

British Columbia Integrated Surveillance of Foodborne Pathogens (BCISFP) Annual Summary of *Salmonella* Findings

2017

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Introduction

BC Integrated Surveillance of Foodborne Pathogens (BCISFP) was initiated in October 2006 with the mission of providing surveillance along the food chain for safe food and healthy people in British Columbia (BC). *Salmonella* is an ideal candidate for integrated surveillance because it is cultured within all sectors (animal, food and humans), is recovered at high rates, and affects a great variety of food commodities. For more information please visit: www.bccdc. ca/integratedfoodchainsurveillance.

This is the BCISFP's eighth annual summary. The purpose of the summary is to provide integrated information about the occurrence of *Salmonella* in BC among humans and at select points along the food chain. Data are sourced from four distinct sectors: human, animal (farm, companion, domestic, and wildlife), abattoir and food. Details about the data sources and how they are integrated are described in BC Integrated Surveillance of Foodborne Pathogens Methods available at www.bccdc.ca/integratedfoodchainsurveillance.

2017 marked the introduction of prospective Whole Genome Sequencing for all human *Salmonella* isolates in Canada. This year's report will be the last to include phage type (PT) data, as it was phased out as a subtyping method in all sectors in 2017. In this report we describe how this shift in laboratory surveillance methods is changing our work.





Results-overview

In 2017, Salmonella was isolated from 553 locally-acquired human specimens, 178 food specimens, 29 abattoir specimens and 759 animal specimens (Table 1). A total of 87 different serotypes were observed from all sectors in 2017. Among the 20 most common serotypes that spanned multiple sectors, two serotypes (S. Enteritidis, S. Kentucky) were found in all four sectors (human, animal, abattoir and food); ten serotypes were found in three sectors and eight serotypes in two sectors. As in previous years, serotypes overlapped primarily between humans, chicken/turkey meat products and samples from on-farm chickens and their environments, likely due to the large number of isolates from these sources.

In 2017, the most commonly detected serotype in BC was *S*. Enteritidis, which has been the most common serotype historically in BC within all sectors. It was the most common serotype for locally-acquired human infections, fresh chicken meat, chicken nuggets, abattoir chicken, chickens on-farm, and domestic ducks and geese (see *Salmonella* Enteritidis section). For the second year in a row, the incidence of *S*. Enteritidis in BC declined to the lowest rate of locally-acquired infections since 2013 (Figure 1).

As in 2016, the second most common serotype was *S*. Kentucky. This serotype is particularly common in chickens and chicken food products, but rarely causes human illness; in 2017 there were only two locally acquired human infections of *S*. Kentucky.

In contrast to 2016, *S.* Enteritidis has dropped to the second most common serotype detected in turkey meat and was rarely recovered from on-farm turkeys. In turkey meat, *S.* Reading was the most common serotype identified in 2017, while *S.* Hadar was the most common serotype identified in on-farm turkeys. Similar to 2016, turkey had a variety of distinct serotypes that were different than those detected in chicken meat.

In 2017, 1069 human isolates were identified. Travel was associated with 32.4% of human *Salmonella* isolates and the remainder were locally-acquired. The most common serotypes of travel-related *Salmonella* infection include: Enteritidis (142), Typhi (38), Paratyphi (22), 4,5,12:i:- (17), and Typhimurium (12). Amongst the locally-acquired human isolates, 55 different serotypes were observed, 54.5% of which had no crresponding isolates identified from food, abattoir, or animal isolates.





Table 1: Salmonella serotypes reported in two or more sectors (human, food, abattoir, animal) in BC*, 2017

Serotype	Locally- acquired human infections	Food				Abattoir	Animal								
		Fresh Chicken	Chicken Nuggets	Pork	Turkey	Chicken	Cattle	Chicken ¹	Domestic Duck/Goose	Exotic /Zoo²	Swine	Turkey ³	Wildlife ⁴	Other ⁵	Total
Enteritidis	365	63	17		12	17	1	262	9	1		1		5	753
Kentucky	2	22	4		1	5		203				1			238
Senftenberg	1					2		22				15		1	41
Hadar	2				7			1	2			27			39
Reading	7				16							10			33
4,5,12:i:-	23							8						1	32
Mbandaka	3	4	3					19	1						30
Typhimurium	22		1					5					1	1	30
Infantis	11	3	2					12							28
Braenderup	11	1	1					9							22
Anatum	3				1			3	1			13			21
Heidelberg	11		4		1										16
Agona	1				1			2				10			14
Dublin	1			1			10								12
Worthington					1			8							9
Cubana					1	3		4							8
Thompson	2	1						4							7
Montevideo	1							1				4			6
Rissen	3							2			1				6
Uganda	1							2				3			6
Other	83	4	2	0	4	2	1	50	4	2	1	21	1	2	177
Total	553	98	34	1	45	29	12	617	17	3	2	105	2	10	1528

^{*}Includes serotypes with five or more isolates across all sectors.







^{1.} Samples taken from on -farm chickens and their environments. In 2017, these include 114 diagnostic isolates, 416 environmental isolates taken from chicken hatcheries/farms, and 78 CIPARS/FoodNet Canada farm isolates (pre-harvest only).

^{2.} Exotic/Zoo includes 1 jaguar, 1 reptile and 1 snake

^{3.} In 2017, the turkey isolates include 18 diagnostic isolates, 3 environmental isolates and 84 CIPARS/FoodNet Canada farm isolates (pre-harvest only).

^{4.} Wildlife includes 1 snake and 1 heron.

^{5.} Other animals include 1 mink, 1 sheep and 8 various poultry species.

Salmonella Enteritidis

BC has been experiencing a *S.* Enteritidis outbreak since 2008. This outbreak continued in 2017, where the BC human incidence was 12.3/100,000 population (Figure 1). In 2017, *S.* Enteritidis accounted for 66% of locally-acquired *Salmonella* infections in humans. While human incidence in BC declined in 2017 from historically high rates seen in 2015 and 2016, it remained notably higher than the incidence reported prior to the start of the outbreak that ranged from 2.9-7.0/100,000 population between 2001 and 2007. In 2017, seven *S.* Enteritidis clusters of human illness were investigated in BC. Five of these investigations were national and two investigations had cases only in BC. The two provincial investigations involved cases from the Lower Mainland. One was associated with farm-gate eggs from a local farm and the other was associated with a holiday event where no source was identified. Two of the five national investigations were related to frozen, breaded chicken products. The Canadian Food Inspection Agency (CFIA) issued health hazard alerts in both of these situations (1,2). The remaining three national investigations were hypothesized to be caused by chicken meat based on case exposure information and chicken meat isolates that were genetically related to human isolates.

The incidence of human *S*. Enteritidis in BC remained notably higher than the national average (8.9/100,000) in 2017 (Figure 1). Between 2008 and 2014, the trends seen in the national incidence closely reflected the trends seen in BC, which suggested that the rate of *S*. Enteritidis in BC had a strong influence on national incidence. Between 2015 and 2017, BC and national trends showed different patterns. National incidence remained relatively constant between 2014 and 2017; the significant increase and subsequent drop seen in BC incidence since 2015 was not reflected in the national incidence.

Analysis of *S*. Enteritidis exposure data reported between 2014 and 2017 showed that cases were statistically significantly more likely to have the following exposures than the healthy population: chicken meat consumption (74% of cases vs 69% of controls), egg consumption (68% of cases vs 54% of controls), breaded chicken product consumption (22% of cases vs 15% of controls), contact with live poultry (11% of cases vs 3% of controls), and to have fed their pet a raw food diet (8% of cases vs 5% of controls) (3).

S. Enteritidis continues to be the most commonly detected serotype of Salmonella in chicken meat (i.e., fresh chicken, chicken nuggets), in samples taken from chicken at abattoirs, and in samples from on-farm chickens and their environments (Table 1). There have been similar trends over time in human cases and in fresh chicken meat (Figure 2), suggesting an association between the level of S. Enteritidis contamination in fresh chicken meat and human disease rates.





Figure 1: Salmonella Enteritidis human incidence (all), Canada vs BC, 2008-2017

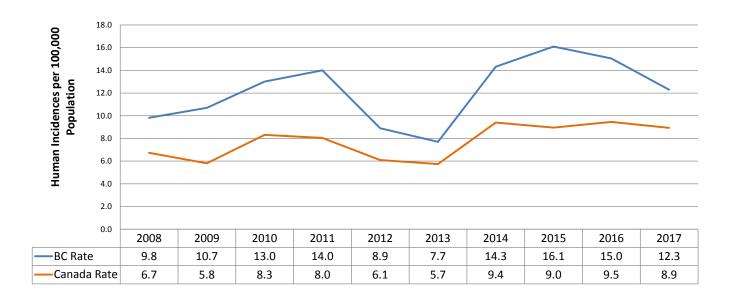
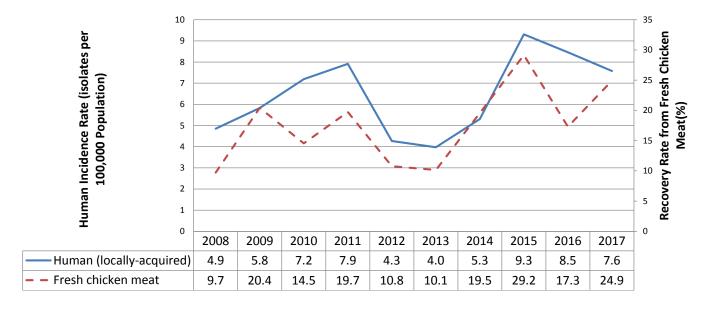


Figure 2: Salmonella Enteritidis human incidence (locally-acquired) and recovery rate from chicken meat, BC, 2008-2017







Transition to Whole Genome Sequencing

In May 2017, prospective whole genome sequencing (WGS) of all *Salmonella* human isolates was implemented across Canada. Prior to this, surveillance relied on phage typing for *S*. Enteritidis and *S*. Heidelberg, and pulsed-field gel electrophoresis (PFGE) for other *Salmonella* serotypes. WGS provides more discriminatory power than the traditional subtyping methods, and allows for the detection of smaller, more closely-related clusters. This has resulted in the detection and investigation of more *Salmonella* clusters, and in particular *S*. Enteritidis clusters.

A limitation of WGS is that it did not become available prospectively for all *Salmonella* isolates from food, animal, and abattoir sectors in 2017. The food data that is available has been helpful to outbreak investigation activities, particularly when WGS demonstrated a genetic link between a specific food product and human isolates. This was the case in two investigations associated with frozen breaded chicken in 2017, where a *Salmonella* isolate from a food consumed by outbreak cases was found to be related to the human by WGS. Comprehensive prospective WGS for food and animal isolates is expected to be implemented in the coming years, allowing for the ongoing integrated analysis of *Salmonella* surveillance data from all sectors.





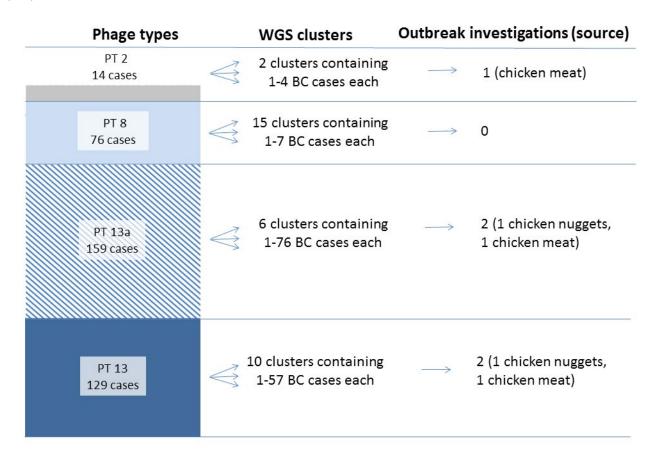


Impact of WGS on S. Enteritidis outbreak detection

Phage typing has historically been used to detect clusters of *S*. Enteritidis amongst humans, as well as to characterize isolates from food and animal sectors. However, it was discontinued in all sectors at different times in 2017 as WGS was implemented. The most common phage types (PTs) detected amongst on-farm chickens and their environments in 2017 were PT 13 (n=51), PT 13a (n=14), and PT 23 (n=9). Similarly, in the human sector, the most common phage types were PT 13 (n=129), PT 13a (n=159), and PT 8 (n=76), which is consistent with previous years. No food PT data is available for 2017. Investigation of human SE outbreaks associated with these phage types has historically been associated with poultry sources.

Between May and December 2017, prospective WGS separated the four most common human phage types in 2017, PTs 13, 13a, 8, and 2, into 33 distinct clusters of related isolates (Figure 3). Five of these clusters led to national outbreak investigations based on geographic or temporal clustering, interesting demographic profile, or suspect source. Of these five outbreak investigations, two were associated with frozen breaded chicken and three were associated with chicken, which was also the suspect source for the corresponding phage type investigations in previous years.

Figure 3: Human *Salmonella* Enteritidis clusters and outbreak investigations detected by prospective WGS, by phage type, BC, 2017







Utility of WGS during S. Braenderup investigation

Among the serotypes that spanned two or more sectors, *S*. Braenderup was the tenth most common serotype in 2017 (<u>Table 1</u>). There was a total of 22 isolates; 11 from locally-acquired human cases, two from food, and nine from animals. All of the food and animal isolates were from chicken samples.

An outbreak of human *S*. Braenderup occurred nationally in 2017. A total of 51 cases were identified that matched based on WGS; ten of these cases were in BC. Case onset dates were reported from March to October, 2017. In addition, there were seven isolates from chicken meat or chicken samples from on-farm that were related to the human cases by WGS, two of these were collected in BC. Investigation identified chicken as the source of this outbreak based on case exposure information (reported by 94% of cases), food safety investigation and traceback, and laboratory data that indicated similarity between the food, animal and human isolates. This investigation demonstrated the use of WGS across sectors to help identify a possible source of human illness.

Conclusion

Ongoing surveillance across sectors is important in order to assess changes and trends in *Salmonella* strains over time to improve our knowledge about *Salmonella* along the farm to fork continuum in BC.

The current model of integrated surveillance in BC continues to be a good platform for data sharing, integration and analysis across human, food and animal sectors for *Salmonella*. Successful surveillance depends on a strong and supported network of individuals and agencies. The connectivity among partners in this system supports surveillance of *Salmonella* and sharing of data and information.

The transition from traditional laboratory subtyping tools to whole genome sequencing of *Salmonella* in 2017 has posed some challenges, particularly due to the delayed implementation in non-human sectors, but is promising to provide a more specific and therefore useful tool to link human cases to each other and to non-human sources, leading to an improved ability to detect and control enteric illnesses and outbreaks.









References

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