



BC Integrated Surveillance of Foodborne Pathogens (BCISFP) Methods

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2006-2017



Background

BC Integrated Surveillance of Foodborne Pathogens (BCISFP) was initiated in October 2006. The mission is to provide surveillance along the food chain for safer food and healthy people in British Columbia (BC). Integrated surveillance expands on traditional surveillance by monitoring and comparing the multiple components of a system (e.g. food chain) to better understand the sources of disease and transmission routes. The overall goal of integrated surveillance is to gain a better understanding of the sources of human illness in a system in order to prevent and control them.

Data are sourced from four distinct sectors: human, food, animal (including livestock, pets and wildlife) and abattoir (Appendix 1). *Salmonella* is the first pathogen under surveillance because it is cultured within all sectors, is recovered at high rates, has several subtyping methods available, and affects a great variety of food commodities. For more information about BCISFP please visit: www.bccdc.ca/integratedfoodchainsurveillance.

Data Sources

The data sources, data flow, typing information, and commodities tested over time are outlined in Appendices 1, 2 and 3. This documents outlines the typing information used by the BCISFP; the programs providing data may have additional typing results not currently used by the BCISFP.

Human

Human salmonellosis cases are reportable in British Columbia (BC). Local laboratories forward all *Salmonella* isolates to the BCCDC Public Health Laboratory (BCCDC PHL) for serotyping.

Up until March 2012, the BCCDC PHL conducted pulsed-field gel electrophoresis (PFGE) on all *Salmonella* isolates. From April 2012 to May 2016, BCCDC PHL conducted PFGE on all *Salmonella* isolates, except serotypes Enteritidis and Heidelberg. Starting in June 2016, BCCDC PHL conducts (PFGE) on isolates with the five most common serotypes (excluding Enteritidis and Heidelberg), any serotype with three or more isolates over a 60 day period, and serotypes requested to support outbreak/cluster investigations. As of June 1, 2018, PFGE for human isolates was discontinued.

The National Microbiology Laboratory of the Public Health Agency of Canada (NML) conducted phage typing for BC's *Salmonella* isolates. Until March 2012, the BCCDC PHL forwarded S. Enteritidis and S. Heidelberg isolates from the first 15 days of the month to the NML for phage typing. Starting in April 2012, phage typing was expanded to include all *Salmonella* serotypes from the first 15 days of the month plus all S. Enteritidis and S. Heidelberg isolates from the entire month. As of January 1, 2018 phage typing for human isolates was discontinued.

As of May 1, 2017 prospective whole genome sequencing has been conducted by the NML on all human *Salmonella* isolates.

The BCCDC PHL provides available attributes on all human *Salmonella* isolates to the BCISFP.

During follow-up with salmonellosis cases, Environmental Health Officers in BC ask about travel and other exposures during the incubation period (for further details see the Salmonellosis Follow-up form at <http://www.bccdc.ca/health-professionals/professional-resources/surveillance-forms>). Travel information is recorded in the public health information systems (PARIS for Vancouver Coastal Health Authority; iPHIS (to September 2014) and Panorama (from September 2014) for all other Health Authorities).

Using the data from the public health information systems, cases are classified into one of three groups:

- Locally-acquired: cases who did not travel outside of Canada during their exposure period.

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- Travel-related (possible or confirmed): cases who had spent any time during their exposure period outside of Canada.
- Unknown: no, or incomplete, travel information was available (e.g., case could not be reached, information was not collected or entered, adequate detail was not provided to classify as local/travel, etc.).

As of 2012, travel exposure data for the cases are linked to the isolate information (serotype, phage type and PFGE) for the annual analysis. Except for analyses examining cases by travel status, all human analyses in the annual reports are based only on isolates from cases reported as locally-acquired. *Salmonella* Typhi and Paratyphi (except for Paratyphi B var. Java) are rarely locally acquired and rarely foodborne, and are therefore excluded from the analyses.

Food

The Public Health Agency of Canada (PHAC) provides data on *Salmonella* isolates from meat samples collected in BC through the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) Retail Meat Program (<http://www.phac-aspc.gc.ca/cipars-picra/pubs-eng.php>). Data on samples of fresh chicken parts and fresh pork (2007-present), and fresh ground turkey (2011-present) are collected as part of the core program. Samples of frozen raw breaded chicken products (2011-2014), fresh black silkie chicken (2010-2013), and fresh seafood (2008-present) are also collected, although the number of samples collected is routinely lower than the core retail commodities. The NML (formerly Laboratory for Foodborne Zoonoses (LFZ) of the Public Health Agency of Canada) is responsible for primary isolation of pathogens and serotyping for all CIPARS meat samples. As of August 31, 2017, phage typing for *S. Enteritidis*, *S. Typhimurium* and *S. Heidelberg* isolates from CIPARS meat samples was discontinued (Appendix 2). Whole genome sequencing is not routinely being conducted on CIPARS meat isolates.

As of 2015, PHAC also provides data on *Salmonella* isolates from meat samples collected by the BC FoodNet sentinel site (<http://www.phac-aspc.gc.ca/foodnetcanada/index-eng.php>). Data on samples of fresh chicken breasts, and fresh ground beef (2015-present) are collected as part of the core program. Samples of frozen raw breaded chicken products (2015-present), fresh ground pork (2016), and fresh and frozen veal (2017) are also collected on a targeted basis. The Lab Services Division, University of Guelph conducts the primary isolation of pathogens from FoodNet samples. All *Salmonella* isolates are then forwarded to NML; there, FoodNet isolates go through the same process as CIPARS isolates (serotyping of all isolates; phage typing of *S. Enteritidis*, *S. Typhimurium* and *S. Heidelberg* was discontinued as of August 31, 2017). Whole genome sequencing started in May 2017 on FoodNet meat samples.

CIPARS and FoodNet provide the BCISFP with data on the number of meat samples tested for *Salmonella*. These data are used as denominators to calculate recovery rates.

Animal

The Animal Health Centre (AHC), BC Ministry of Agriculture (BC MAgr) provides data on *Salmonella* isolates from all animals tested. While over 80% of *Salmonella* isolates from BC MAgr are from chickens and their environments, other animal species are included (e.g. turkey, cattle, dogs, cats, reptiles, wild birds, etc.).

Two categories of data are included – diagnostic and monitoring. Diagnostic samples represent submissions to the AHC from the animals' owners or their veterinarians. These are generally specimens from individual animals.

Monitoring samples represent submissions from apparently healthy animals and their environments sampled as part of government monitoring or industry monitoring/research programs. Government monitoring samples are submitted from ongoing, routine animal health programs (at present, the only such programs are in the poultry industry). These specimens are collected in a systematic manner, and are submitted to look specifically for *Salmonella* species. These samples generally represent a flock, rather than an individual animal.

There is one major industry monitoring program: "Start Clean—Stay Clean", administered by the Canadian Egg Marketing Agency (CEMA). The program is for producers of table eggs, and looks specifically for *Salmonella* Enteritidis. The program involves the collection of environmental samples at three times during the life of the flock: once for pullets (i.e. young birds), and twice during the lay period. Environmental samples may include feathers, and swabs from floors, ventilation fans, egg belts, and walls. Eggs from barns positive for *S. Enteritidis* are diverted for pasteurization and/or the flock is depopulated. The barn(s) are thoroughly cleaned and must test negative prior to the introduction of a new flock.

BC MAgr *Salmonella* isolates from projects and research are not included in these analyses. Animal data from BC MAgr may include multiple isolates of *Salmonella* from the same animal or premises.

As of 2015, CIPARS and FoodNet Canada provide data on *Salmonella* isolates from on-farm animals (chicken and turkey) in BC. The farm surveillance component is a shared responsibility between the two larger surveillance programs. Only samples collected close to the time of slaughter (pre-harvest) are included in these analyses; samples collected when the chicks/poults are placed in the barns (placement) are not included. More details about the farm program are available in the program reports available at: <http://www.phac-aspc.gc.ca/cipars-picra/pubs-eng.php> and <http://www.phac-aspc.gc.ca/foodnetcanada/publications-eng.php>.

The *Salmonella* typing data available are shown in Appendix 2. The Animal Health Centre conducts primary isolation for the BC MAgr samples. The NML (formerly LFZ-PHAC) conducts primary isolation for CIPARS/FoodNet Canada farm samples. In 2006-2007, the BCCDC

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PHL conducted serotyping and PFGE (*S. Enteritidis*) for the BC MAgri isolates. The NML (formerly LFZ-PHAC) performs serotyping (all *Salmonella*) and phage typing (*S. Enteritidis*, *S. Typhimurium* and *S. Heidelberg*) for the CIPARS, FoodNet and BC MAgri isolates. Phage typing on BC MAgri, CIPARS, and FoodNet isolates was stopped in August 2017. Whole genome sequencing of FoodNet-CIPARS shared farm isolates as of August 2018.

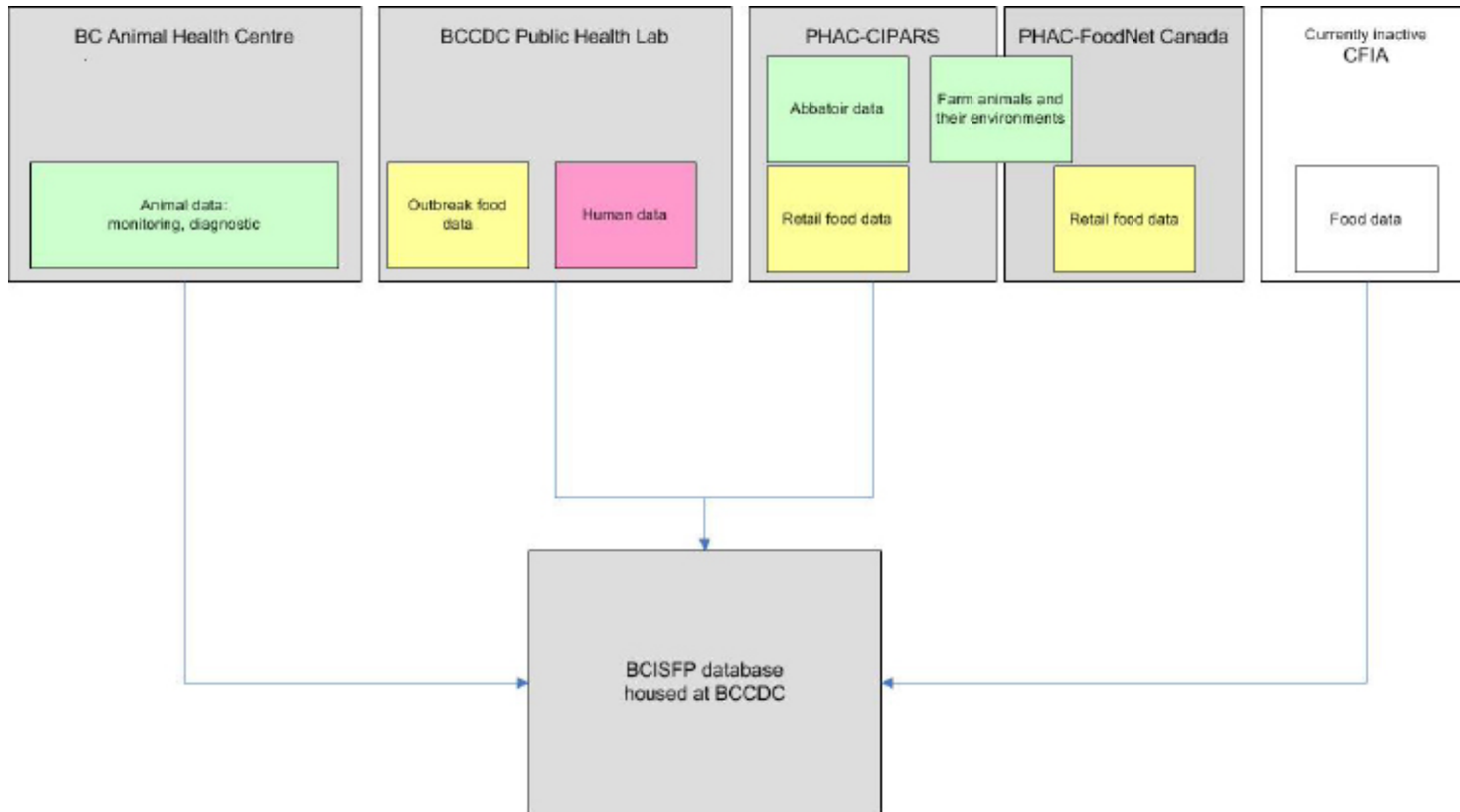
Abattoir

CIPARS routinely tests for *Salmonella* in cecal content samples collected from pigs and chickens slaughtered at federally inspected abattoirs across Canada. As of 2011, CIPARS provides data on *Salmonella* isolates from animals that were located in BC prior to slaughter (these data do not reflect the location of the abattoirs). The NML (formerly LFZ-PHAC) conducts primary isolation, serotyping (all *Salmonella*) and phage typing (*S. Enteritidis*, *S. Typhimurium* and *S. Heidelberg*) for CIPARS abattoir samples. Phage typing on CIPARS abattoir isolates was stopped in August 2017. Whole genome sequencing is not routinely being conducted on abattoir isolates.

Analysis

All data are extracted from their respective information systems and compiled in a single Microsoft Access database at BCCDC. Data tables are prepared and reviewed bimonthly by the BC Integrated Surveillance Epidemiology Sub-Group which is made up of representatives from BCCDC, BC MAgri and CIPARS. Each sector's data are reviewed individually, and then all data are integrated and reviewed to identify common strains and trends over time. Rates and trends in *Salmonella* are compared across sectors and over time.

Appendix 1. BCISFP Data Sources and Data Flow



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Appendix 2. Typing Data Available by Program and Year, BCISFP

Sector	Program	Typing Method	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
Animal	BC MAgri	Serotype	All Salmonella											
		Phage Type		S. Enteritidis, S. Typhimurium & S. Heidelberg										Stopped in August
		PFGE	S. Enteritidis											
	CIPARS/ FoodNet	Serotype											All Salmonella	
Phage Type												S. Enteritidis, S. Typhimurium & S. Heidelberg	Stopped in August	
Abattoir	CIPARS	Serotype	All Salmonella											
		Phage Type											S. Enteritidis, S. Typhimurium & S. Heidelberg	Stopped in August
Food	CIPARS	Serotype	All Salmonella											
		Phage Type		S. Enteritidis, S. Typhimurium & S. Heidelberg										Stopped in August
	FoodNet	Serotype											All Salmonella	
		Phage Type											S. Enteritidis, S. Typhimurium & S. Heidelberg	Stopped in August
		Whole Genome Sequencing												All Salmonella as of May 1
Human	BCCDC PHL	Serotype	All Salmonella											
		PFGE [‡]	All Salmonella							All except S. Enteritidis & S. Heidelberg			Select [‡]	
	NML	Phage Type [†]	S. Enteritidis & S. Heidelberg from first 15 days of the month.				All S. Enteritidis & S. Heidelberg. All other serotypes from first 15 days of the month.							
		Whole Genome Sequencing												All Salmonella as of May 1

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Appendix 3. Commodities Tested by Program and Year, BCISFP

