haiti)	28 (15%)
Haiti	22 (12%)
Africa	21 (11%)
Central America	7 (4%)
South America	6 (3%)
Other Destinations	9 (5%)
Multiple Destinations	4 (2%)
Unknown Destination	11 (6%)
Total	**191**

There was a considerable increase in the number of infections reported with travel history to Haiti; 22 cases were reported in 2010 compared with 3 in 2009. This may have been due to increased travel to and immigration from Haiti due to global events. All of the reported cases were associated with parasitic infections, unlike other Caribbean destinations which are most frequently associated with bacterial infections.

Parasitic infections were the most common travel-related infection, accounting for 43% of travel associated cases reported through NESP. These cases were most often reported among people who recently immigrated from, or travelled to Haiti, Africa or South Asia. *Giardia* was the most frequent pathogen associated with international travel, accounting for more than a quarter (27%) of all travel cases.

Salmonella was the second leading cause of travel-associated gastroenteritis, with 63 cases reported to NESP. The most common travel destinations identified were Mexico and the Caribbean.

Mexico was the country with the highest number of travel-acquired infections; this has been the case for the past eleven years. *Salmonella* was the most common enteric pathogen associated with travel to Mexico, but other bacterial and parasitic infections were also reported. In 2010, there were multi-

provincial clusters of *E. coli* O157, *S*. Enteritidis and *S.* Typhimurium linked to Canadian travellers returning from Mexico.

Table 12. Travel-acquired infections reported to NESP in 2010

Organism	No. of Cases	Country (No. > 1)
Campylobacter	**16 (8%)**	
C. coli	1	India
C. jejuni	13	Mexico (3), Cuba (2), Africa, Chile, Dominican Republic, Ethiopia, India, Jamaica, Nepal and Multiple destinations (Guatemala & USA)
C. jejuni/coli	1	Tahiti
Campylobacter sp.	1	Ethiopia
E. coli	**6 (3%)**	
E. coli O157	6	Mexico (4), Jamaica and Multiple destinations (Mexico & Europe)
Parasites	**83 (43%)**	
Cryptosporidium	1	Mexico
Cyclospora	2	Mexico and El Salvador
Entamoeba histolytica/dispar	29	Haiti (14), Africa (3), Burma (3), India (3), Eritrea (2), Bhutan, Ghana, Honduras and Pakistan
Giardia	51	Burma (8), Haiti (8), Bhutan (7), Ethiopia (5), Nepal (4), Caribbean (2), India (2), Colombia, France, Honduras, Mexico, Pakistan, Somalia, Multiple destinations (Madagascar, South Africa & Thailand) Unknown (8)
Salmonella	**63 (33%)**	
S. Enteritidis	29	Mexico (11), Cuba (5), Dominican Republic (3), USA (2), Argentina, Bosnia, Congo, Lebanon, Panama, Peru, Ukraine and Multiple Destinations (Greece & Turkey)
S. Newport	2	Cuba (2)
S. Paratyphi A	2	India and Bangladesh
S. Paratyphi B var. Java	2	Mexico and Bolivia
S. Saintpaul	2	Africa and Colombia
S. Typhi	2	India (2)
S. Typhimurium	7	Mexico (6) and Kenya
Other (15 serovars)	17	Mexico (5), Costa Rica (2), Jamaica (2), Caribbean, Cuba, India, Nepal, Thailand, USA and Unknown (2)
Shigella	**17 (9%)**	
S. dysenteriae 3	1	India
S. flexneri	6	India (3), Ethiopia, Mexico and Unknown
S. sonnei	10	Cuba (3), Africa (2), Dominican Republic (2), Costa Rica, Indonesia and Mexico
Vibrio	**4 (2%)**	
V. cholerae O1	1	Thailand
V. cholerae non-O1/O139	1	Dominican Republic
V. parahaemolyticus	2	Mexico (2)
Yersinia	**2 (1%)**	
Y. enterocolitica	2	Belgium and Cuba
Total	**191**	

Appendix 1. Species and Serotype data reported to NESP in 2010

Organism	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YT	NT	NU	Total
Campylobacter														
C. coli	54	15	5	5	102	34	2	1		1				**219**
C. concisus		1												**1**
C. fetus ssp *fetus*	5	6			5	18								**34**
C. hyointestinalis	1		1			1								**3**
C. jejuni	423	279	143	126	178	62	88	10		24	4	2	4	**1343**
C. jejuni/coli				1			2	21	88	8				**120**
C. lari	2		1		2	9	2						1	**17**
C. upsaliensis	21	6	4		10	7			1					**49**
Campylobacter sp.	1		1	1			44		1	3				**51**
Total *Campylobacter*	**507**	**307**	**155**	**133**	**297**	**131**	**138**	**32**	**90**	**36**	**4**	**2**	**5**	**1837**
Escherichia coli														
E. coli				1										**1**
E. coli Non-Typed VTEC	49			16										**65**
E. coli O26				2										**2**
E. coli O26:NM	1													**1**
E. coli O111:NM	4													**4**
E. coli O127				1										**1**
E. coli O157 VTEC	39	58	9	55	154	55	9	2					1	**382**
E. coli O157:NM	3	4			3	3	2		7					**22**
Total *Escherichia coli*	**96**	**62**	**9**	**75**	**157**	**58**	**11**	**2**	**7**	**0**	**0**	**0**	**1**	**478**
Listeria														
Listeria monocytogenes	8	4	1	2	38	37	3		4					**97**
Parasites														
Cryptosporidium	9	3	16	21	36	7	15	3	25	1				**136**
Cyclospora	3		1	1	39	5			2					**51**
Entamoeba histolytica/dispar	129	11	20	29	244	188	1		15					**637**
Giardia	91	21	95	96	157	92	94	9	64	42				**761**
Total Parasites	**232**	**35**	**132**	**147**	**476**	**292**	**110**	**12**	**106**	**43**	**0**	**0**	**0**	**1585**
Salmonella														
S. Aberdeen	1				3									**4**
S. Abony					1									**1**
S. Adelaide		2			1	1								**4**
S. Ago						1								**1**
S. Agona	14	12	6	2	29	11			1	2		1		**78**
S. Alachua		1			1									**2**
S. Albany	2	1			6				3					**12**
S. Altona				1	1									**2**
S. Amager		1												**1**
S. Anatum	5	3			5	3								**16**
S. Apapa					1	1								**2**
S. Apeyeme	3													**3**
S. Arechavaleta					1									**1**
S. Bardo									1					**1**

Organism	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YT	NT	NU	Total
S. Bareilly	2			1	13	1								**17**
S. Barranquilla						1								**1**
S. Berta				1	12	5								**18**
S. Blijdorp					1									**1**
S. Blockley				1	12									**13**
S. Bonariensis					5									**5**
S. Bovismorbificans	3				2	3								**8**
S. Braenderup	8	8	1	1	44	6	1		4					**73**
S. Brancaster										1				**1**
S. Brandenburg	13	6			18	6	1		1					**45**
S. Bredeney		1			3									**4**
S. Brunei					1									**1**
S. California				1										**1**
S. Cannstatt					1									**1**
S. Carmel						1								**1**
S. Carrau		1			2	1								**4**
S. Cerro	1		1		4	1								**7**
S. Chester	34	3	2		3									**42**
S. Coeln	1		1											**2**
S. Colindale					2				1					**3**
S. Concord	1			1										**2**
S. Corvallis	5	3		1	3				1					**13**
S. Cotham		1			3	1								**5**
S. Cubana		1												**1**
S. Curacao					1									**1**
S. Daytona	2													**2**
S. Derby	3	1	1		9	7	1	1						**23**
S. Dublin		2			6									**8**
S. Durban	1				3		1							**5**
S. Eastbourne	2				3									**5**
S. Ebrie		1			1									**2**
S. Emek		1			1									**2**
S. Enteritidis	556	420	61	99	1035	439	69	21	83	27	3	2	12	**2827**
S. Epinay					1									**1**
S. Florida		1												**1**
S. Fluntern					1	1								**2**
S. Freetown					1									**1**
S. Galiema				1	1									**2**
S. Gatuni					4									**4**
S. Give	2	1		1	5		1				1			**11**
S. Goelzau									2					**2**
S. Goettingen					3									**3**
S. Goverdhan	1													**1**
S. Grumpensis				1										**1**
S. Hadar	15	4	6	4	55	8	1		2					**95**
S. Haifa					8	2								**10**
S. Hartford		5			14	10			3					**32**
S. Havana					6	2								**8**
S. Heidelberg	64	128	11	21	276	238	28	5	13	3				**787**
S. Herston					1									**1**

Organism	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YT	NT	NU	Total
S. Hithergreen		1												**1**
S. Hull					2									**2**
S. Hvittingfoss		1			2	1								**4**
S. Indiana					2	1								**3**
S. Infantis	14	15	1		56	11	2		5	2				**106**
S. Inpraw					1									**1**
S. Irumu					1									**1**
S. Isangi					1									**1**
S. Istanbul					1									**1**
S. Jangwani	1													**1**
S. Javiana	5	9	1	1	42	25	4		2	1				**90**
S. Johannesburg				1	2					1				**4**
S. Jukestown					1									**1**
S. Kentucky	8	4	1		6	1				1				**21**
S. Kiambu	1	12	1	2	14	2								**32**
S. Kintambo		2			2									**4**
S. Kisarawe								1						**1**
S. Kokomlemle	1													**1**
S. Kottbus		3			1									**4**
S. Larochelle			1			1								**2**
S. Lattenkamp		2												**2**
S. Limete					2									**2**
S. Litchfield	4	3			9	2								**18**
S. Liverpool	1													**1**
S. Livingstone	1					1								**2**
S. Llandoff					1									**1**
S. Lomalinda			1											**1**
S. London					2	3								**5**
S. Manchester					1									**1**
S. Manhattan	1			1	8	1								**11**
S. Matadi		1												**1**
S. Matopeni						1								**1**
S. Mbandaka	13	5	1		8	1	1							**29**
S. Meleagridis	1			4	1	1								**7**
S. Miami					2	3								**5**
S. Michigan	1				1				1					**3**
S. Minnesota			1											**1**
S. Mississippi	2				11	1								**14**
S. Molade					1									**1**
S. Monschaui									5					**5**
S. Montevideo	6	2		1	23	7	1							**40**
S. Muenchen	4	5	2	3	17	4	1		2					**38**
S. Muenster	1			1	6	1								**9**
S. Napoli					1									**1**
S. Nessziona				1										**1**
S. Newport	19	16	4	7	79	17	1		2	1				**146**
S. Nima		1			3	1								**5**
S. Nottingham						2								**2**
S. Nyanza					1									**1**
S. Ohio	4				2	2		1						**9**

Organism	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YT	NT	NU	Total
S. Oranienburg	4	6	1	2	81	8	1		1					**104**
S. Orientalis		1												**1**
S. Oslo	1	1			5	1				1				**9**
S. Overschie					1									**1**
S. Panama	4	12		3	9	1								**29**
S. Paratyphi A	20	10			49	11			1					**91**
S. Paratyphi B	4		1	1	12				1					**19**
S. Paratyphi B var. Java	9	9		3	31	13		1				1		**67**
S. Plymouth		1												**1**
S. Pomona					2	1								**3**
S. Poona	4	9			13	14						1		**41**
S. Potsdam	2				1									**3**
S. Praha						1								**1**
S. Reading	1	1		1	1									**4**
S. Richmond	1													**1**
S. Rissen	2	2			7	3								**14**
S. Romanby					1									**1**
S. Rubislaw					1	1								**2**
S. Saintpaul	12	10	2	5	35	12	3	1	1	3			4	**88**
S. Sandiego	3	9	2		5	8	1		1					**29**
S. Schwarzengrund	3	2		3	9	4	1							**22**
S. Senftenberg	6	1	1	1	10	5					1			**25**
S. Singapore					1									**1**
S. Soahanina					1									**1**
S. Stanley	15	2	3	7	26	7								**60**
S. Stanleyville		1		1	2	1								**5**
S. Telelkebir					3	1								**4**
S. Tennessee	2			1	8	1								**12**
S. Texas					1									**1**
S. Thompson	5	14	5	2	57	19	1	1	2	1				**107**
S. Tornow					1									**1**
S. Tudu					1									**1**
S. Typhi	34	20	2	8	96	18		1	1					**180**
S. Typhimurium	100	131	55	15	347	139	14		17	4	1	1	3	**827**
S. Uganda		2			9	1								**12**
S. Urbana					1	1								**2**
S. Victoria				1										**1**
S. Virchow	8	4		1	24	3			2	1				**43**
S. Virginia		1												**1**
S. Wagenia					1									**1**
S. Weltevreden	13	2			6	1								**22**
S. Woodinville						1								**1**
S. Worthington	1	1		1										**3**
S. ssp I						2			1	2				**5**
S. ssp I 3,10:r:-	1													**1**
S. ssp I 4,[5],12:-:-		2			2									**4**
S. ssp I 4,[5],12:-:e,n,z15				1		1								**2**
S. ssp I 4,[5],12:b:-	1	7			64	18								**90**
S. ssp I 4,[5],12:d:-		16												**16**
S. ssp I 4,[5],12:e,h:-					1									**1**

Organism	BC	AB	SK	MB	ON	QC		PE	NS	NL	YT	NT	NU	Total
S. ssp I 4,[5],12:i:-	46	65	15	25	55	61	8		2				1	**278**
S. ssp I 6,7:-:1,6	1													**1**
S. ssp I 6,7:c:-		1			1		1							**3**
S. ssp I 6,7:c:1,5					1									**1**
S. ssp I 6,7:e,h:-						3								**3**
S. ssp I 6,7:k:-						1								**1**
S. ssp I 6,7:r:-					9									**9**
S. ssp I 6,7:z4,z23:-						1								**1**
S. ssp I 6,8:-:-	1													**1**
S. ssp I 6,8:-:1,2						1								**1**
S. ssp I 6,8:e,h:-		1			1	1								**3**
S. ssp I 8,20:i:-					1									**1**
S. ssp I 9,12:-:-	4			2	2									**8**
S. ssp I 9,12:-:1,5	3	2			3	4	1							**13**
S. ssp I 9,46:-:-					1									**1**
S. ssp I 13,22:z:-						1								**1**
S. ssp I 13,23:b:-					1									**1**
S. ssp I 13,23:d:-						1								**1**
S. ssp I 13,23:i:-		1												**1**
S. ssp I 16:b:-					3									**3**
S. ssp I 16:d:-		1												**1**
S. ssp I 17:b:-					1									**1**
S. ssp I Rough-O:-:-		5	1		5									**11**
S. ssp I Rough-O:b:-					1									**1**
S. ssp I Rough-O:e,h:1,2		1												**1**
S. ssp I Rough-O:f,g,s:-		1												**1**
S. ssp I Rough-O:i:-		1												**1**
S. ssp I Rough-O:r:-		1												**1**
S. ssp I Rough-O:r:1,2		1				1								**2**
S. ssp I Rough-O:untypable					1	1								**2**
S. ssp I Rough-O:z10:-		1												**1**
S. ssp II	1				1									**2**
S. ssp II 4,12:d:-					1									**1**
S. ssp II 6,7:g,t:e,n,x					1									**1**
S. ssp II 16:m,t:-					1									**1**
S. ssp II 50:b:z6					1									**1**
S. ssp IIIa				2										**2**
S. ssp IIIa 18:z4,z23:-						1								**1**
S. ssp IIIa 41:z4,z23:-	1	1	2	1	1									**6**
S. ssp IIIb 35:k:e,n,x,z15					1									**1**
S. ssp IIIb 47:-:-		1												**1**
S. ssp IIIb 47:k:-						1								**1**
S. ssp IIIb 47:k:z35					1									**1**
S. ssp IIIb 50:k:z						1								**1**
S. ssp IIIb 50:l,v:z35	1													**1**
S. ssp IIIb 50:r:z		1												**1**
S. ssp IIIb 50:z:z52					1									**1**
S. ssp IIIb 53:z10:-	1													**1**
S. ssp IIIb 61:c:z35						1								**1**
S. ssp IIIb 61:l,v:1,5,7	1													**1**

Organism	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YT	NT	NU	Total
S. ssp IIIb 61:r:z						1								**1**
S. ssp IIIb 61:z52:z53					1									**1**
S. ssp IIIb Rough-O:r:e,n,x,z15		1												**1**
S. ssp IV	1			1										**2**
S. ssp IV 17:z29:-									2					**2**
S. ssp IV 44:z4,z23:-					2									**2**
S. ssp IV 48:g,z51:-		1			2									**3**
S. ssp IV 48:z4,z32:-					3									**3**
S. ssp IV 50:g,z51:-	1													**1**
S. ssp IV 50:z4,z23:-						1								**1**
Salmonella sp.			1	5	1		1	1	5					**14**
Total *Salmonella*	**1145**	**1054**	**195**	**252**	**2955**	**1219**	**145**	**34**	**169**	**51**	**6**	**6**	**20**	**7251**
Shigella														
S. boydii	1								2					**3**
S. boydii 1	2	1			1									**4**
S. boydii 2	1	1			1									**3**
S. boydii 4	1	1			6	2								**10**
S. boydii 12					1									**1**
S. boydii 13					2									**2**
S. boydii 14						1								**1**
S. boydii 17	1													**1**
S. boydii 18	1										1			**2**
S. boydii 19						1								**1**
S. boydii 20	1													**1**
S. dysenteriae				1										**1**
S. dysenteriae 1	3													**3**
S. dysenteriae 2		2			5	2								**9**
S. dysenteriae 3		2			1	1								**4**
S. dysenteriae 12		1												**1**
S. flexneri	1		5	6			2		2					**16**
S. flexneri 1	47	3									1			**51**
S. flexneri 1a					3									**3**
S. flexneri 1b					55	28								**83**
S. flexneri 2	20	13												**33**
S. flexneri 2a					22	13								**35**
S. flexneri 2b					2									**2**
S. flexneri 3	11	5												**16**
S. flexneri 3a					6	1								**7**
S. flexneri 3b					6	3								**9**
S. flexneri 4	1	1				1								**3**
S. flexneri 4a					5									**5**
S. flexneri 5	3													**3**
S. flexneri 5a					1									**1**
S. flexneri 5b	2													**2**
S. flexneri 6	5	4			10	4								**23**
S. flexneri Prov. SH-104	2	1			4	1								**8**
S. flexneri var. X		2												**2**
S. flexneri var. Y	3				6			1						**10**
S. sonnei	80	82	6	42	109	42	5	2	7	2				**377**

Organism	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	YT	NT	NU	Total
Shigella sp.	1	2												**3**
Total *Shigella*	**187**	**121**	**11**	**49**	**246**	**100**	**7**	**3**	**11**	**2**	**2**	**0**	**0**	**739**
Vibrio														
V. alginolyticus	1								1					**2**
V. cholerae								1						**1**
V. cholerae O1	1													**1**
V. cholerae O1 Inaba		1												**1**
V. cholerae non-O1/O139		3					1							**4**
V. fluvialis		1						2						**3**
V. mimicus	1													**1**
V. parahaemolyticus	14	8	1	2	4		2	3	1				2	**37**
Vibrio sp.							1							**1**
Total *Vibrio*	**17**	**13**	**1**	**2**	**4**	**0**	**4**	**6**	**2**	**0**	**0**	**0**	**2**	**51**
Viruses														
Adenovirus	51			42	98		2	1	2					**196**
Astrovirus					8									**8**
Enterovirus				6				1						**7**
Norovirus	388	264	273	82	1140	966	105	28	219	158				**3623**
Rotavirus	96	47	377	50	167		62	6	7	14		1	1	**828**
Total Viruses	**535**	**311**	**650**	**180**	**1413**	**966**	**169**	**36**	**228**	**172**	**0**	**1**	**1**	**4662**
Yersinia														
Y. enterocolitica	42	35	16	5	184	17	3		1					**303**
Y. frederiksenii	13		5											**18**
Y. intermedia		5	1											**6**
Y. kristensenii	3	1												**4**
Y. mollaretii	1													**1**
Y. pseudotuberculosis	4		1											**5**
Yersinia sp.				4										**4**
Total *Yersinia*	**63**	**41**	**23**	**9**	**184**	**17**	**3**	**0**	**1**	**0**	**0**	**0**	**0**	**341**
Total Organisms	**2790**	**1948**	**1177**	**849**	**5770**	**2820**	**590**	**125**	**618**	**304**	**12**	**9**	**29**	**17041**

Appendix 2. Phage types of isolates reported in 2010, NML*

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
Escherichia coli												
E. coli O157:H7	2		5		5	9	6					**25**
	4		2		1	3	2					**8**
	8	1	5			11	6					**23**
	14	1	9	3	1	22	5					**41**
	14a		31	6	36	96	29	8	1	9		**216**
	14c						1					**1**
	21	1	4									**5**
	23					1						**1**
	27					1						**1**
	31		4			1						**5**
	32		3									**3**
	34				1		3	1				**5**
	38		1									**1**
	39					1						**1**
	42					1						**1**
	45		1									**1**
	48					1				1		**2**
	49		2				1					**3**
	51		1									**1**
	54		1			2	1					**4**
	67		1									**1**
	70					2						**2**
	74					1						**1**
	87	1			2	1						**4**
	Atypical	1	1	1		7	1					**11**
	Untypable					1						**1**
	Subtotal	**5**	**71**	**10**	**46**	**161**	**55**	**9**	**1**	**10**	**0**	**368**
E. coli O157:H Nonmotile	2		1									**1**
	4					1						**1**
	8				1		2					**3**
	14					1	1	2	1			**5**
	14a		1			2				1		**4**
	14c		1			1	1					**3**
	87		1			1						**2**
	Atypical		2			1						**3**
	Subtotal	**0**	**6**	**0**	**1**	**7**	**4**	**2**	**1**	**1**	**0**	**22**
Total *Escherichia coli*		**5**	**77**	**10**	**47**	**168**	**59**	**11**	**2**	**11**	**0**	**390**
Salmonella												
S. Enteritidis	1	22	22	2	1	120	62	5	1	10	1	**246**
	1a		1									**1**
	1b	1	3			7	1					**12**

* These values include isolates submitted to the NML for research purposes and may also include a small number of strains that represent multiple isolates from the same patient.

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	2	1	2			3	5					**11**
	3	1				5						**6**
	3a		1			1						**2**
	4	12	10	2		35	18			1		**78**
	4b					1	1					**2**
	5a					1						**1**
	5b	6	6	2	3	68	40	3	1	6	1	**136**
	6	1				3	3					**7**
	6a	32	28	3	4	20	4					**91**
	6c					1						**1**
	7					1	2					**3**
	7a	3	6	2		6	2					**19**
	8	295	135	29	65	265	106	22	8	31	11	**967**
	9b					1						**1**
	11b			1								**1**
	12	2	2									**4**
	13	49	56	6	4	108	60	2	1	3		**289**
	13a	61	61	5	11	246	96	29	6	19	1	**535**
	14b	3	1	1	1	9	3					**18**
	14c					1	1					**2**
	15	1	1									**2**
	15a					3						**3**
	18					1						**1**
	19		2		1	4	5	3				**15**
	20	3	1									**4**
	21	3	3		1	11	2			1		**21**
	21c	1	1			6	1					**9**
	22		2	1		17	6	2	3	4	4	**39**
	23	2	4			6	1			1	1	**15**
	27					7	2					**9**
	30					1						**1**
	31	1	1									**2**
	34	1	40			1						**42**
	35	3		1		1						**5**
	37						1					**1**
	41	12	7	3	1	13					1	**37**
	43						1					**1**
	47					1						**1**
	51	17	8	2	2	16	5	2		1		**53**
	53			1								**1**
	55					5	1					**6**
	57	2				2		1				**5**
	194					1						**1**
	Atypical	21	23	1	4	34	12	1	1	2	1	**100**
	Untypable	9	12			9	2	1			2	**35**
	Subtotal	**565**	**439**	**62**	**98**	**1041**	**443**	**71**	**21**	**79**	**23**	**2842**
S. Hadar	2	1	3		1	22		1		1		**29**
	5					2						**2**
	10					3						**3**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	11	1	1	2	2	3	1					**10**
	13					1						**1**
	19	1										**1**
	43					1						**1**
	47	1		4	1		1					**7**
	48			1								**1**
	51					1						**1**
	56					1						**1**
	58					1						**1**
	Atypical					2				1		**3**
	Untypable	4										**4**
	Subtotal	**8**	**4**	**7**	**4**	**37**	**2**	**1**	**0**	**2**	**0**	**65**
S. Heidelberg	1					2	3					**5**
	2	2	3	2	6	15	27	2				**57**
	4					2	5					**7**
	5			1		10	2	3		1	1	**18**
	6						1					**1**
	6a										1	**1**
	9		1		1		1					**3**
	10					8	2	1				**11**
	11	1				1						**2**
	11a					2						**2**
	13			1	2							**3**
	16					4	6	2	1			**13**
	17			1		8	10					**19**
	18	5	2	1		1						**9**
	18a					3	1					**4**
	19	10	93	2	5	143	94	11	2	3	1	**364**
	19a					3	4	1		1		**9**
	19b						1					**1**
	20				2	1						**3**
	21						1					**1**
	22					2	2					**4**
	24		1									**1**
	25				2				1			**3**
	26				1	12	27	4		3		**47**
	29	12	19		2	35	16	1		1		**86**
	29a	1	4									**5**
	32	2				2	6			1		**11**
	32a								1			**1**
	32b					1				1		**2**
	35							1				**1**
	39									1		**1**
	41	4	3	1	1	7	7	1				**24**
	42					1	1					**2**
	44					1		1				**2**
	47					1	1					**2**
	51						1					**1**
	52					2						**2**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	53					2						**2**
	54		1									**1**
	55								1			**1**
	56				1							**1**
	58					1	1					**2**
	60					2	2					**4**
	Atypical	2	1	1	2	11	10			1		**28**
	Untypable									1		**1**
	Subtotal	**39**	**128**	**10**	**25**	**283**	**232**	**28**	**6**	**14**	**3**	**768**
S. Infantis	1					1				1		**2**
	4		4			7	1					**12**
	6					2						**2**
	7	4	5	1		8	1	2		1		**22**
	8		3			2						**5**
	9		1			2						**3**
	12					2						**2**
	13					4					1	**5**
	26		1			1	1					**3**
	27					1						**1**
	Atypical									1	1	**2**
	Untypable		1			1						**2**
	Subtotal	**4**	**15**	**1**	**0**	**31**	**3**	**2**	**0**	**3**	**2**	**61**
S. Newport	1					2						**2**
	2	1		1		4						**6**
	3	3		1	2	13	1					**20**
	4	1	1		1	2						**5**
	8	1										**1**
	9	2				23	2				1	**28**
	10	4	1			1						**6**
	11					1						**1**
	13				1	2	1	1				**5**
	14					1	2					**3**
	14a	1		1	1	1						**4**
	14b	4	6		1	3	1	1				**16**
	14c	1		1			1					**3**
	15		1			7	1			2		**11**
	16		1			1	2					**4**
	17a					3	2					**5**
	17c					1						**1**
	17e		2				1					**3**
	Atypical	1	4		2	9	3					**19**
	Subtotal	**19**	**16**	**4**	**8**	**74**	**17**	**2**	**0**	**2**	**1**	**143**
S. Oranienburg	1									1		**1**
	2		1									**1**
	6		3		2	3	2	1				**11**
	8					1						**1**
	9					45						**45**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	11		2			4	4					**10**
	12	1		1								**2**
	13					1						**1**
	Atypical				1	8						**9**
	Untypable					1						**1**
	Subtotal	**1**	**6**	**1**	**3**	**63**	**6**	**1**	**0**	**1**	**0**	**82**
S. Panama	A		4									**4**
	F		1									**1**
	G		3		1	1						**5**
	H		1			1						**2**
	Atypical		1			2						**3**
	Untypable		4		3							**7**
	Subtotal	**0**	**14**	**0**	**4**	**4**	**0**	**0**	**0**	**0**	**0**	**22**
S. Paratyphi B	3b var. 2	1										**1**
	Battersea					1	1					**2**
	Dundee					2	1					**3**
	Dundee var. 2	1				6	2			1		**10**
	Worksop			1								**1**
	Atypical					4	1					**5**
	Subtotal	**2**	**0**	**1**	**0**	**13**	**5**	**0**	**0**	**1**	**0**	**22**
S. Paratyphi B var. Java	3b var. 2	1			2	2						**5**
	Battersea	3					1					**4**
	Dundee	1	2		1	6	4					**14**
	Dundee var. 2	1	1				1					**3**
	Stirling						1					**1**
	Worksop		2	1		1						**4**
	Atypical	2	4			7	2		1			**16**
	Untypable		1		3							**4**
	Subtotal	**8**	**10**	**1**	**6**	**16**	**9**	**0**	**1**	**0**	**0**	**51**
S. ssp (I) 4,[5],12:b:-	1 var. 6						1					**1**
	3b var. 2					5						**5**
	3b var. 7					4						**4**
	Battersea	1	3			23	13					**40**
	Dundee						1					**1**
	Dundee var. 1		1									**1**
	Dundee var. 2					8						**8**
	Worksop						1					**1**
	Atypical	2	2			10	2				1	**17**
	Untypable	3	2			10						**15**
	Subtotal	**6**	**8**	**0**	**0**	**60**	**18**	**0**	**0**	**0**	**1**	**93**
S. ssp (I) 4,[5],12:i:-	12						1					**1**
	21	2				1						**3**
	35						4					**4**
	41		1			1	1					**3**
	41a			1								**1**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	51						1					**1**
	99							1				**1**
	110b					1	1					**2**
	120		2			4	2					**8**
	151					1						**1**
	191	4	19	6	16	13	5		1	1		**65**
	191a	7	30	5	4		1					**47**
	193	4	2			13	29	2				**50**
	195	2					1					**3**
	203			1		1						**2**
	UT1						1					**1**
	UT2					1	1					**2**
	UT6		1									**1**
	UT7					2						**2**
	U291	1	3	1	2	12	4				1	**24**
	U302		1				6					**7**
	Atypical	2	10	2	1	8	2	5		1		**31**
	Untypable					2						**2**
	Subtotal	**22**	**69**	**16**	**23**	**60**	**60**	**8**	**1**	**2**	**1**	**262**
S. ssp (I) Rough-O:i:1,2	UT3					1						**1**
S. ssp (I) Vi:d:-	Untypable	1				1						**2**
S. Thompson	1		4	4		14	2					**24**
	2		2			1				1		**4**
	3			1		6	6					**13**
	11					2						**2**
	21		1		1	1		1	1		1	**6**
	22					1						**1**
	25	3	6		1							**10**
	26									1		**1**
	Atypical					1	1					**2**
	Untypable		1			1						**2**
	Subtotal	**3**	**14**	**5**	**2**	**27**	**9**	**1**	**1**	**2**	**1**	**65**
S. Typhi	28	1			1	2						**4**
	38					1						**1**
	40		2			1						**3**
	A	1			1	4	1					**7**
	B1		1									**1**
	D2					1						**1**
	DVS	1				1	1					**3**
	E1	13	7	2	5	40	7			1		**75**
	E2	2										**2**
	E9 var	6	7		2	12	2					**29**
	E14	2										**2**
	J1	1				1						**2**
	K1					1						**1**
	M1					1			1			**2**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	T	1										**1**
	UVS	1				4						**5**
	UVS (I+IV)	4	1			15	5					**25**
	Untypable	2	1	1	4	8	4					**20**
	Subtotal	**35**	**19**	**3**	**13**	**92**	**20**	**0**	**1**	**1**	**0**	**184**
S. Typhimurium	1		3	1	1	12	1	2				**20**
	2	1				8	1					**10**
	3 aerogenic	1								1		**2**
	4						1					**1**
	6						1					**1**
	8	1	2			1						**4**
	9					2						**2**
	10	1	1	1	1	15	5			1	2	**27**
	12	1	1		1	12	8					**23**
	15a	5	2	1				1				**9**
	21	2				1	1					**4**
	22		1			1	2	1		1		**6**
	29					1	1					**2**
	35						2					**2**
	39					1	1					**2**
	40	1	1			1						**3**
	41	1	2			4	5					**12**
	42					1		1				**2**
	46					1						**1**
	51					1						**1**
	66					1				1		**2**
	67				1							**1**
	69					5	2					**7**
	82					1	3					**4**
	94					1						**1**
	99	1				4						**5**
	104	4	21	1		30	14			2		**72**
	104a		4			15	2					**21**
	104b		2	1		4	1					**8**
	108	1		1	1	19	5	1				**28**
	110						1					**1**
	110b		7	2		8	5			1		**23**
	117					1						**1**
	120		1			10	4					**15**
	132		2			3	3	1				**9**
	135	1				1				1		**3**
	136	1				2	1					**4**
	143						1					**1**
	146						1					**1**
	151					1						**1**
	153					2						**2**
	160		1			1						**2**
	169					1						**1**
	170	6	15	41	4	89	32	1		1	1	**190**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	180						1					**1**
	191					1	1			1		**3**
	192					1						**1**
	193		5	2		19	5	1				**32**
	194					2	1					**3**
	195					3	3	1		1	2	**10**
	203		2		1	2		1				**6**
	204b					1						**1**
	208		2			2						**4**
	UT1	4	5	1		1	2					**13**
	UT2	4	52		1	2	1					**60**
	UT5		2			2						**4**
	UT6					1						**1**
	UT7		5		2	1						**8**
	U284	2										**2**
	U302	1	2			16	7	2				**28**
	U310						1					**1**
	Atypical	7	8	2	2	35	12	2		6		**74**
	Untypable					5	1					**6**
	Subtotal	**46**	**149**	**54**	**15**	**355**	**139**	**15**	**0**	**17**	**5**	**795**
Total *Salmonella*		**759**	**891**	**165**	**201**	**2158**	**963**	**129**	**31**	**124**	**37**	**5458**
Shigella												
Shigella boydii 1	13									1		**1**
	Atypical		1									**1**
	Subtotal	**0**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**0**	**2**
Shigella boydii 2	6		1									**1**
	13									1		**1**
	Subtotal	**0**	**1**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**0**	**2**
Shigella boydii 4	13		1									**1**
Shigella boydii 13	Untypable					1						**1**
Shigella boydii 14	13						1					**1**
Shigella boydii 19	3	1										**1**
Shigella boydii 20	3	1										**1**
Shigella sonnei	1		65	3		25		2	1	3	1	**100**
	2			1								**1**
	10					1		1				**2**
	15		4			1						**5**
	18					1						**1**
	19		6									**6**
	21		1									**1**
	26							1				**1**

Organism	Phage Type	BC	AB	SK	MB	ON	QC	NB	PE	NS	NL	Total
	S14		1									**1**
	Atypical		7	2		2			1	4	1	**17**
	Subtotal	**0**	**84**	**6**	**0**	**30**	**0**	**4**	**2**	**7**	**2**	**135**
Total *Shigella*		**2**	**87**	**6**	**0**	**31**	**1**	**4**	**2**	**9**	**2**	**144**
Total Organisms		**766**	**1055**	**181**	**248**	**2357**	**1023**	**144**	**35**	**144**	**39**	**5992**