

# Enhancing Foodborne Disease Surveillance Across Australia

**OzFoodNet**

**Annual Report 2020**



**Queensland  
Government**

## Enhancing Foodborne Disease Surveillance Across Australia – OzFoodNet Annual Report, 2020

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# Abbreviations

CDNA	Communicable Diseases Network Australia
cgMLST	core genome Multi-Locus Sequence type
FSANZ	Food Standards Australia New Zealand
HHS	Hospital Health Service
HUS	Haemolytic Uraemic Syndrome
IGAS	Invasive Group A Streptococcal Disease
MDU	Microbiological Diagnostic Unit, Doherty Institute for Infection and Immunity
MDR	Multi-drug resistant
MLVA	Multilocus Variable Number Tandem Repeats Analysis
MLST	Multilocus sequence type
MSM	Men who have sex with men
NNDSS	National Notifiable Diseases Surveillance System
PCR	Polymerase chain reaction (nucleic acid amplification)
PHLN	Public Health Laboratory Network
SNP	Single Nucleotide Polymorphism
STEC	Shiga toxin-producing E. coli
STm	Salmonella Typhimurium
QHFSS	Queensland Health Forensic and Scientific Services
WGS	Whole genome sequencing

# Introduction

OzFoodNet, established in 2000 by the Commonwealth Department of Health and Ageing, is a collaborative network of epidemiologists conducting enhanced surveillance, outbreak investigations and applied research into foodborne disease across six Australian States, the Northern Territory, and the Australian Capital Territory. The OzFoodNet surveillance network actively investigates foodborne disease at both the national and local level to improve our knowledge of this disease and describe more effectively its epidemiology, and to provide information to assist public health efforts in minimising its incidence in Australia. Recent Australian studies estimate that around 4.1 million cases of foodborne disease occur each year in Australia, costing A\$1.2 billion annually.<sup>1</sup>

Enhanced communication and cooperation among network members have strengthened Australia's capacity to detect and respond to emerging foodborne diseases and multi-jurisdictional outbreaks that cross state and territory borders. In 2020, the coverage of the network included the entire Australian population, which was estimated at 25,693,059 as at 30 September 2020.<sup>2</sup>

To improve detection, management and prevention of foodborne diseases, OzFoodNet in Queensland works collaboratively with a range of other units and agencies, including other state and territory health departments, Queensland public health units, Queensland Health Food Safety Standards and Regulation, the Public Health Microbiology and Virology laboratories (Forensic and Scientific Services), the Public Health Laboratory Network (PHLN), the Doherty Institute for Infection and Immunity (MDU), Food Standards Australia New Zealand (FSANZ), SafeFood Production Queensland, and local councils. At a national level, OzFoodNet is a member of the Communicable Diseases Network Australia (CDNA), which is Australia's peak body for communicable disease control.

OzFoodNet in Queensland has state responsibility to provide surveillance functions and epidemiological capacity to monitor enteric disease incidence and enable the early detection and investigation of outbreaks of foodborne disease including multi-jurisdictional outbreaks. Data collected from outbreak investigations and from epidemiological studies of sporadic disease provide information on local risk factors and

emerging pathogens, and inform prevention efforts, risk assessments and policy. This report describes and summarises the surveillance and outbreak investigation activities undertaken by the Queensland OzFoodNet site (Communicable Diseases Branch) during 2020, in collaboration with Queensland public health units, Food Safety Standards and Regulation Unit, and the Public Health Microbiology Laboratory (QHFSS).



## Data Sources and Methods

Incidence data are derived from statutorily notified cases of infection collated by the Communicable Diseases Branch, Queensland Health. Notified cases of foodborne illness also include those residents who acquired their infection outside of Australia but were diagnosed in Queensland. Surveillance data is summarised for the following fifteen pathogens/conditions: *Salmonella*, *Campylobacter*, Cholera, *Cryptosporidium*, *Listeria monocytogenes*, Shiga toxin-producing *E. coli* (STEC), *Shigella*, *Yersinia enterocolitica*, Typhoid Fever, Paratyphoid Fever, Ciguatera poisoning, *Clostridium botulinum*, Hepatitis A, Hepatitis E and Haemolytic Uraemic Syndrome (HUS).

The number of notifications reported for each condition was extracted from the Queensland Health Notifiable Conditions database by date of onset or if this was unknown, the pathology request date or earliest date of specimen collection or notification date between 1 January 2020 and 31 December 2020. Notifications were collated and analysed using Microsoft Excel for Office 365. National data was sourced from the National Notifiable Diseases Surveillance System (NNDSS).<sup>3</sup>

Crude notification rates were calculated using the Australian Bureau of Statistics mid-year estimated resident population figures for a single year between 2011 and 2019 as the denominator.<sup>4</sup>

Serotype and genotype data were obtained from the Public Health Microbiology Reference Laboratory, Queensland Health Forensic and Scientific Services (QHFSS). Outbreak data were obtained from the OzFoodNet Gastrointestinal Illness Outbreak Register, Communicable Diseases Branch, Queensland Department of Health.

An **'outbreak'** is defined as the occurrence of cases of the same disease in excess of what would normally be expected in a specified population from a given area, over a particular period of time.

A **'foodborne outbreak'** is defined as the occurrence of 2 or more cases of a similar illness after consuming a common food or meal, and analytic epidemiological evidence and/or microbiological evidence (including food and/or environmental) implicates the meal or food as the source of illness; or in the absence of analytic and/or microbiological

evidence, the aetiology of the outbreak can only result through foodborne transmission (e.g. ciguatera poisoning, *Listeria monocytogenes*).

A **'probable foodborne outbreak'** is defined as an incident where 2 or more persons experience a similar illness after consuming a common food or meal and compelling descriptive epidemiological evidence implicates the meal or food as the suspected source of illness. This includes outbreaks where the mode of transmission is suspected to be from person to food to person (e.g. ill food handler).

A **'waterborne outbreak'** is defined as the occurrence of 2 or more cases of a similar illness with an established or putative epidemiological or microbiological link to a water source.

A **'zoonotic'** outbreak is defined as the occurrence of 2 or more cases of a similar illness associated with direct or indirect transmission of a pathogen from vertebrate animals to humans.

A **'cluster'** is defined as an increase in cases of disease (in excess of expected numbers) that are epidemiologically related in time, place, or person where investigations were unable to implicate a common exposure, mode of transmission or source of infection.

# Incidence of Foodborne Disease 2020

- Number of notifiable enteric pathogens/conditions: 13,406
- Overall notification rate per 100,000 population: 263.1
- Foodborne / probable foodborne outbreaks: 12 (107 cases, 27 hospitalisations)
- Zoonotic outbreaks: 1 (38 cases, 9 hospitalisations)
- Non-foodborne outbreaks: 675 (12,470 cases, 156 hospitalisations)
- Multi-jurisdictional foodborne outbreaks (QLD lead agency): 1
  - Total cases: 1,063
    - QLD: 687
    - NSW 228
    - VIC: 96
    - SA 21:
    - ACT: 13
    - TAS: 9
    - NT: 6
    - WA: 3

**Table 1.** Foodborne pathogen notification numbers and crude rates per 100,000 population, Queensland 2020, 2019, and 5-year (2015–2019) mean

Pathogen	Notification Count			Notification Rate per 100,000 population		
	2020	2019	5-year mean*	2020	2019	5-year mean
<b>BACTERIAL</b>						
<i>Clostridium botulinum</i> (Botulism)	0	0	0	0.0	0.0	0.0
<i>Campylobacter</i>	7660	9152	7968	150.4	179.6	161.7
<i>Listeria monocytogenes</i> (Listeriosis)	6	11	13	0.1	0.2	0.3
<i>Salmonella</i> (non-typhoidal)	4131	3815	4335	81.1	74.9	88.0
<i>Salmonella</i> Typhi (Typhoid)	10	25	24	0.2	0.5	0.5
<i>Salmonella</i> Paratyphi (Paratyphoid)	2	15	9	0.0	0.3	0.2
STEC <sup>a</sup>	30	29	27	0.6	0.6	0.5
<i>Shigella</i>	280	609	324	5.5	12.0	6.6
<i>Vibrio cholerae</i> (Cholera)	0	0	0	0.0	0.0	0.0
<i>Yersinia enterocolitica</i>	579	691	735	11.4	13.6	14.9
<b>PARASITIC</b>						
<i>Cryptosporidium</i>	670	724	1352	13.2	14.2	27.4
<b>VIRAL</b>						
Hepatitis A	15	25	31	0.3	0.5	0.6
Hepatitis E	6	4	6	0.1	0.1	0.1
<b>OTHER</b>						
Ciguatera poisoning	13	21	20	0.3	0.4	0.4
HUS <sup>b</sup>	4	3	3	0.1	0.1	0.1
<b>Total</b>	<b>13,406</b>	<b>15,124</b>	<b>14,847</b>	<b>263.1</b>	<b>296.9</b>	<b>301.3</b>

\* 5-year mean (2015–2019)

<sup>a</sup> STEC: *Shiga toxin-producing Escherichia coli*

<sup>b</sup> HUS: *Haemolytic Uraemic Syndrome*

## Notable changes in incidence in 2020

- 54% decrease in *Shigella* notifications between 2019 and 2020<sup>i</sup>
- 8% increase in *Salmonella* notifications between 2019 and 2020
- 16% decrease in *Campylobacter* notifications between 2019 and 2020
- *Campylobacter* notification rate in 2020 (150.4 per 100,000) was 7% lower than the 5-year (2015–2019) annual mean (161.7 per 100,000)

**Table 2.** Notifications for selected pathogens by diagnostic test type (PCR and Culture), 2020

Pathogen	Culture only		PCR only		Culture and PCR		Total
	Number	%	Number	%	Number	%	
<i>Campylobacter</i>	1608	21	2741	36	3309	43	7658 <sup>^</sup>
<i>Salmonella</i>	1333	32	340	8	2456	59	4129 <sup>†</sup>
<i>Shigella</i>	50	18	162	58	68	24	280
<i>Yersinia enterocolitica</i>	19	3	374	65	186	32	579
Total	3,010	24	3,618	29	6,018	48	12,646

<sup>^</sup> 2 cases were not specified

<sup>†</sup> 2 cases were not specified

- 36% of *Campylobacter* notifications in 2020 were detected by PCR only (Table 2)
- 8% of *Salmonella* notifications in 2020 were detected by PCR only
- 58% of *Shigella* notifications in 2020 were detected by PCR only
- 65% of *Yersinia* notifications in 2020 were detected by PCR only

<sup>i</sup> The national case definition for notification of *Shigella* spp was modified on 1 July 2018 to include all cases diagnosed through PCR testing only as ‘probable cases.’ Prior to this date, only culture positive *Shigella* infections were notified. From 1 July 2018, notifications of *Shigella* are categorised as either ‘confirmed’ (culture positive cases) or ‘probable’ (PCR positive only).

# *Salmonella*

## Summary 2020

- Total notifications: 4,131
- Notification rate per 100,000: 81.1
- Median age: 26 years (range <1–100 years)
- 2,178 (53%) female
- 6 outbreaks investigated (82 cases, 24 hospitalisations)
- 1 multi-jurisdictional outbreak investigated (Total 1,063 cases: 65% from QLD)
- 2 clusters investigated (18 cases, 3 hospitalisations)

## Other Key Information

- 3,767 isolates serotyped (91% notified cases)
- 340 (8%) detected through PCR only (Figure 1)
- 24 (<1%) culture positive and serotype unknown
- 85 different serotypes reported in 2020 (25% associated with single notifications)

## Changes in incidence

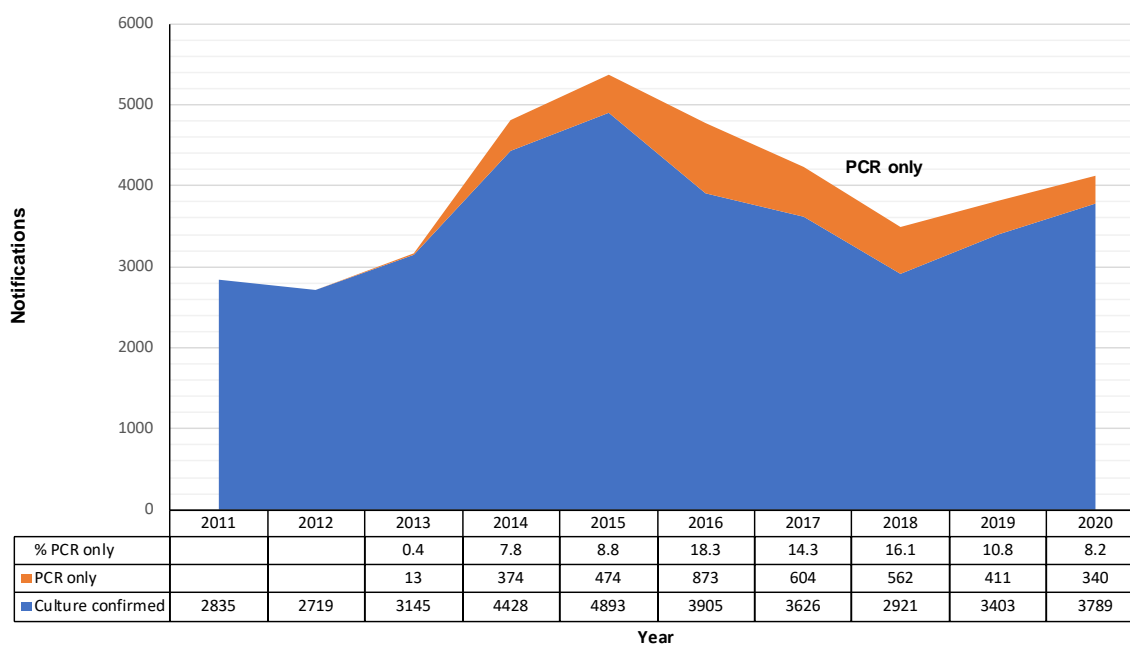
- 8% increase in 2020 notifications (4,131) compared to 2019 (3,815) (Table 1)
- *Salmonella* notification rate in 2020 (81.1 per 100,000) was 8% lower than the 5-year (2015–2019) annual mean (88.0 per 100,000) (Table 1)
- Following a steady decline over the period 2015 to 2018, *Salmonella* notification rates have trended upwards in both 2019 (74.9 per 100,000) and 2020 (81.1 per 100,000) (Figure 2)
- Notification rates in Queensland have been consistently higher than the Australian rates across the past 10 years (Figure 3)

## Groups with highest notification rate

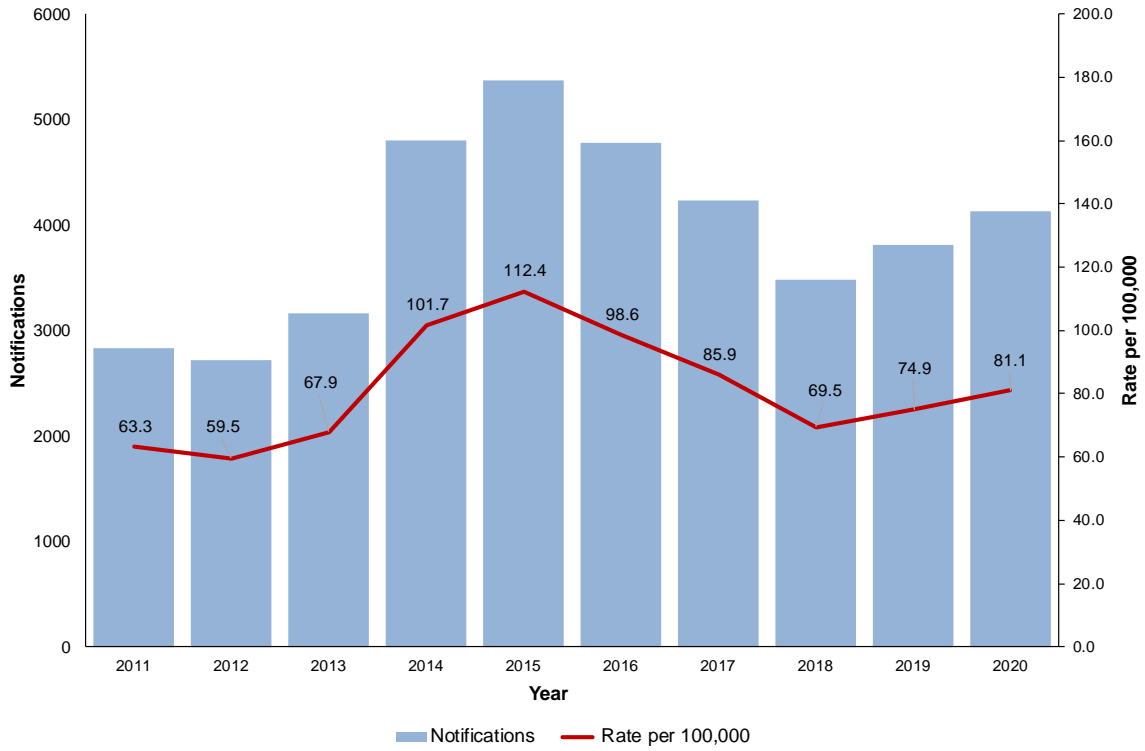
- Age group: 0–4 years (28% of cases – 367.2 cases per 100,000 population); children aged <1 year (843.1 per 100,000) (Table 3, Figure 4)
- HHS: Central West (<1% of cases – 155.0 per 100,000) (Table 4)

## Seasonality

- Notifications typically peak in warmer months, particularly between January and March each year (Figure 5)



**Figure 1.** *Salmonella* notifications in Queensland by method of diagnosis, 2011–2020

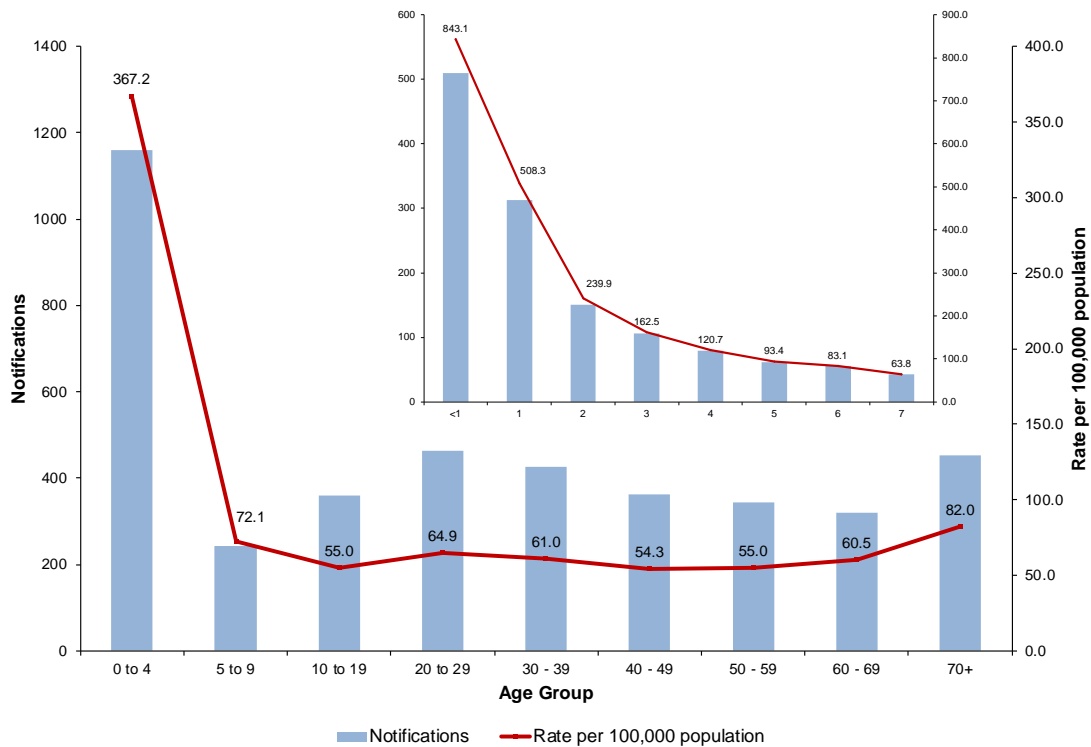


**Figure 2.** *Salmonella* notifications and rate per 100,000 population by year, Queensland 2011–2020





**Figure 3.** *Salmonella* notification rate by year in Queensland and Australia (sourced from the national notifiable diseases surveillance system), 2011–2020



**Figure 4.** *Salmonella* notifications and rate per 100,000 population by age group (inset: age in years 0–7), Queensland 2020

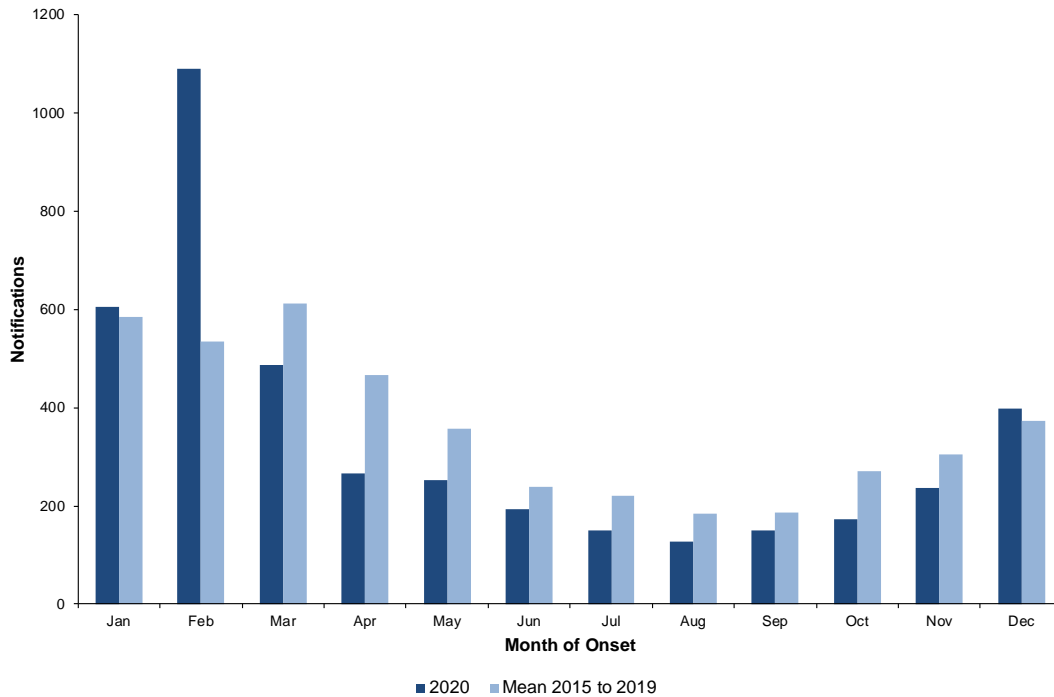
**Table 3.** *Salmonella* notifications and rate per 100,000 population by age group and sex, Queensland 2020

Age Group (years)	Male		Female		Total	
	Number	Rate	Number	Rate	Number	Rate
0-4	625	385.6	534	347.8	1159	367.2
5-9	136	78.6	108	65.4	244	72.1
10-19	168	50.1	191	60.1	359	55.0
20-29	193	54.1	270	75.7	463	64.9
30-39	178	52.0	249	69.7	427	61.0
40-49	154	47.1	209	61.2	363	54.3
50-59	135	44.1	210	65.3	345	55.0
60-69	152	59.0	167	61.9	319	60.5
70 +	212	82.0	240	82.0	452	82.0
All ages	1953	77.5	2178	84.6	4131	81.1

**Table 4.** Salmonella notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	230	253	88.8	99.3
Central Queensland	269	283	122.5	129.9
Central West	16	21	155.0	196.7
Darling Downs	202	207	71.0	73.5
Gold Coast	472	502	74.2	82.8
Mackay	195	177	112.7	102.5
Metro North	679	750	65.0	74.7
Metro South	800	878	67.5	76.8
North West	36	67	130.9	239.5
South West	35	34	145.8	139.6
Sunshine Coast	394	398	90.2	95.5
Torres and Cape	30	39	106.9	146.6
Townsville	307	278	127.1	115.9
West Moreton	243	230	79.8	80.3
Wide Bay	223	217	101.6	100.8
<b>QLD Total</b>	<b>4131</b>	<b>4335</b>	<b>81.1</b>	<b>88.0</b>

\* 5-year mean (2015–2019)



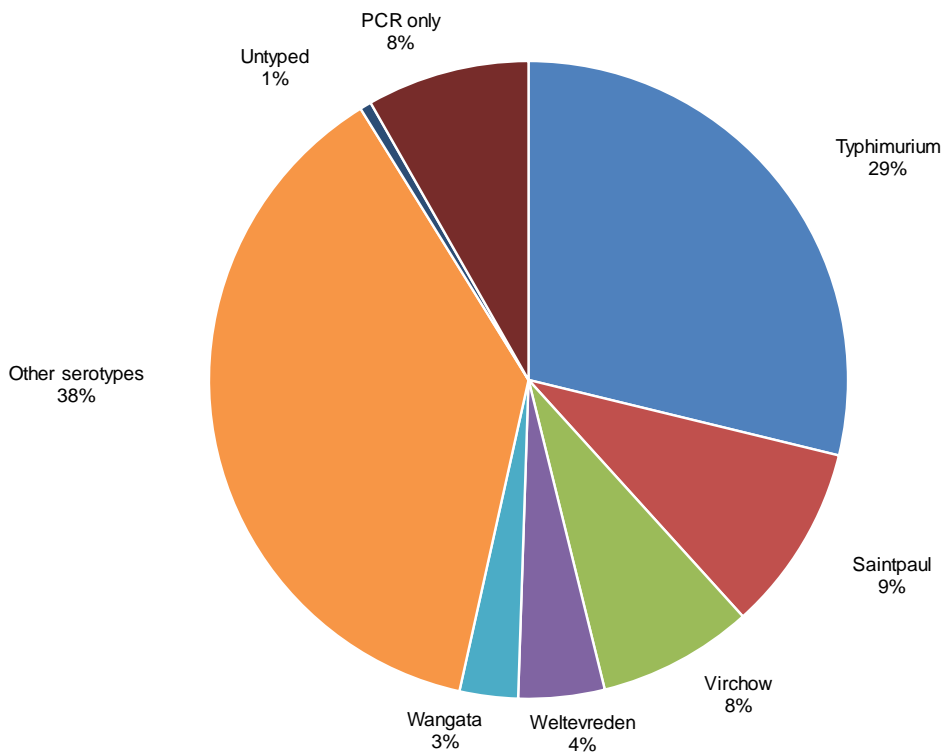
**Figure 5.** *Salmonella* notifications in 2020 by month of onset, compared with mean number of notifications for the five-year period, 2015–2019 in Queensland

## Serotypes

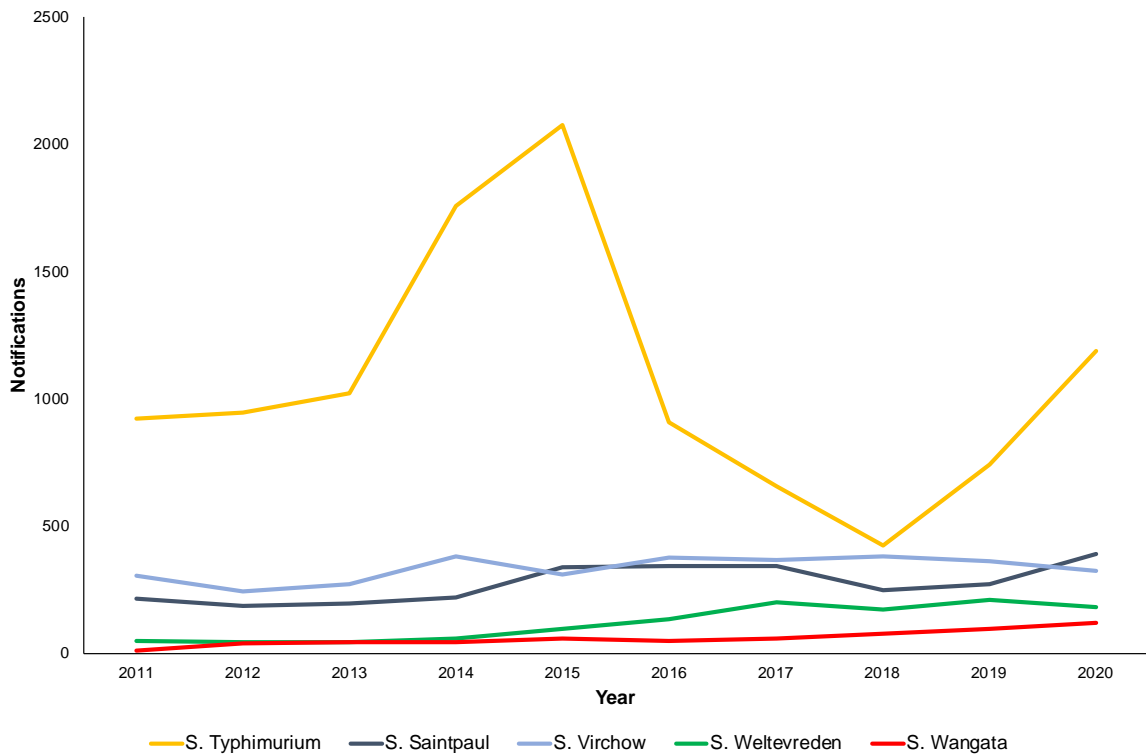
- The ten most frequently reported *Salmonella* serotypes accounted for 72% of all salmonellas that were serotyped during 2020 (Table 5, Figure 6)
  - *Salmonella* Typhimurium notifications increased by 60% in comparison to 2019
  - *Salmonella* Saintpaul increased by 43% in comparison to 2019
  - *Salmonella* Wangata increased by 30% in comparison to 2019
  - *Salmonella* Enteritidis had the largest decrease in notifications (among the top 10) in comparison to 2019 (56% decrease)
- Historical (2011–2020) notification data for the top 5 *Salmonella* serotypes reported in 2020 are shown (Figure 7). The number and magnitude of outbreaks that occur each year is the major contributing factor for the large fluctuation in *Salmonella* Typhimurium trends
- 750 (63%) *Salmonella* Typhimurium notifications received in 2020 were associated with known outbreaks.

**Table 5.** Top ten *Salmonella* serotypes (notifications) by year of onset in Queensland, 2016 to 2020

Rank	2016	2017	2018	2019	2020
1	Typhimurium (909)	Typhimurium (655)	Typhimurium (424)	Typhimurium (743)	Typhimurium (1190)
2	Virchow (374)	Virchow (367)	Virchow (380)	Virchow (363)	Saintpaul (392)
3	Saintpaul (345)	Saintpaul (345)	Saintpaul (249)	Saintpaul (274)	Virchow (325)
4	Aberdeen (221)	Enteritidis (200)	Enteritidis (196)	Weltevreden (211)	Weltevreden (180)
5	Enteritidis (204)	Weltevreden (199)	Weltevreden (172)	Enteritidis (208)	Wangata (122)
6	Hvittingfoss (145)	Hvittingfoss (145)	Birkenhead (95)	Aberdeen (141)	Aberdeen (121)
7	Weltevreden (136)	Aberdeen (136)	Aberdeen (92)	Birkenhead (102)	Hvittingfoss (106)
8	Birkenhead (105)	Birkenhead (126)	Wangata (77)	Wangata (94)	Birkenhead (103)
9	Waycross (101)	Waycross (113)	Hvittingfoss (75)	Hvittingfoss (88)	Waycross (99)
10	Subsp 3b (79)	Subsp 3b (71)	Waycross (75)	Waycross (82)	Enteritidis (92)



**Figure 6.** Percentage of all *Salmonella* notifications by serotype, QLD 2020



**Figure 7.** Annual notifications for the top 5 reported serotypes reported in 2020

## *Salmonella* Typhimurium

- *Salmonella* Typhimurium (1,190 notifications) in 2020 increased 60% in comparison to 2019 (743 notifications).
- *Salmonella* Typhimurium notification rate in 2020 (23.4 per 100,000) was 20% higher than the 5-year (2015–2019) annual mean (961 cases; 19.5 per 100,000).
- All human *Salmonella* Typhimurium isolates are routinely genotyped in Queensland using a PCR-based technique called Multi-locus Variable Number Tandem Repeats Analysis (MLVA or VNTR typing). A 5-loci MLVA code is generated for *Salmonella* Typhimurium isolates using the coding system of Lindstedt et al<sup>5</sup> and Gilbert.<sup>6</sup>
- MLVA profile results were available for 1,147 (96%) notifications
- 174 different MLVA profiles were reported among the 1,147 notifications; 9% were associated with single notifications.<sup>ii</sup>
- The most frequently reported MLVA profile in 2020 was 05-16-13-11-490 (653 cases) (Table 6). 651 of these cases were associated with a multi-jurisdictional outbreak in which a bagged/package salad product was the likely source of infection. This MLVA profile had only been reported with 2 previous cases in Queensland in 2016 and 2019.
- There were 4 other MLVA genotypes among the top 10 reported in 2020 that were associated with known outbreaks:
  - 27/49 cases of *Salmonella* Typhimurium 03-11-10-08-523 were outbreak associated. The likely source of infection was contact with backyard poultry (chicks)
  - 13/37 cases of *Salmonella* Typhimurium 03-12-12-09-523 were outbreak associated. A source of infection was not identified
  - 8/11 cases of *Salmonella* Typhimurium 03-17-09-12-523 were outbreak associated. Eggs were the likely source of infection (aioli)

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<sup>ii</sup> On 24 April 2019, the Queensland reference laboratory began recording allele 524 as 523 when reporting MLVA profiles for *Salmonella* Typhimurium.

- 4/60 cases of *Salmonella* Typhimurium 03-20-11-10-523 were outbreak associated. Eggs were the likely source of infection (eggs benedict / poached egg).
- Two cluster investigations were conducted in which no common exposure or source of infection was identified: 12 cases of *Salmonella* Typhimurium MLVA 03-12-12-09-523 and 6 cases of *Salmonella* Typhimurium 03-11-10-08-523.



**Table 6.** Top 10 *Salmonella* Typhimurium MLVA profiles by year in Queensland, 2016–2020

Rank	2016	2017	2018	2019	2020
1	03-17-09-11-523 (116)	03-12-10-10-523 (29)	04-15-11-00-490 (12)	03-20-11-10-523 (256)	05-16-13-11-490 (653)
2	03-12-12-09-523 (66)	03-12-12-11-523 (27)	03-12-10-12-523 (11)	03-12-13-09-523 (17)	03-20-11-10-523 (60)
3	03-26-13-08- 523 (37)	05-15-16-11-490 (19)	03-12-11-12-523 (10)	03-09-07-14-523 (13)	03-11-10-08-523 (49)
4	03-12-13-09-523 (29)	03-12-10-11-523 (18)	05-17-09-13-490 (8)	03-13-10-08-523 (10)	03-12-12-09-523 (37)
5	03-12-10-11-523 (27)	03-12-11-11-523 (17)	03-15-10-13-523 (8)	03-20-12-10-523 (9)	06-11-10-10-490 (18)
6	03-12-09-11-523 (22)	04-15-11-00-490 (16)	03-16-10-17-523 (7)	03-13-12-08-523 (9)	03-17-09-12-523 (11)
7	03-26-13-11-523 (20)	03-17-09-11-523 (15)	03-12-10-11-523 (7)	03-15-00-00-517 (8)	03-13-10-08-523 (10)
8	04-15-11-00-490 (20)	03-16-09-11-523 (13)	03-23-13-11-523 (7)	03-16-11-09-523 (7)	03-15-10-13-523 (10)
9	04-16-06-00- 490 (18)	03-12-12-08-523 (13)	03-15-00-00-517 (7)	03-17-11-10-523 (7)	03-12-11-09-523 (7)
10	03-12-11-09-523 (17)	03-12-12-09-523 (12)	03-16-09-11-523 (7)	03-11-14-09-523 (5)	04-15-11-00-490 (7)

*Colour code indicates same MLVA profile*

## Salmonella Enteritidis

- 92 notifications in 2020 which compares with 208 notifications in 2019 (Table 7)
  - Travel restrictions implemented in March 2020 associated with the COVID-19 pandemic contributed to this decline in notifications.
- *Salmonella* Enteritidis 2020 notification rate (1.8 per 100,000) was 56% lower than the 5-year (2015–2019) annual mean (4.1 per 100,000).
- Epidemiological information was collected on 38 (41%) cases
  - 17 (45%) cases reported no overseas travel and were designated as locally acquired infections.
  - There were no outbreaks of locally acquired infections during 2020.
- Among the 21 cases who reported overseas travel, 11 (52%) had been to Indonesia.
- Whole genome phylogenetic analysis of *S. Enteritidis* isolates were conducted on 84 (91%) case isolates:
  - 51 (61%) were grouped as either Clade A or Clade C (predominantly locally acquired infection) (Table 8).
  - 33 (39%) were designated as Clade B (predominantly overseas-acquired infections).
- Among the 8 isolates that were not sequenced; 1/8 reported overseas travel and 1/8 was locally acquired. Travel history for the remaining cases was unknown.
- Phage typing was not conducted on any *Salmonella* Enteritidis isolates during 2020 (phage typing no longer performed).

**Table 7.** *Salmonella* Enteritidis notifications and case reported travel, 2015 – 2020

Year	Locally acquired	Overseas Travel	No travel information	Total
2015	10	60	126	196
2016	54	92	58	204
2017	47	84	69	200
2018	17	72	107	196
2019	24	72	112	208
2020	17	21	54	92

**Table 8.** *Salmonella* Enteritidis whole genome sequencing analysis (grouped as Clade A, B or C) and case reported travel, 2020\*

SNP Clade	Locally acquired	Overseas Travel	No Travel information	Total
A	1	6	29	36
B	18	5	10	33
C	1	5	9	15
<b>Total</b>	<b>20</b>	<b>16</b>	<b>48</b>	<b>84</b>

*\*Isolates sequenced = 84/92; travel information available for 36/84 cases*

# *Campylobacter*

## Summary 2020

- Total notifications: 7,660
- Notification rate per 100,000: 150.4
- Median age: 40 years (range <1–99 years)
- 4,195 (55%) male
- No outbreaks reported

## Other Key Information

- 2,741 (36%) detected through PCR only (Figure 8)
- Notification rate among males was consistently higher than females among all age groups, particularly for cases aged <10 years and those aged 70+ (Figure 9).

## Changes in incidence

- 16% decrease in the 2020 notifications (7,660) compared to 2019 (9,152) (Table 1).
- Pathology Queensland ceased the use of multiplex PCR for the detection of enteric pathogens in faeces between March and December 2020 to preserve reagents for COVID-19 testing. In addition, stool culture for *Campylobacter* was only performed on specific request during this period.
- *Campylobacter* notification rate in 2020 (150.4 per 100,000) was 7% lower than the 5-year (2015–2019) annual mean (161.7 per 100,000) (Table 1).
- Annual notification rates steadily increased between 2016 and 2019 before declining again in 2020; 2019 having the highest notification rate during the past 10 years (Figure 10).
- The marked increase in notification rates in 2014 and 2015 was largely due to the introduction of multiplex PCR testing by diagnostic pathology laboratories for routine testing of faecal specimens (Figure 10).<sup>7</sup>

- Notification rates for *Campylobacter* infection in Queensland have been higher than the Australian notification rate since 2014 (Figure 11).

## Groups with highest notification rate

- Age group: 0–4 years (10% of cases – 249.6 per 100,000) (Table 9)
- Sex: Males (166.5 per 100,000) (Table 9)
- HHS: Townsville (7% of cases – 216.1 per 100,000) and South West (<1% of cases – 258.2 per 100,000) (Table 10)

## Seasonality

- Notifications were typically slightly higher in the warmer months (Figure 12).  
Temporary ceasing of PCR testing in March may have had some impact.

**Table 9.** *Campylobacter* notifications and rate per 100,000 population by age group and sex in Queensland, 2020

Age group (years)	Male		Female		Total	
	Number	Rate	Number	Rate	Number	Rate
0–4	471	290.6	317	206.4	788	249.6
5–9	213	123.1	121	73.3	334	98.7
10–19	380	113.3	268	84.3	648	99.2
20–39	1022	146.3	949	132.9	1971	139.5
40–59	1017	160.6	875	132.0	1892	146.0
60+	1092	211.5	935	166.3	2027	188.0
<b>All ages</b>	<b>4195</b>	<b>166.5</b>	<b>3465</b>	<b>134.5</b>	<b>7660</b>	<b>150.4</b>

**Table 10.** *Campylobacter* notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	404	466	156.0	182.8
Central Queensland	328	329	149.3	150.8
Central West	15	14	145.3	131.8
Darling Downs	480	460	168.6	163.4
Gold Coast	826	855	129.9	141.1
Mackay	280	274	161.8	158.6
Metro North	1522	1682	145.6	167.7
Metro South	1762	1755	148.7	153.6
North West	28	44	101.8	157.8
South West	62	45	258.2	186.4
Sunshine Coast	689	780	157.8	187.1
Torres and Cape	21	22	74.9	80.3
Townsville	522	514	216.1	214.0
West Moreton	412	453	135.3	158.3
Wide Bay	309	276	140.8	127.8
<b>QLD Total</b>	<b>7660</b>	<b>7968</b>	<b>150.4</b>	<b>161.7</b>

\*5-year mean (2015–2019)

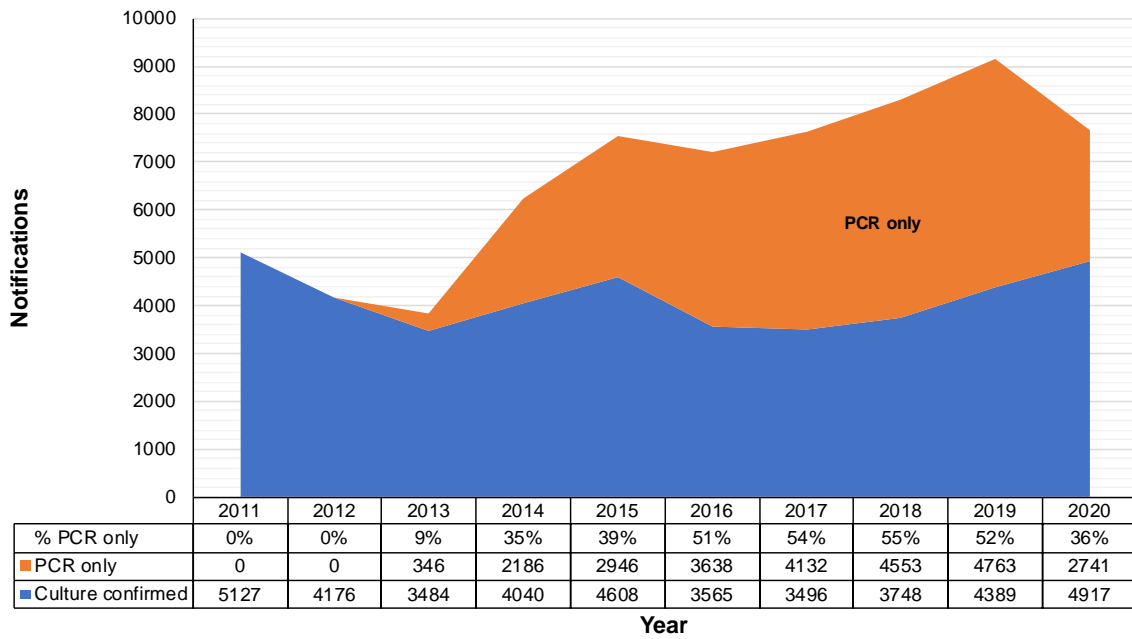


Figure 8. *Campylobacter* notifications Queensland by method of diagnosis, 2011–2020

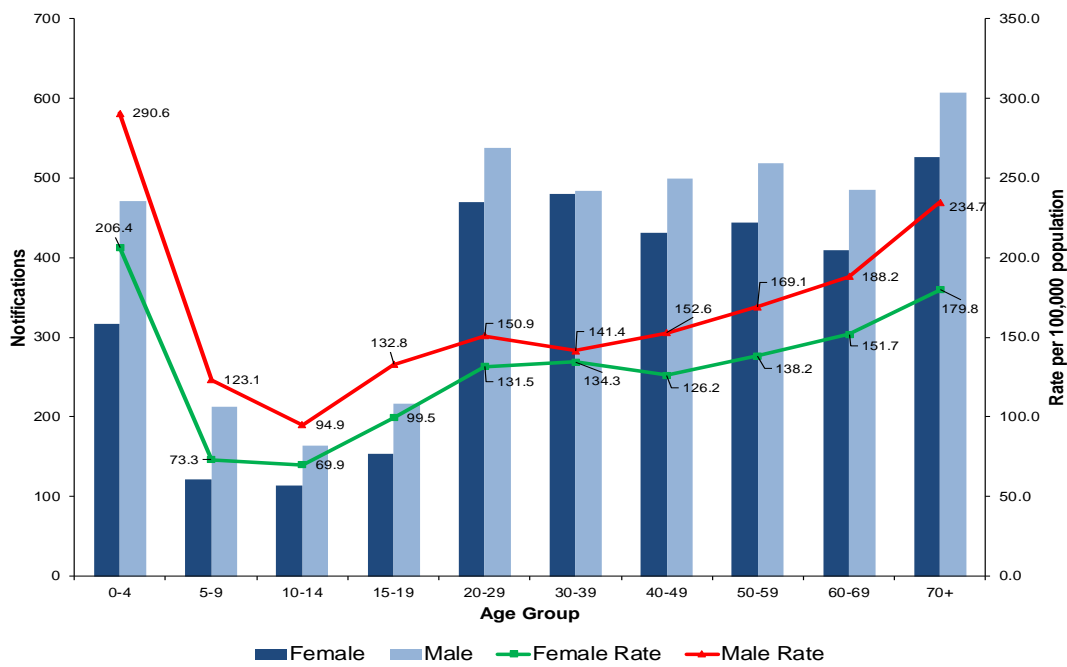


Figure 9. *Campylobacter* notifications and rate per 100,000 population by age group and sex in Queensland, 2020

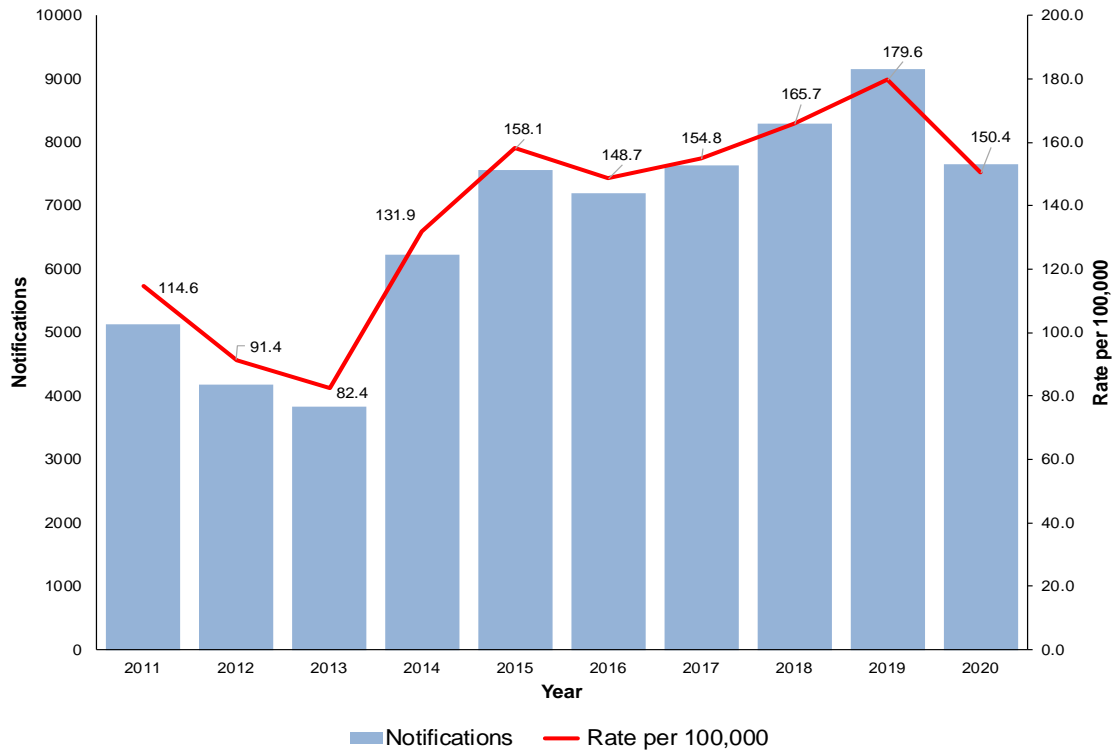


Figure 10. *Campylobacter* notifications and rate per 100,000 population by year, Queensland 2011–2020

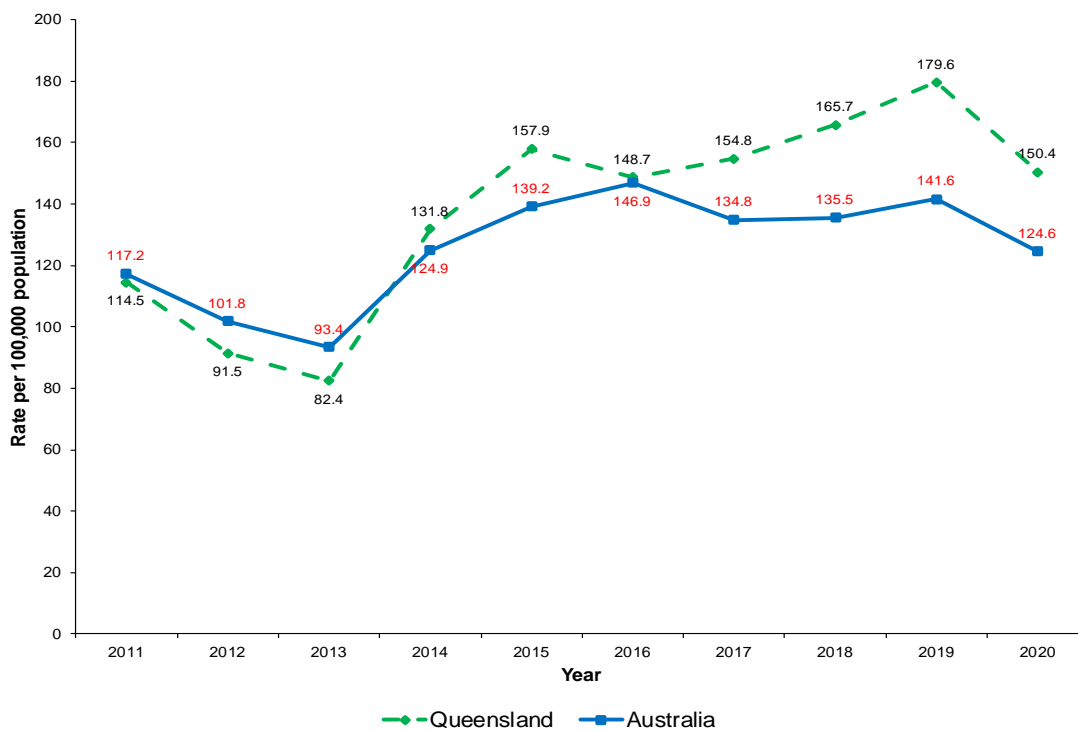
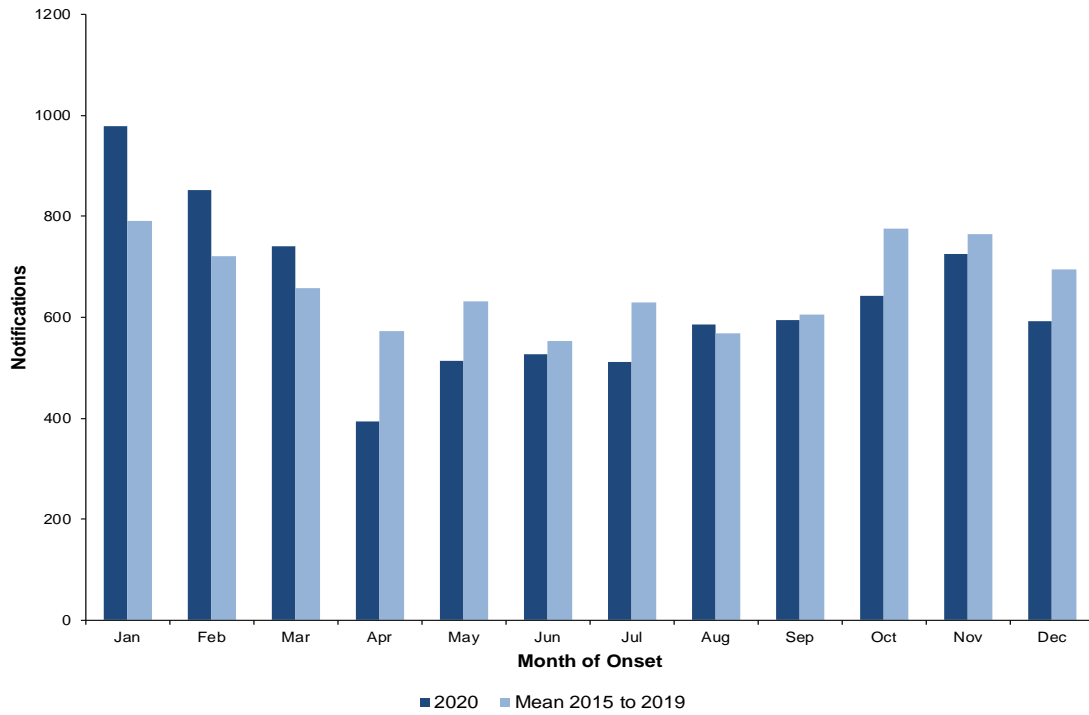


Figure 11. *Campylobacter* notification rates by year, for Queensland and Australia, 2011–2020 [Source: NNDSS]





**Figure 12.** *Campylobacter* notifications by month of onset in 2020 compared to the mean number of notifications by month for 2015–2019 in Queensland

# Cryptosporidiosis

## Summary 2020

- Total notifications: 670
- Notification rate per 100,000: 13.2
- Median age: 24 years (range <1–95 years)
- 335 (50%) female
- No outbreaks reported.

## Other Key Information

- 656 (98%) detected through PCR; 6 by microscopy only; 8 unknowns.

## Changes in incidence

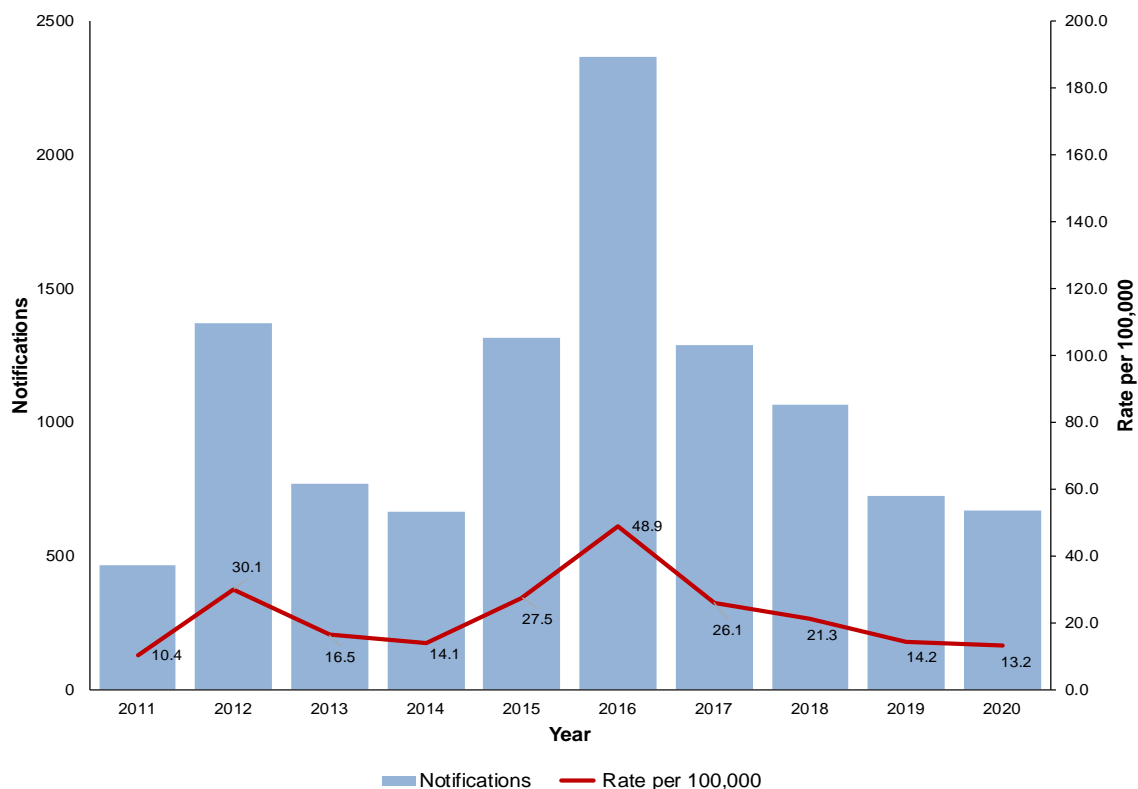
- 7% decrease in the 2020 notifications (670) compared to 2019 (724), (Table 1).
- Cryptosporidiosis notification rate in 2020 (13.2 per 100,000) was 52% lower than the 5-year (2015–2019) annual mean (27.4 per 100,000) (Table 1).
- Decreasing trend in annual notifications and rates observed over the period 2016–2020 (Figure 13).

## Groups with highest notification rate

- Age group: 0–4 years (28% of cases – 58.6 per 100,000) (Table 11)
- HHS: Mackay (10% of cases – 38.1 per 100,000) and South West (3% of cases – 75.0 per 100,000) (Table 12).

## Seasonality

- 71% (474) cases were reported during the first quarter 2020; peak in March (227 cases – no geographical clustering).



**Figure 13.** Cryptosporidiosis notifications and rate per 100,000 population by year, Queensland 2011–2020

**Table 11.** Cryptosporidiosis notifications and rate per 100,000 population by age group and sex, Queensland 2020

Age Group (years)	Male		Female		Total	
	Number	Rate	Number	Rate	Number	Rate
0–4	124	76.5	61	39.7	185	58.6
5–9	39	22.5	27	16.3	66	19.5
10–19	24	7.2	28	8.8	52	8.0
20–29	41	11.5	63	17.7	104	14.6
30–39	52	15.2	91	25.5	143	20.4
40–49	29	8.9	29	8.5	58	8.7
50–59	9	2.9	19	5.9	28	4.5
60–69	10	3.9	10	3.7	2	3.8
70 +	17	2.7	7	2.4	14	2.5
<b>All ages</b>	<b>335</b>	<b>13.3</b>	<b>335</b>	<b>13.0</b>	<b>670</b>	<b>13.2</b>

**Table 12.** Cryptosporidiosis notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	84	92	32.4	36.3
Central Queensland	30	74	13.7	34.1
Central West	2	4	19.4	42.0
Darling Downs	56	88	19.7	31.1
Gold Coast	58	128	9.1	21.2
Mackay	66	27	38.1	15.6
Metro North	94	276	9.0	27.5
Metro South	94	306	7.9	26.8
North West	8	12	29.1	44.1
South West	18	11	75.0	43.5
Sunshine Coast	33	111	7.6	26.5
Torres and Cape	4	10	14.3	35.7
Townsville	72	102	29.8	42.6
West Moreton	23	91	8.2	31.8
Wide Bay	26	20	11.8	9.1
<b>QLD Total</b>	<b>670</b>	<b>1352</b>	<b>13.2</b>	<b>27.4</b>

\* 5-year mean (2015–2019)

# *Listeria monocytogenes*

## Summary 2020

- Total notifications: 6
- Notification rate per 100,000: 0.1
- Median age: 69 years (range 27–81 years)
- 4 (67%) female.

## Other Key Information

- Non-perinatal cases count: 6
- Perinatal cases: 0
- No deaths reported
- One case of *Listeria monocytogenes* serotype 1/2a, binary gene type 59, MLST 7 was highly related on phylogenetic analysis to case isolates from a multi-state outbreak in the United States, associated with the consumption of enoki mushrooms, imported from the Republic of Korea (Table 13).
  - A total of 6 cases were subsequently identified in Australia associated with this international outbreak (outbreak cases also identified in Canada)
  - Cases were notified between October 2017 and March 2020
  - 3/6 cases were notified in Queensland during this same period
  - Very high levels of *Listeria monocytogenes* were detected in 2 samples of implicated, unopened enoki mushrooms, sampled by Queensland Health
  - The food isolates were the same serotype and binary gene type as the human case isolates, and all isolates were highly related on phylogenetic analysis following whole genome sequencing
  - Two national consumer level food recalls were conducted on 10 and 14 April 2020
- All other isolates reported in 2020 were not genetically related.

## Changes in incidence

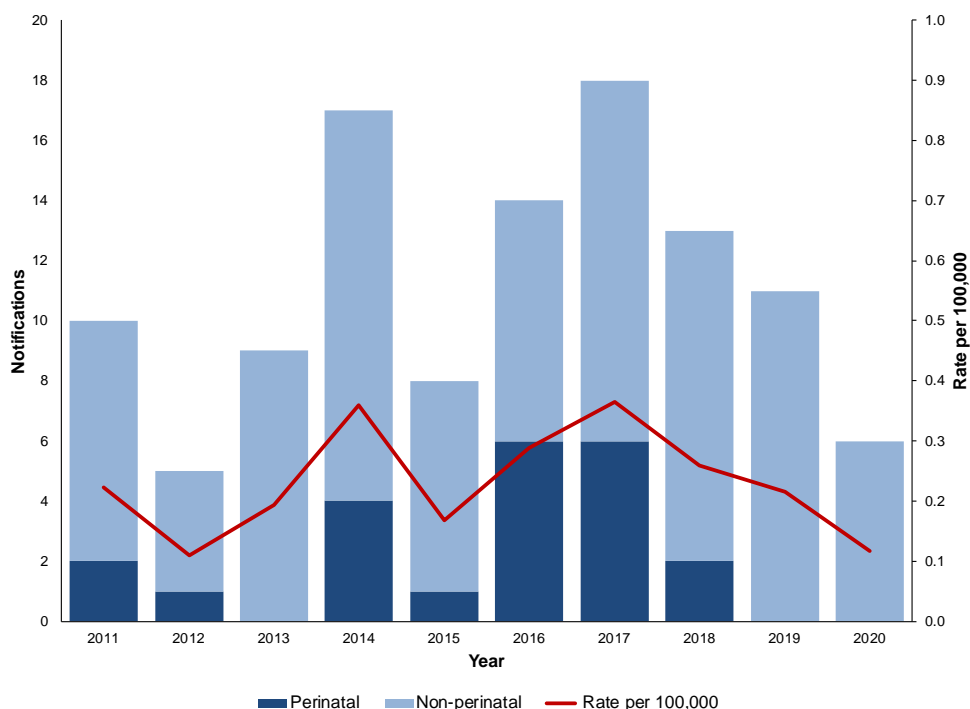
- 6 cases reported 2020 compared to 11 cases in 2019 (Table 1).
- *Listeria* notification rate in 2020 (0.1 per 100,000) was slightly lower than the 5-year (2015–2019) annual mean (0.3 per 100,000) (Table 1).
- Annual notifications have fluctuated between 5 and 18 cases per year over the past 10-year period (Figure 14).
- Average of 2 perinatal cases reported per year, over the past 10-year period (range 0–6 cases).

## Groups with highest notification rate

- Age group: 75+ years (50% of cases – 0.1 per 100,000)
- Sex: Female (67% of cases – 0.1 per 100,000).

## Seasonality

- 4/6 cases were reported during the first quarter 2020.



**Figure 14.** Invasive *Listeria monocytogenes* notifications and rate per 100,000 population by year, Queensland 2011–2020

**Table 13.** Laboratory typing results of invasive *Listeria monocytogenes* infections, Queensland, 2020

Serotype	Binary Gene Type	MLST	Number of Cases
1/2a	58	321	2
1/2a	59	7	1
1/2a	82	204	1
1/2b	158	3	1
4a	30	202	1

# *Shigella*

## Summary 2020

- Total notifications: 280
- Notification rate per 100,000: 5.5
- Median age: 30 years (range <1–91 years)
- 161 (58%) male
- 2 outbreaks investigated (14 cases, 9 hospitalisations).

## Other Key Information

- Indigenous: 52 (19%) – Indigenous status unknown for 5 cases
- 118 confirmed cases (culture positive)
- 162 (58%) detected through PCR only (Figure 15)
- Change in case definition occurred 1 July 2018 to include PCR positive (probable) cases as notifiable (see footnote, page 10)
- All 118 culture positive cases were speciated (Table 14, Figure 16):
  - 75 (64%) *S. sonnei*
  - 43 (36%) *S. flexneri*.

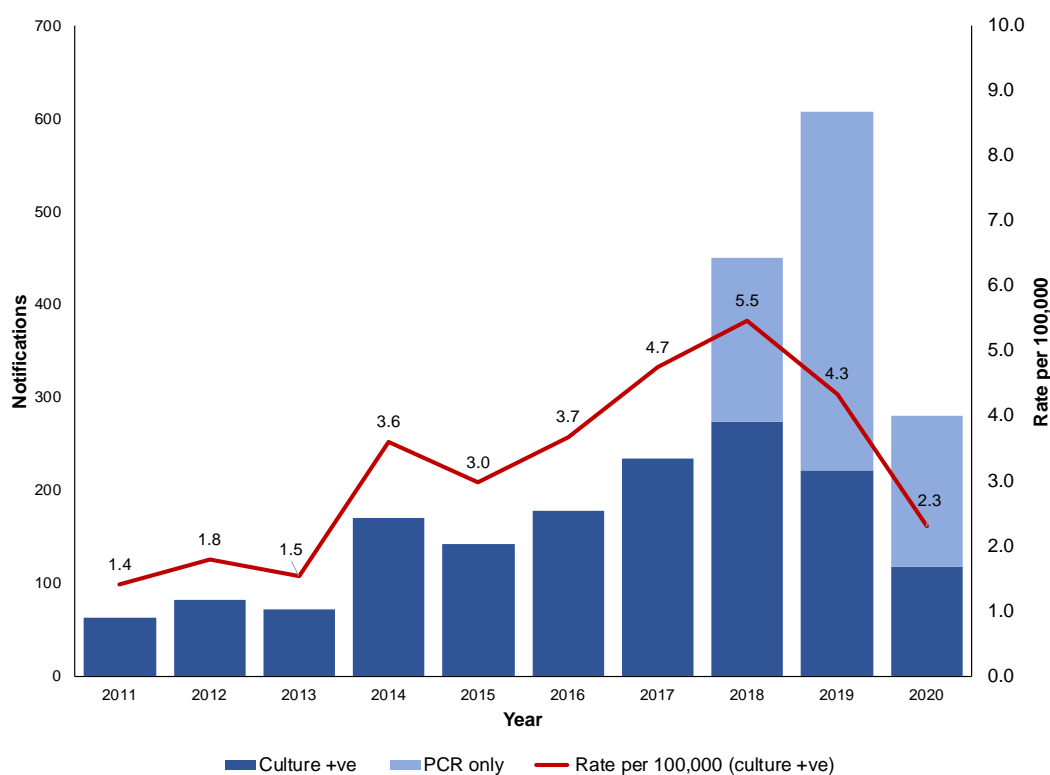
## Changes in incidence

- 54% decrease in notifications received in 2020 (280) compared to 2019 (609 notifications) (Table 1, Figure 15). Travel restrictions associated with the COVID-19 pandemic would have been a major contributor to this decline.
- *Shigella* notification rate in 2020 (5.5 per 100,000) was 17% lower than the 5-year annual mean (6.6 per 100,000) (Table 1).

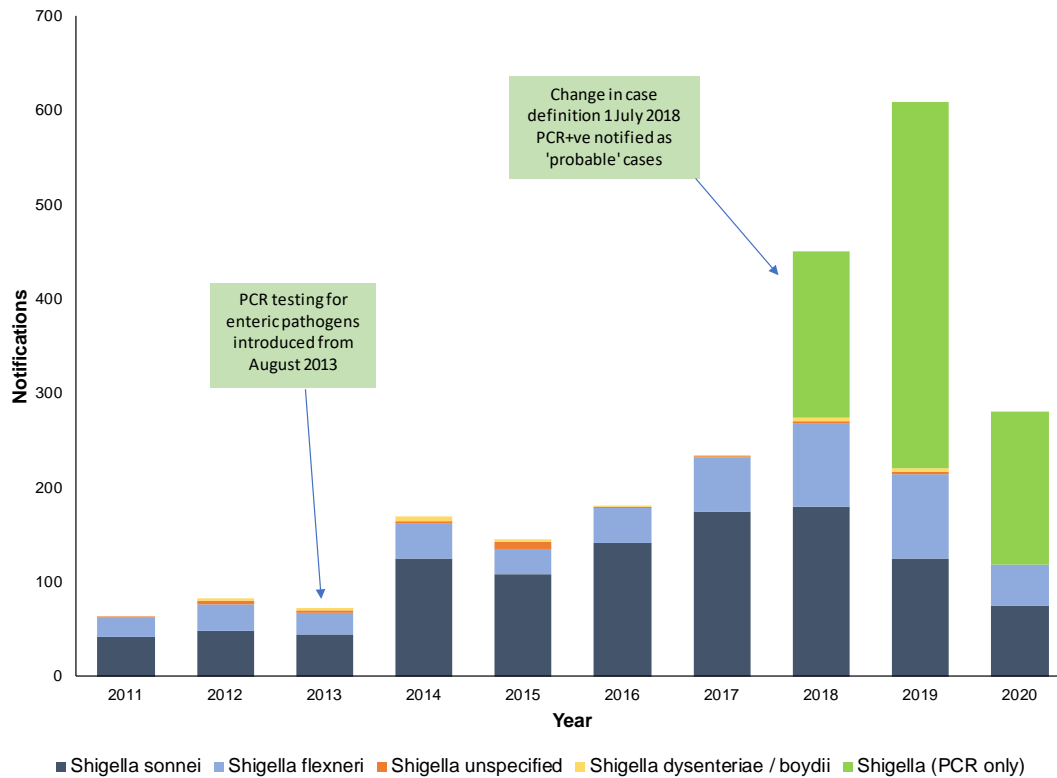


**Table 14.** *Shigella* species by year, Queensland, 2020

Species	2015	2016	2017	2018	2019	2020
<i>Shigella dysenteriae / boydii</i>	2	1	2	4	4	0
<i>Shigella flexneri</i>	27	37	57	88	90	43
<i>Shigella sonnei</i>	108	141	175	180	125	75
<i>Shigella</i> unspecified	8	2	1	2	1	0
<i>Shigella</i> (PCR only)	0	0	0	176	389	162
<b>Total</b>	<b>145</b>	<b>181</b>	<b>235</b>	<b>450</b>	<b>609</b>	<b>280</b>



**Figure 15.** *Shigella* notifications by method of diagnosis and culture-positive rate per 100,000 population, Queensland 2011–2020



**Figure 16.** *Shigella* notifications in Queensland by species, 2011–2020

## *Shigella sonnei*

- Total cases: 75
- Median age: 36 years (range <1–76 years)
- Indigenous: 9/75 (12%)
- Overseas travel: 13/50 (26%) – unknown for 25 cases
- 56 (75%) male (49 cases aged 18 years or older)
  - MSM: 26/28 (93%) males aged ≥18 years – MSM unknown for 21 cases
- HHS with highest notification rate: North West (18.2 per 100,000) (Table 15)
- Biotypes
  - Biotype a (20 cases)
  - Biotype g (54 cases)
  - Biotype f (1 case).

- MDR<sup>iii</sup> *Shigella sonnei*: 40 cases:
  - 39/54 (72%) biotype g isolates were MDR.
    - 35 (90%) male
    - All male cases (n=35) were aged 18 years or older – MSM reported by 21/22 (95%); unknown / not stated for 13 cases.
    - 3/39 MDR *S. sonnei* biotype g cases were identified in recently returned overseas travellers (1/3 female, 2/3 MSM unknown).
    - 1/20 (5%) biotype a isolates was MDR.
      - Identified in an Indigenous adult female.

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<sup>iii</sup> MDR: Multi-Drug Resistant - resistant to 3 or more of the following antibiotic combinations: ampicillin/amoxicillin, ciprofloxacin/norfloxacin, co-trimoxazole, ceftriaxone/cefotaxime/ceftazidime, or azithromycin.

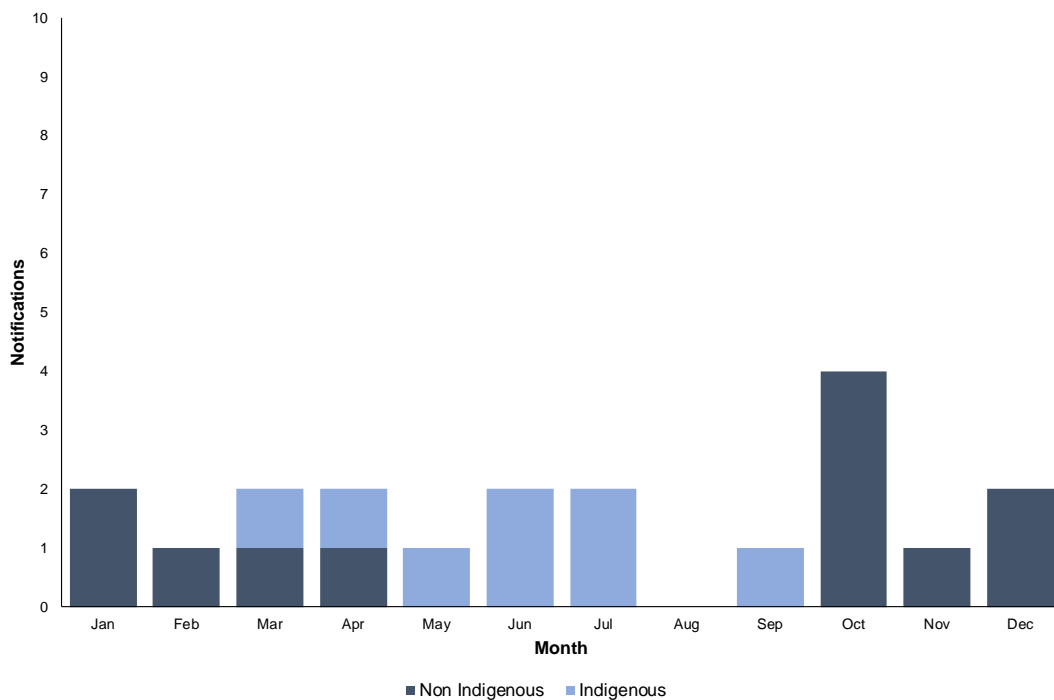
**Table 15.** *Shigella sonnei* notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	1	13	0.4	5.1
Central Queensland	0	7	0.0	3.2
Central West	0	0	0.0	0.0
Darling Downs	0	9	0.0	3.2
Gold Coast	10	14	1.6	2.3
Mackay	1	1	0.6	0.6
Metro North	29	32	2.8	3.2
Metro South	10	25	0.8	2.2
North West	5	4	18.2	14.2
South West	0	0	0.0	0.0
Sunshine Coast	2	9	0.5	2.2
Torres and Cape	1	9	3.6	33.5
Townsville	12	16	5.0	6.7
West Moreton	4	4	1.3	1.4
Wide Bay	0	2	0.0	0.9
<b>QLD Total</b>	<b>75</b>	<b>146</b>	<b>1.5</b>	<b>3.0</b>

\*5-year mean (2015–2019)

## Biotype a

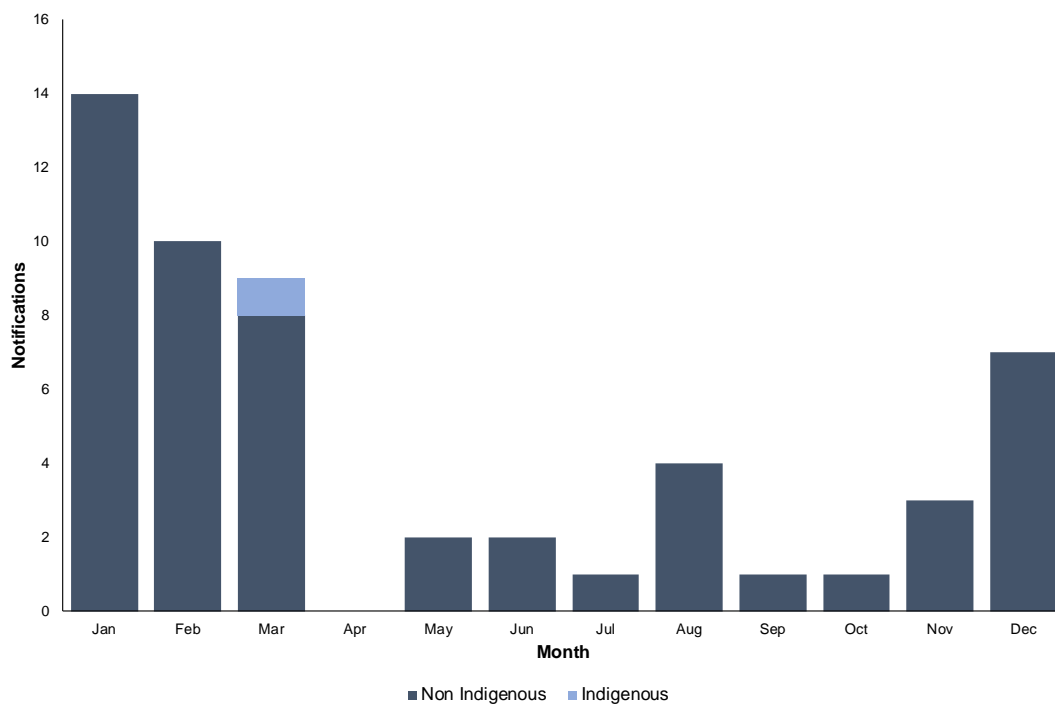
- 20 notifications (27% of all *Shigella sonnei*)
- Median age: 33 years (range 1–59 years)
- 10 (50%) male
- 8 (40%) Indigenous (Figure 17)
- Overseas travel: 3/10 (30%) – travel history unknown for 10 cases
- MSM: no cases reported
- One case of MDR *Shigella* biotype a identified
- One community-wide outbreak investigated in Northern Queensland (5 laboratory confirmed cases, 5 hospitalisations)



**Figure 17.** Monthly *Shigella sonnei* biotype a notifications in Queensland by reported Indigenous status, 2020

## Biotype g

- 54 notifications (72% of all *Shigella sonnei*).
- Median age: 36 years (range <1–76 years)
- 46 (85%) male
- One (2%) Indigenous (Figure 18)
- Overseas travel: 10/40 (25%) – travel history unknown for 14 cases
- MSM: 26/27 (96%) – MSM unknown for 17 cases, not applicable for 2 cases (children)
- MDR: 39/54 (72%) isolates (35 males, 4 females).



**Figure 18.** Monthly *Shigella sonnei* biotype g notifications in Queensland by reported Indigenous status, 2020

## Biotype f

- One notification in a 55-year-old female
- Travel and exposure history unknown.

## *Shigella flexneri*

- Total cases: 43
- Median age: 12 years (range 1–65 years)
- 30 (71%) Indigenous (Indigenous status unknown for 1 case)
- Overseas travel: 2/12 (17%) – unknown for 31 cases
- 28 (65%) male (14 cases aged 18 years or older)
- MSM: 2/3 males aged ≥18 years – MSM unknown for 11 cases
- HHS with highest notification rate: North West (10.9 per 100,000) (Table 16)
- Serotypes
  - Serotype 1b: 2 cases
  - Serotype 1c: 3 cases
  - Serotype 2a: 13 (30%) cases
  - Serotype 2b: 22 (51%) cases
  - Serotype 3b: 2 cases
  - Untyped: 1 case.
- 20/21 (95%) *Shigella flexneri* 2b cases reported among Indigenous persons (Indigenous status unknown for 1 case)
  - One outbreak investigated (4/9 cases laboratory confirmed, 4 hospitalisations)
    - Outbreak reported among residents of a Northern Queensland Indigenous community.
- 7 (54%) *Shigella flexneri* 2a cases reported among Indigenous persons
- MDR *Shigella flexneri*: 3 cases
  - All cases reported among non-indigenous persons
  - 2/3 were serotype 1c
    - Both cases MSM
  - 1/3 was serotype 2a
    - Recent travel to both India and Malaysia.

**Table 16.** *Shigella flexneri* notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	16	6	6.2	2.4
Central Queensland	8	1	3.6	0.5
Central West	0	0	0.0	0.0
Darling Downs	0	2	0.0	0.7
Gold Coast	0	4	0.0	0.7
Mackay	0	0	0.0	0.0
Metro North	7	10	0.7	1.0
Metro South	2	11	0.2	1.0
North West	3	9	10.9	32.0
South West	0	0	0.0	0.0
Sunshine Coast	0	3	0.0	0.7
Torres and Cape	2	8	7.1	29.8
Townsville	5	3	2.1	1.2
West Moreton	0	2	0.0	0.7
Wide Bay	0	0	0.0	0.0
<b>QLD Total</b>	<b>43</b>	<b>60</b>	<b>0.8</b>	<b>1.2</b>

\* 5-year mean (2015–2019)



# *Yersinia*

## Summary 2020

- Total notifications: 579
- Notification rate per 100,000: 11.4
- Median age: 41 years (range <1–96 years)
- 377 (65%) female
- No outbreaks reported.

## Other Key Information

- 205 (35%) culture positive (201 biotyped); 374 (65%) detected through PCR only
- The most frequently reported biotype: 1a – 65% (131 notifications) (Table 17).

## Changes in incidence

- 16% decrease in the 2020 notifications (579) compared to 2019 (691) (Table 1)
- *Yersinia* notification rate in 2020 (11.4 per 100,000) was slightly lower in comparison to the 5-year (2015–2019) annual mean (14.9 per 100,000) (Table 1)
- The increase in notifications from 2013 to 2015 was largely due to the introduction of multiplex PCR testing by diagnostic pathology laboratories for routine testing of faecal specimens.<sup>7</sup>
- *Yersinia* notification rates have since declined following a peak in 2016 (16.3 per 100,000) (Figure 19).

## Groups with highest notification rate

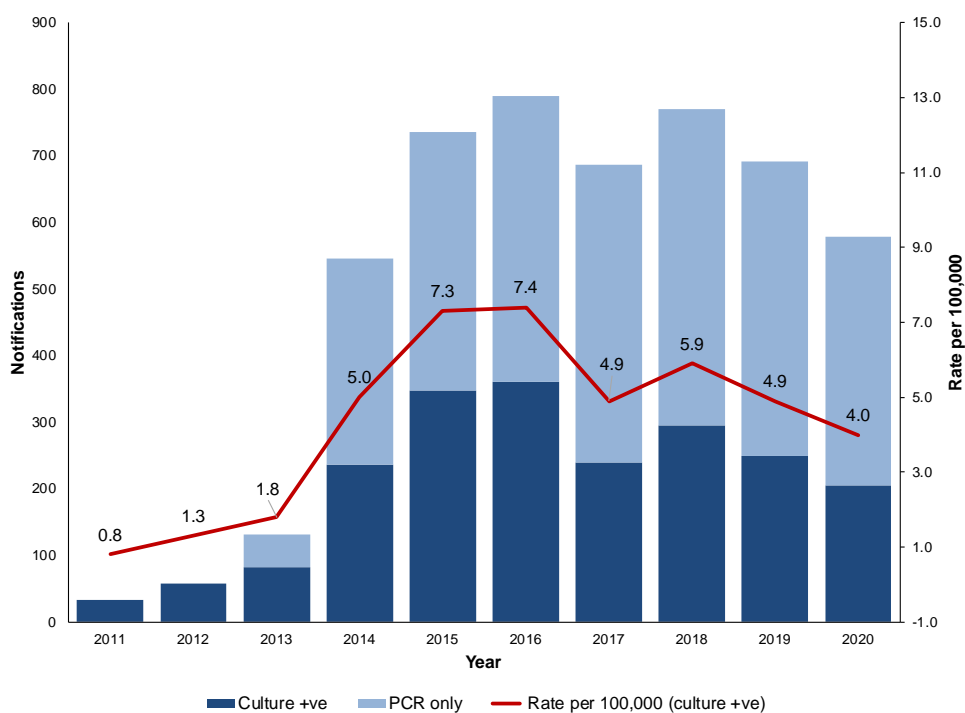
- Age group: 70+ years (15% of cases – 15.2 per 100,000) (Table 18)
- HHS: Metro North (23% of cases – 13.0 per 100,000) (Table 19).

## Seasonality

- Notifications peak during the warmer months (Figure 20).

**Table 17.** *Yersinia enterocolitica* notifications by bio/serotype in Queensland, 2020

Bio/serotype	Count	%
Biotype 1a non-typeable	123	61.2
Biotype 1a O:5	1	0.5
Biotype 1a O:8	7	3.5
Biotype 3 non-typeable	13	6.5
Biotype 4 O:3	57	28.4
Total	201	100



**Figure 19.** *Yersinia enterocolitica* notifications and rate per 100,000 population by year, Queensland 2011–2020

**Table 18.** *Yersinia enterocolitica* notifications and rate per 100,000 population by age group and sex, Queensland 2020

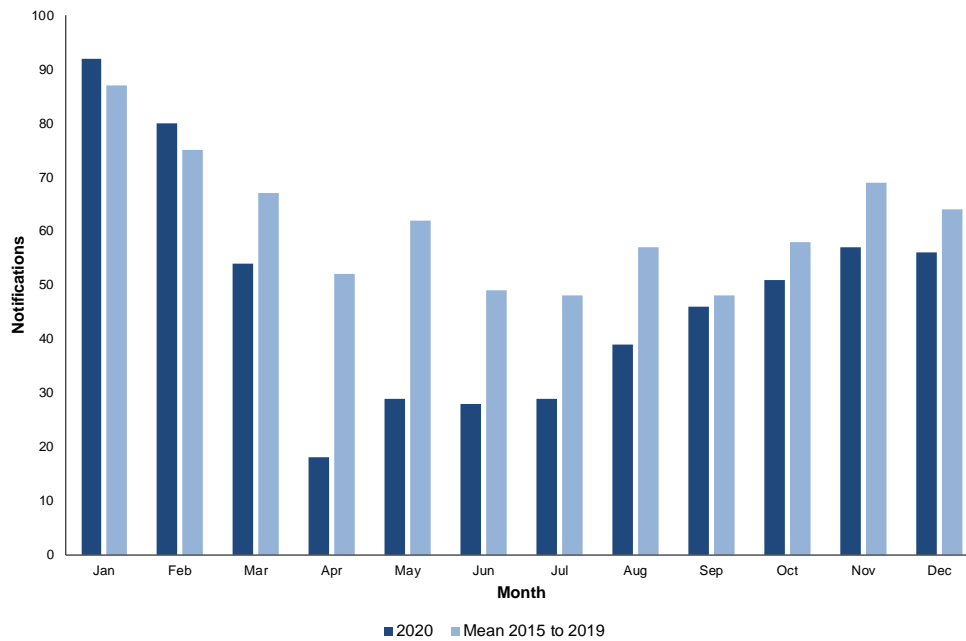
Age Group (years)	Male		Female		Total	
	Number	Rate	Number	Rate	Number	Rate
0-4	19	11.7	19	12.4	38	12.0
5-9	11	6.4	15	9.1	26	7.7
10-19	18	5.4	23	7.2	41	6.3
20-29	30	8.4	51	14.3	81	11.4
30-39	33	9.6	64	17.9	97	13.9
40-49	19	5.8	54	15.8	73	10.9
50-59	25	8.2	49	15.2	74	11.8
60-69	15	5.8	50	18.5	65	12.3
70 +	32	12.4	52	17.8	84	15.2
<b>All ages</b>	<b>202</b>	<b>8.0</b>	<b>377</b>	<b>14.6</b>	<b>579</b>	<b>11.4</b>

**Table 19.** *Yersinia enterocolitica* notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	33	50	12.7	19.6
Central Queensland	26	30	11.8	13.7
Central West	1	0	9.7	0.0
Darling Downs	34	28	11.9	9.9
Gold Coast	66	87	10.4	14.4
Mackay	22	28	12.7	16.2
Metro North	136	155	13.0	15.5
Metro South	145	172	12.2	15.1
North West	1	3	3.6	10.7
South West	3	2	12.5	8.2
Sunshine Coast	50	80	11.5	19.2
Torres and Cape	1	1	3.6	3.7
Townsville	24	44	9.9	18.3
West Moreton	22	34	7.2	11.9

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	Wide Bay	15	20	6.8
QLD Total	579	735	11.4	14.9

\* 5-year mean (2015–2019)



**Figure 20.** *Yersinia enterocolitica* notifications in 2020 by month of onset, and mean notifications for the 5-year period, 2015 to 2019 in Queensland

# Shiga toxin-producing *E. coli* (STEC)

## Summary 2020

- Total notifications: 30
- Notification rate per 100,000: 0.6
- Median age: 36 years (range 2–85 years)
- 16 (53%) female
- No outbreaks reported

## Other Key Information

- 8 (27%) hospitalised; no deaths reported
- 4 cases notified with HUS
- 15 (50%) cases with culture positive stools:
  - Most frequent serogroups:
    - O91 (2 cases)
    - O111 (2 cases)
    - O128 (2 cases)
  - Individual serogroups identified in the remaining cases:
    - O8, O76, O139, O82, O145, O112, O157, O26 and O non-typeable
- STEC target genes:
  - 6 cases (20%) PCR +ve for stx1 gene only
  - 15 cases (50%) PCR +ve for stx2 gene only
  - 9 cases (30%) PCR +ve for both stx1 and stx2 genes
- 29/30 (97%) locally acquired infections. No confirmed source of infection among these cases:
  - 10/29 cases had exposure to one or more of the following risk factors:
    - a rural property / setting (including camping), untreated water or contact with farm animals (and/or animal manure)

- 1 asymptomatic case (serogroup O128) was a faecal microbiota transplant (FMT) donor who reported weekly consumption of either raw steak or mince
  - This case was identified via traceback, following a positive *Campylobacter* infection in an FMT recipient who was given a pooled faeces sample from 4 donors
  - STEC was not identified in the recipient
- A source of infection was not identified for the remaining 18 cases
- 1/30 cases reported overseas travel during their exposure period:
  - Travel to Papua New Guinea for work and also travelled to Canada during their exposure period
    - Serogroup ONT:H7 detected
- 8/30 cases were diagnosed by the Melbourne Diagnostic Unit, with these isolates referred from NutriPATH Integrative Pathology Services (Victoria) who provide diagnostic services for medical and complementary healthcare practitioners:
  - 1 case reported frequent contact with cattle during their exposure period
  - 7 cases reported non-acute illness and no risk factors identified
  - 6/8 cases with culture positive results:
    - Serogroups O111, O112, O128, O76, O8 and O91 identified
- 6/30 cases were asymptomatic:
  - 1 case was identified via household screening (rural / animal exposure)
  - 1 case was an FMT donor
  - 4 cases had visited a naturopath / nutritionist for non-acute, chronic gastrointestinal conditions

## Changes in incidence

- 2020 notifications (30) were comparable to 2019 (29) (Table 1)
- Notifications and rates have remained relatively stable over the period 2014–2020 (Figure 21)
- Increase in incidence in during 2013 was primarily due to a zoonotic outbreak (57 cases)

## Groups with highest notification rate

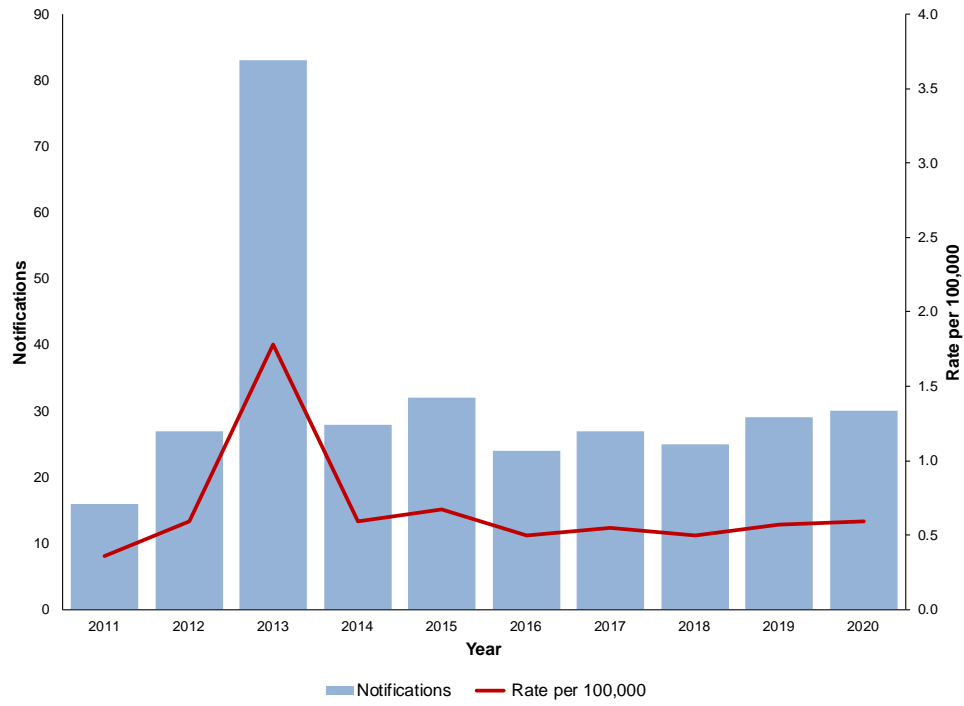
- Gender: Male (53% of cases - 0.6 per 100,000) (Table 20)
- Age group: 70+ years (20% of cases – 1.1 per 100,000)
- HHS: Central Queensland (3 cases – 1.4 per 100,000) (Table 21)

## Seasonality

- Peak notifications during 2020 occurred in spring (12 cases) and summer (11 cases)
- Notifications by quarter: Q1 (9), Q2 (2), Q3 (3), Q4 (16)

**Table 20.** STEC notifications and rate per 100,000 population by age group and sex, Queensland 2020

Age Group (years)	Male		Female		Total	
	Number	Rate	Number	Rate	Number	Rate
0–4	0	0.0	1	0.7	1	0.3
5–9	0	0.0	1	0.6	1	0.3
10–19	3	0.9	1	0.3	4	0.6
20–29	4	1.1	3	0.8	7	1.0
30–39	1	0.3	3	0.8	4	0.6
40–49	0	0.0	2	0.6	2	0.3
50–59	1	0.3	1	0.3	2	0.3
60–69	2	0.8	1	0.4	3	0.6
70 +	5	1.9	1	0.3	6	1.1
<b>All ages</b>	<b>16</b>	<b>0.6</b>	<b>14</b>	<b>0.5</b>	<b>30</b>	<b>0.6</b>



**Figure 21.** STEC notifications and rate per 100,000 population by year, Queensland 2011–2020



**Table 21.** STEC notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	1	1	0.4	0.4
Central Queensland	3	2	1.4	0.9
Central West	0	0	0.0	0.0
Darling Downs	3	4	1.1	1.4
Gold Coast	5	3	0.8	0.5
Mackay	2	0	1.2	0.0
Metro North	3	5	0.3	0.5
Metro South	6	5	0.5	0.4
North West	0	0	0.0	0.0
South West	0	0	0.0	0.0
Sunshine Coast	2	3	0.5	0.7
Torres and Cape	0	0	0.0	0.0
Townsville	0	1	0.0	0.4
West Moreton	3	2	1.0	0.7
Wide Bay	2	1	0.9	0.5
<b>QLD Total</b>	<b>30</b>	<b>27</b>	<b>0.6</b>	<b>0.5</b>

\*5-year mean (2015–2019)

# Haemolytic Uraemic Syndrome (HUS)

## Summary 2020

- Total notifications: 4
- Notification rate per 100,000: 0.1
- Median age: 62.5 years (range 5–85 years)
- 2 (50%) female
- Clinical diagnosis

## Other Key Information

- All cases associated with STEC infections:
- Isolates from all 4 cases were PCR +ve for stx2 gene (stx1 -ve)
  - 1/4 cases had culture positive stools: Serogroup O82
  - 3/4 cases had exposure to cattle in a rural environment during their exposure period
- No confirmed source of infection among cases
- No deaths were reported

## Changes in incidence

- 2020 notifications (4) were comparable to 2019 (3) and the 5-year mean (3) (Table 1)

# Enteric Fever

## Typhoid Fever

### Summary 2020

- Total notifications: 10
- Notification rate per 100,000: 0.2
- Median age: 31.5 years (range 3–75 years)
- 6 (60%) female

### Changes in incidence

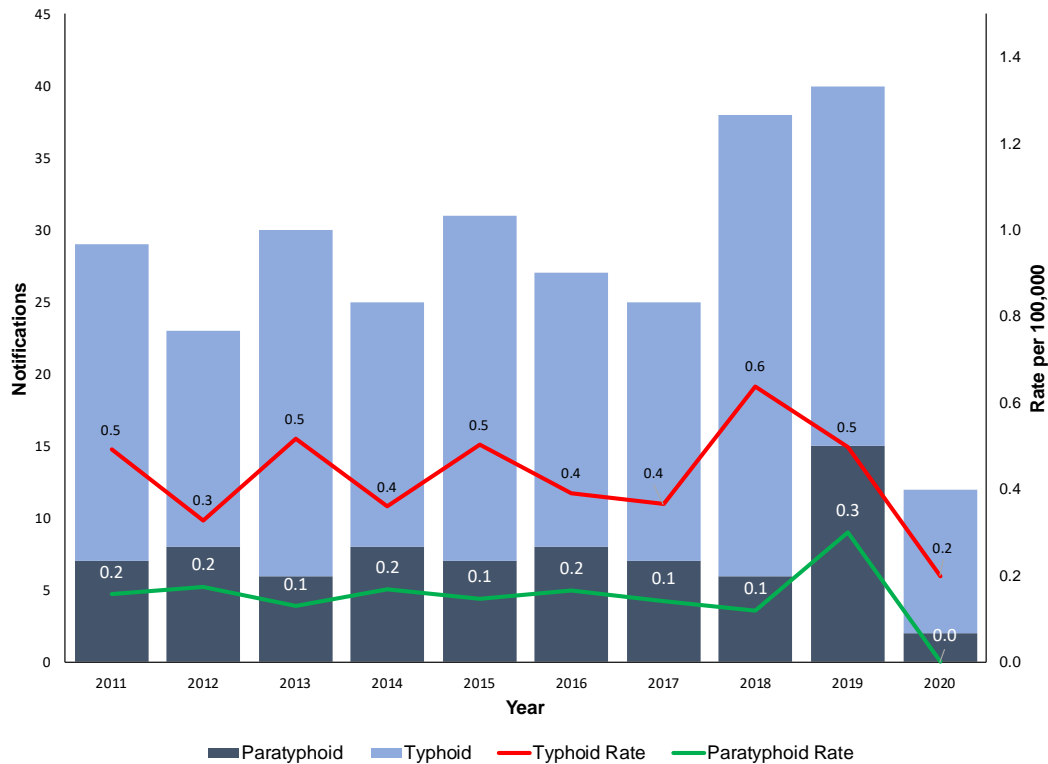
- 2020 notifications (10) were 60% lower in comparison to 2019 (25) and 58% lower than the 5-year mean (24) (Table 1, Figure 22)

### Groups with highest notification rate

- Age group: 0 – 4 years (20% of cases – 0.6 per 100,000).

### Place of Acquisition

- Overseas acquired: 9 (90%)
- India (6)
- Indonesia (1)
- Pakistan (1)
- Samoa (1)
- Locally acquired: 1 (household contact of 2 cases that were notified in September 2019)



**Figure 22.** Typhoid / Paratyphoid notifications and rate per 100,000 population by year, Queensland 2011–2020

## Paratyphoid Fever

### Summary 2020

- Total notifications: 2
- Notification rate per 100,000: 0.0
- Median age: 22.5 (cases aged 17 and 28 years).
- 1 (50%) female

### Changes in incidence

- 2020 notifications (2) were 7.5 times lower than 2019 (15) (Table 1, Figure 22)

## Groups with highest notification rate

- Not applicable

## Place of Acquisition

- Both cases were likely overseas acquired infections (India)

# Hepatitis A

## Summary 2020

- Total notifications: 15
- Notification rate per 100,000: 0.3
- Median age: 11 years (range 3–45 years)
- 10 (67%) male
- No foodborne outbreaks; 1 non-foodborne outbreak (7 cases)

## Other Key Information

- MSM: No cases reported
- Indigenous: No cases reported
- 5 (33%) infections were genotyped (Table 22)
  - Genotype IB was identified in 4 cases; all were from the same local outbreak
  - Genotype IIIA was identified in 1 case (overseas acquired)
- An outbreak involving 7 cases (6 children, 1 adult) was reported across 2 households
  - Both households had children who attended the same primary school
  - 5 cases were asymptomatic (all children)
  - Person to person transmission

## Changes in incidence

- 2020 notifications (15) decreased by 40% in comparison to 2019 (25) (Table 1)
- 2020 notification rate (0.3 per 100,000) was lower than the 5-year annual mean (0.6 per 100,000) (Table 1)
- Notable decline in notifications from 2018 to 2020. Overseas travel restrictions due to the COVID-19 outbreak was largely responsible for the small number of cases in 2020 (Figure 23)

## Groups with highest notification rate

- Age group: 5 – 9 years (27% of cases – 1.2 per 100,000) (Table 23)
- HHS: West Moreton (8 cases – 2.6 per 100,000) (Table 24).
- 7/8 cases were from the same outbreak

## Place of acquisition

- Overseas travel reported: 8 (53%) (Table 25)
- All 8 cases had travelled overseas prior to the COVID-19 travel restrictions.

**Table 22.** Hepatitis A notifications by genotype, Queensland 2020

Genotype	Locally acquired infections	Overseas acquired infections	Total
IIIA	0	1	1
IB	4	0	4
Not typed	3	7	10
<b>Total</b>	<b>7</b>	<b>8</b>	<b>15</b>

**Table 23.** Hepatitis A notifications and rate per 100,000 population by age group and sex, Queensland 2020

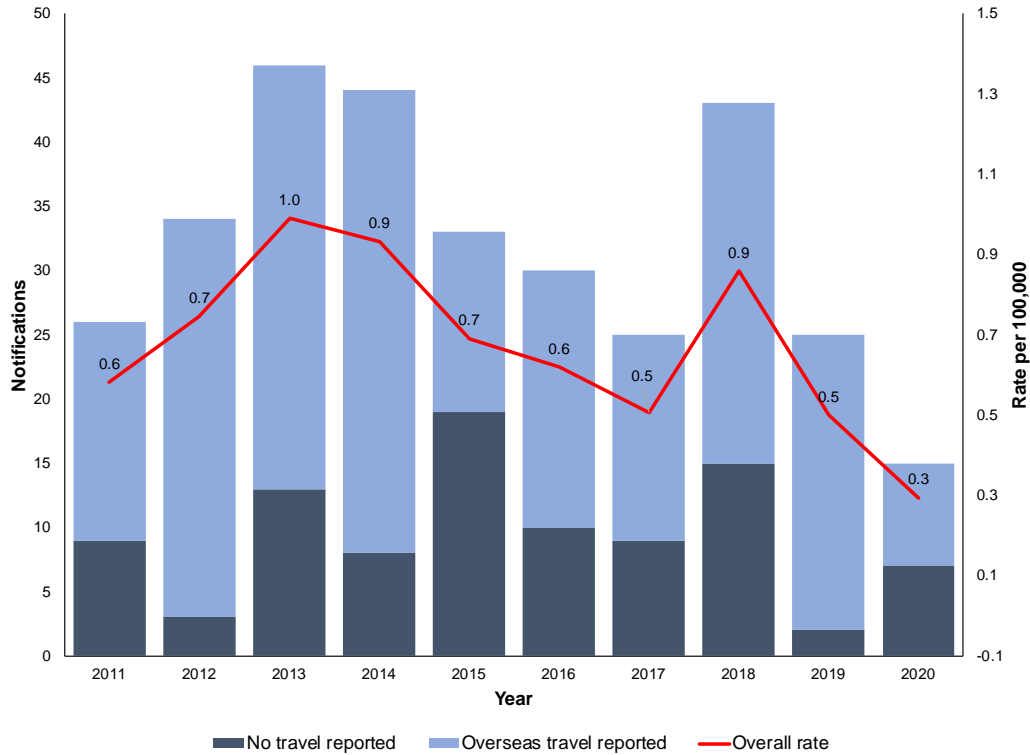
Age Group (years)	Male		Female		Total	
	Number	Rate	Number	Rate	Number	Rate
0–4	2	1.2	1	0.7	3	1.0
5–9	4	2.3	0	0.0	4	1.2
10–19	1	0.3	0	0.0	1	0.2
20–29	1	0.3	1	0.3	2	0.3
30–39	1	0.3	3	0.8	4	0.6
40–49	1	0.3	0	0.0	1	0.1
50–59	0	0.0	0	0.0	0	0.0
60–69	0	0.0	0	0.0	0	0.0
70 +	0	0.0	0	0.0	0	0.0
<b>All ages</b>	<b>10</b>	<b>0.4</b>	<b>5</b>	<b>0.2</b>	<b>15</b>	<b>0.3</b>

**Table 24.** Hepatitis A notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	1	1	0.4	0.4
Central Queensland	0	1	0.0	0.5
Central West	0	0	0.0	0.0
Darling Downs	0	1	0.0	0.4
Gold Coast	2	6	0.3	1.0
Mackay	0	0	0.0	0.0
Metro North	2	7	0.2	0.7
Metro South	1	10	0.1	0.9
North West	0	0	0.0	0.0
South West	0	0	0.0	0.0
Sunshine Coast	1	2	0.2	0.4
Torres and Cape	0	0	0.0	1.5
Townsville	0	0	0.0	0.0
West Moreton	8	2	2.6	0.6
Wide Bay	0	1	0.0	0.4
<b>QLD Total</b>	<b>15</b>	<b>31</b>	<b>0.3</b>	<b>0.6</b>

\*5-year mean (2015–2019)





**Figure 23.** Hepatitis A notifications by reported travel and overall rate per 100,000 population by year, Queensland 2011 – 2020

**Table 25.** Frequency of Hepatitis A infections by place of acquisition, 2020

Place of Acquisition	Count	%
Australia	7	47
South Korea	3	20
India	2	13
Mexico	2	13
Uzbekistan	1	7
<b>Total</b>	<b>15</b>	<b>100</b>

# Hepatitis E

## Summary 2020

- Total notifications: 6
- Notification rate per 100,000: 0.1
- Median age: 33.5 years (range 26–59 years)
- 4 (67%) male
- No outbreaks reported

## Other Key Information

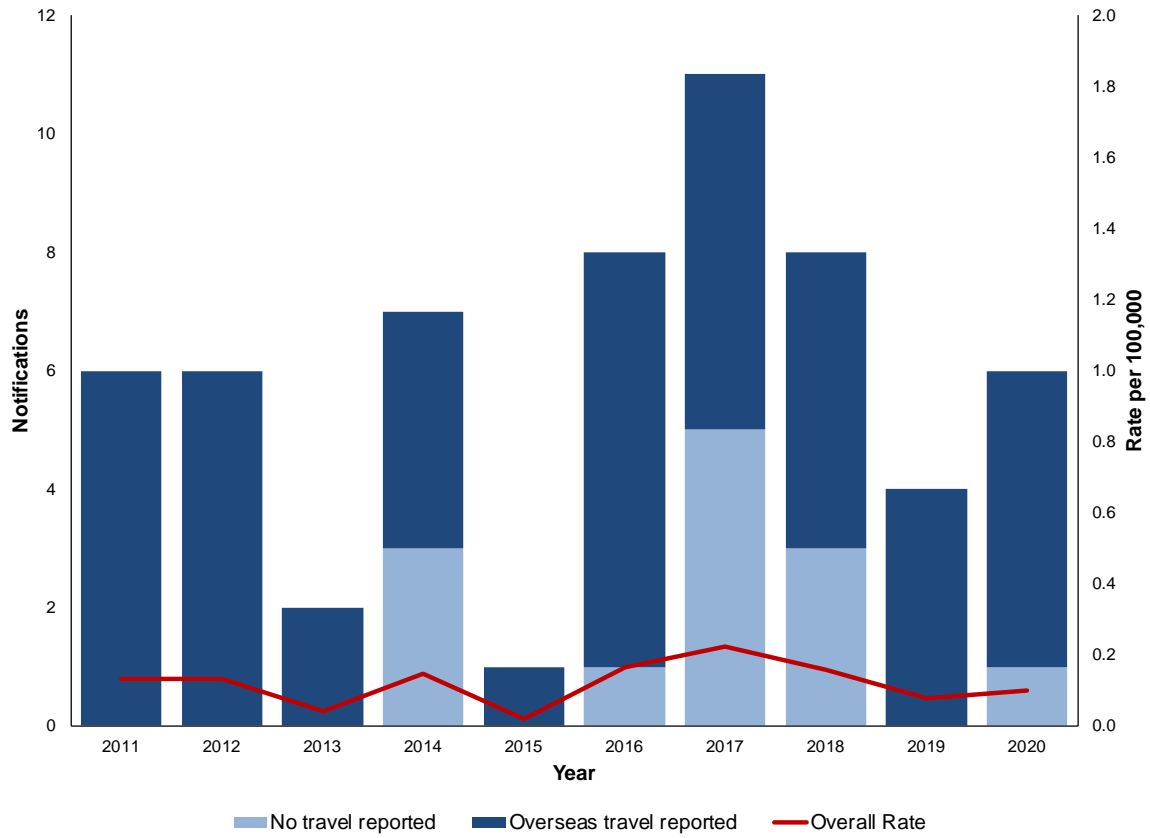
- No genotype available

## Changes in incidence

- 6 notified cases in 2020; compares with 4 notified cases in 2019 and a 5-year mean of 6 cases (Table 1)
- Notifications have ranged from 1 to 11 cases per year during the past 10 years (mean 6 cases) (Figure 24)
  - 78% of cases during the past 10 years were overseas acquired infections

## Place of acquisition

- Overseas travel reported: 5 (83%)
  - India (4), Pakistan (1)
  - All 5 cases had travelled overseas prior to the COVID-19 travel restrictions.
- No recent overseas travel for one case – travelled to South America in March 2019. Potential source of infection unknown.



**Figure 24.** Hepatitis E notifications by reported travel and overall rate per 100,000 population by year, Queensland 2011–2020

# Ciguatera

## Summary 2020

- Total notifications: 13 (1 sporadic, 12 outbreak related cases).
- Notification rate per 100,000: 0.3
- Median age: 34 years (range 2–66 years)
- 8 (62%) female
- 4 outbreaks investigated

## Other Key Information

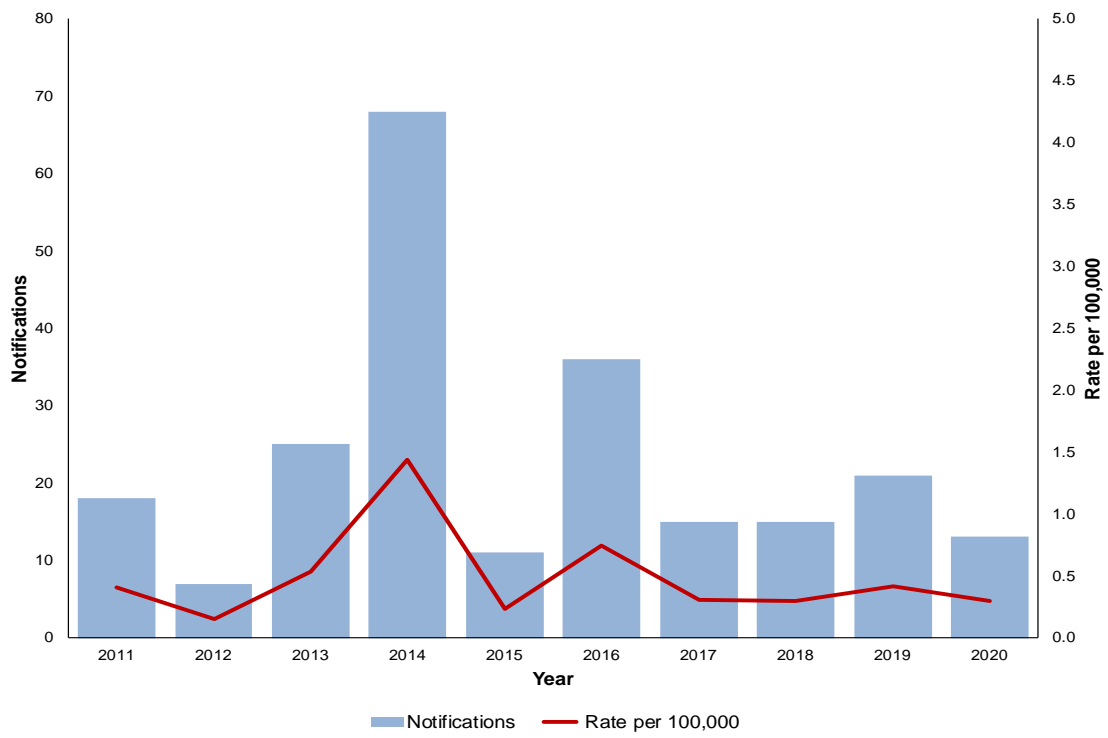
- All ciguatera notifications are based on clinical diagnoses
- All 13 reported neurological symptoms
- 12/13 reported diarrhoea
- 4/13 hospitalised
- Median incubation period: 4 hours (range 1–10.5 hours); information available for 10 cases
- Most frequently implicated fish:
- Spanish mackerel (11 cases); Coral trout (2)
- Ciguatoxin detected in leftover fish for 12/13 cases

## Changes in incidence

- Incidence has been relatively stable since 2017 (Figure 25).
- 2020 notifications (13) were 38% lower in comparison to 2019 (21) (Table 1)
- Ciguatera notification rate in 2020 (0.3 per 100,000) was slightly lower than the 5-year (2015–2019) annual mean (0.4 per 100,000) (Table 1)

## Groups with highest notification rate

- HHS: Metro South (69% cases – 0.8 per 100,000) and Townsville (15% cases – 0.8 per 100,000) (Table 26)



**Figure 25.** Ciguatera notifications and rate per 100,000 population by year, Queensland 2011–2020

**Table 26.** Ciguatera notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2020

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2020	5-year mean*	2020	5-year mean
Cairns and Hinterland	1	3	0.3	1.2
Central Queensland	0	0	0.0	0.2
Central West	0	0	0.0	0.0
Darling Downs	0	1	0.0	0.4
Gold Coast	1	1	0.2	0.2
Mackay	0	2	0.0	1.2
Metro North	0	2	0.0	0.2
Metro South	9	3	0.8	0.3
North West	0	1	0.0	2.1
South West	0	0	0.0	0.0
Sunshine Coast	0	2	0.0	0.5
Torres and Cape	0	0	0.0	0.7
Townsville	2	4	0.8	1.7
West Moreton	0	0	0.0	0.0
Wide Bay	0	1	0.0	0.5
<b>QLD Total</b>	<b>13</b>	<b>20</b>	<b>0.3</b>	<b>0.4</b>

\*5-year mean (2015–2019)

# Gastrointestinal Disease Outbreaks

## Summary 2020

- Total outbreaks: 688
- Total cases: 12,615
- Hospitalisations: 192 (1.5% of cases)
- Foodborne outbreaks (QLD): 12 (107 cases)
- Zoonotic outbreaks: 1 (38 cases)
- Non-foodborne outbreaks: 675 (12,470 cases)
- Multi-jurisdictional foodborne outbreaks: 1 (1,063 cases)

## Foodborne outbreaks

- 12 outbreaks within Queensland involving 107 cases of illness, with 27 hospitalisations (Table 27)
- *Salmonella* was the confirmed aetiological agent in 5 foodborne outbreaks comprising 44 cases and 15 hospitalisations (Table 28)
- Ciguatera fish poisoning was the cause of 4 outbreaks (16 cases) associated with the consumption of Spanish mackerel (3 outbreaks) and Coral Trout (1 outbreak)
- Norovirus was the confirmed aetiological agent in 2 outbreaks that involved 45 cases with 5 hospitalisations. Both were associated with catered gatherings.
- Histamine fish poisoning was the likely cause of one outbreak where both cases were hospitalised
- One multi-jurisdictional foodborne outbreak comprising 1,063 confirmed cases of *Salmonella* Typhimurium MLVA 05-16-13-11-490 with 132 hospitalisations. The large majority (65%) of cases were reported from Queensland (refer to [Multi-jurisdictional outbreak section](#))



## Zoonotic outbreaks

- One outbreak of zoonotic transmission comprising 38 cases of illness, with 9 hospitalisations (Table 28)
  - *Salmonella* Typhimurium MLVA 03-11-10-08-523 was the predominate aetiological agent identified among cases who had exposure to backyard poultry (chicks) that had been sourced from a single poultry supplier

## Non-foodborne outbreaks

- There were 675 non-foodborne related outbreaks associated with 12,470 cases and 156 hospitalisations
- Childcare centres (573 outbreaks, 85%) and aged care facilities (77 outbreaks, 11%) were the most frequently reported outbreak settings, (refer Non-foodborne Disease Outbreaks section)

**Table 27.** Gastrointestinal illness outbreaks by mode of transmission, Queensland 2020

Mode of transmission	No. of Outbreaks	No. ill	No. hospitalised	No. of deaths
Foodborne* / probable foodborne**	12	107	27	0
Zoonotic	1	38	9	0
Person to person	531	10,903	139	1
Unknown	144	1,567	17	0
<b>Total</b>	<b>688</b>	<b>12,615</b>	<b>192</b>	<b>1</b>

**\*Foodborne:** An incident where 2 or more persons experience a similar illness after consuming a common food or meal and analytical epidemiological evidence and/or microbiological evidence (including food and/or environmental) implicates the meal or food as the source of illness; or in the absence of analytic and/or microbiological evidence, the aetiology of the outbreak can only result through foodborne transmission (e.g. ciguatera poisoning, *Listeria monocytogenes*).

**\*\*Probable Foodborne:** An incident where 2 or more persons experience a similar illness after consuming a common food or meal and compelling descriptive epidemiological evidence implicates the meal or food as the suspected source of illness. This includes outbreaks where the mode of transmission is suspected to be from an ill food handler to food to person.

**Table 28.** Gastrointestinal illness outbreaks by mode of transmission and aetiology in Queensland, 2020

Mode of transmission	Aetiology	No. of Outbreaks	No. ill	No. hospitalised	No. of deaths
Foodborne / probable foodborne	Ciguatera fish poisoning	4	16	5	0
	Norovirus	2	45	5	0
	Salmonella Hvittingfoss	1	4	0	0
	Salmonella Saintpaul MLST 50	1	15	6	0
	Salmonella Typhimurium MLVA 03-12-12-09-523	1	13	3	0
	Salmonella Typhimurium MLVA 03-17-09-12-523	1	8	4	0
	Salmonella Typhimurium MLVA 03-20-11-10-523	1	4	2	0
	Histamine fish poisoning	1	2	2	0
	<b>Sub Total</b>	<b>12</b>	<b>107</b>	<b>27</b>	<b>0</b>
Zoonotic	Salmonella Typhimurium MLVA 03-11-10-08-523	1	38	9	0
Person to person	Adenovirus	2	78	1	0
	Blastocystis hominis	1	3	0	0
	Hepatitis A	1	7	1	0
	Norovirus	52	1,273	17	1
	Sapovirus	1	11	0	0
	Shigella flexneri 2b	1	9	4	0
	Shigella sonnei biotype a	1	5	5	0
	Unknown	472	9,517	111	0
	<b>Sub Total</b>	<b>531</b>	<b>10,903</b>	<b>139</b>	<b>1</b>
Unknown mode of transmission	Clostridium difficile	1	9	2	0
	Norovirus	1	25	0	0
	Unknown	142	1,533	15	0
	<b>Sub Total</b>	<b>144</b>	<b>1,567</b>	<b>17</b>	<b>0</b>
<b>TOTAL</b>		<b>688</b>	<b>12,615</b>	<b>192</b>	<b>1</b>

*Note: Table 28 does not include the multi-jurisdictional outbreak of Salmonella Typhimurium that involved 687 Queensland cases (see Multi-jurisdictional outbreak section in this report)*

# Foodborne disease outbreaks

## Summary 2020

- Total outbreaks: 12
- Total cases: 107
- Hospitalisations: 27 (25% of cases)
- No deaths reported.

## Other Key Information

- 5 (42%) outbreaks had a bacterial aetiology (Table 29):
  - *Salmonella* Typhimurium (3), *Salmonella* Hvittingfoss (1), *Salmonella* Saintpaul (1)
- 5 (42%) outbreaks associated with marine toxins:
  - Ciguatera (4), Histamine (1)
  - Ciguatera food vehicles included Spanish mackerel (3 outbreaks) and Coral Trout (1). Histamine food vehicle was linked to Yellow Fin Tuna.
  - Outbreak settings: private residence (4), community (1)
- 2 (17%) outbreaks had a viral aetiology (norovirus)
- A likely food vehicle was identified in 9 (75%) outbreaks
- Outbreak settings: private residence (4), restaurants (3), catered gatherings (2), general community (2), franchised fast food (1)

**Table 29.** Foodborne / probable foodborne outbreaks in Queensland by aetiology and month during 2020

No.	Month	Aetiology	Total cases	Lab confirmed	Vehicle	Likely source	Setting where food was consumed	Evidence <sup>†</sup>
<b>Bacterial</b>								
1	Feb	<i>Salmonella</i> Hvittingfoss	4	2	Wilted rocket salad with butter sauce and parmesan	Unknown	Restaurant	D
2	Jul	<i>Salmonella</i> Saintpaul MLST 50	15	15	Unknown	Unknown	Community	D
3	Sep	<i>Salmonella</i> Typhimurium MLVA 03-12-12-09-523	13	13	Unknown	Unknown	National franchised fast food	D
4	Oct	<i>Salmonella</i> Typhimurium MLVA 03-20-11-10-523	4	4	Eggs benedict	Eggs	Restaurant	D
5	Nov	<i>Salmonella</i> Typhimurium MLVA 03-17-09-12-523	8	8	Aioli	Eggs	Restaurant	D
<b>Marine Toxins</b>								
6	Jun	Histamine	2	-	Yellow Fin Tuna	Fish	Private residence	D
7	Jul	Ciguatera	9	-	Spanish mackerel	Fish	Community	M
8	Sep	Ciguatera	2	-	Spanish mackerel	Fish	Private residence	M
9	Oct	Ciguatera	2	-	Coral Trout	Fish	Private residence	D
10	Dec	Ciguatera	3	-	Spanish mackerel	Fish	Private residence	M
<b>Viral</b>								
11	Nov	Norovirus	20	1	Unknown	Unknown	Catered gathering	D
12	Dec	Norovirus	25	3	Sandwiches (suspected)	Unknown	Catered gathering	D

*† D: Descriptive evidence implicating the suspected vehicle or suggesting foodborne transmission; A: Analytical association between illness and food; M: Microbiological confirmation in suspect vehicle and cases; AM: Analytical and microbiological evidence.*

**Note:** Table 29 does not include the multi-jurisdictional outbreak of Salmonella Typhimurium that involved 687 Queensland cases (see [Multi-jurisdictional outbreak section](#) in this report).

# Significant Foodborne Outbreaks 2020

Salmonella Typhimurium MLVA 05-16-13-11-490 (Multi-jurisdictional)

- Please refer to [Multi-jurisdictional Outbreaks section](#).

# Zoonotic Outbreaks

- One outbreak of gastrointestinal illness associated with zoonotic transmission was investigated during 2020

## *Salmonella* Typhimurium MLVA 03-11-10-08-523

A cluster of six cases of *Salmonella* Typhimurium (STm) MLVA 03-11-10-08-523 was reported in late May, 5 of who were 9 years or younger, prompted an investigation into a potential common source of infection. Historically, there was a single case reported several months earlier in February 2020 with this MLVA profile and only 3 cases during the previous 5 years. Over the course of the investigation a total of 38 outbreak cases of STm were identified with cases reported from Queensland (29), Northern Territory (1), New South Wales (6), South Australia (1) and Victoria (1). Of the 38 cases, 24 (63%) were male; the median age was 5 years (range <1 to 38 years). Additionally, a further 14 possible epidemiologically linked cases were identified across 11 households. Onset dates of illness among laboratory confirmed cases ranged from 10 May to 29 July. Three MLVA profiles were linked to this outbreak during the course of this investigation, including 03-11-10-08-523 (35 cases) and 2 variant profiles, 03-13-09-11-523 (2 cases) and 03-11-10-09-523 (1 case). All 38 cases had contact with live poultry in the week prior to their illness. Thirty-seven cases had exposure to backyard poultry and one case worked as a farmhand at a broiler farm. No other common risk factors were identified among cases.

The large majority of cases who reported exposure to backyard poultry had recently purchased one-week old chicks from either a produce store, pet store or farmer's market. Eighteen of 25 separate produce/pet stores that were linked to outbreak cases had the same poultry supplier (breeder farm). The supplier of chicks for the other 7 stores was unknown.

A total of 77 environmental samples were collected from the breeder farm and 8 samples were taken from the chicken coop environment at the home of one case. One of these 8 samples tested positive for the outbreak strain (STm 03-11-10-08-523). Two of the 3 outbreak strains associated with cases were detected in 13 different environmental farm

samples taken from the hatchery and multiple poultry sheds, with STm 03-11-10-08-523 isolated from 11 samples and STm 03-13-09-11-523 from 2 samples.

Nineteen STm 03-11-10-08-523 outbreak isolates (13 x human; 6 x environmental) and 12 historical isolates with the same MLVA profile were submitted for whole genome sequencing (wgs). The 13 isolates from outbreak cases and the 6 environmental isolates all genotyped as cgMLST complex type 5922 and clustered together with a high level of genetic similarity (0-3 SNPs<sup>iv</sup>). None of the historical isolates were highly related to the outbreak strains. Two STm 03-13-09-11-523 outbreak isolates (1 x human; 1 x environmental) were also sequenced and both genotyped as cgMLST 3454 and were highly related genetically (1 SNP difference).

The investigation provided very strong epidemiological and laboratory evidence to implicate the breeder farm as the source of infection for this outbreak. Transmission was most likely through close contact and handling of one-week old chicks sold through retail produce/feed and pet stores. Control and prevention measures at the farm included flock vaccination, water chlorination, installation of more hand/foot washing facilities, fumigation of sheds between batches, and improved vermin control methods. A media statement was released during the investigation providing public health advice for owners of backyard poultry. Information fact sheets have been developed and made available for both the public and for staff of produce/pet stores to assist in prevention of transmission of *Salmonella* to humans.

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<sup>iv</sup> Single Nucleotide Polymorphisms



# Multi-jurisdictional Outbreaks

- There was one multi-jurisdictional outbreak investigation conducted during 2020 with Queensland appointed the lead agency.

## *Salmonella* Typhimurium MLVA 05-16-13-11-490

OzFoodNet Queensland initiated an investigation on 31 January 2019 following 3 reported cases of *Salmonella* Typhimurium (STm) 05-16-13-11-490 by Public Health Microbiology, Forensic and Scientific Services. On 6 February, another 27 cases of this genotype were reported **with specimen collection dates ranging between 23 and 31 January**. As of 11 February, 65 cases of this genotype had been notified in Queensland. Thirty cases had been interviewed with egg dishes, sushi and other Asian style foods being commonly reported during the week before onset of illness.

On 12 February, Victoria reported 6 cases with this MLVA genotype. This was followed by New South Wales on the 14 February who reported 8 outbreak cases identified through sequencing. A multi-jurisdictional outbreak investigation was commenced on the 20 February. There had been 5 previous cases with this MLVA profile reported in Australia between 2011 and 2019. This included 2 cases from Queensland (2016, 2019), 2 cases from South Australia (2019) and one case from Victoria (2016).

Nationally, there were a total of 1,063 confirmed outbreak cases identified from this investigation with the large majority of cases reported from Queensland (687, 64.6%), followed by New South Wales (228, 21.4%), Victoria (96, 9.0%), South Australia (21, 2.0%), Australian Capital Territory (13, 1.2%), Tasmania (9, 0.8%), Northern Territory (6, 0.6%) and Western Australia (3, 0.3%). Onset/specimen collection dates ranged from 17 January 2020 to 19 May 2020. Case numbers peaked in the first week of February and remained steady throughout February before declining in March. The median age of cases was 33 years (range <1–92 years) and 59.5% were female.

Potential risk factors for infection were identified from binomial probability analyses based on the comparison of food exposure data among 229 interviewed cases with that of the general population using data from a food frequency survey conducted in Victoria between November 2014 and October 2016. This analysis showed that consumption

rates among outbreak cases was significantly higher than the survey population for several food items, with the greatest difference being for ‘salad mix in a sealed bag’.

A case-case study was subsequently designed to test the hypothesis that the outbreak was associated with consumption of any salad mix in a sealed bag. Fifty-one *Salmonella* Typhimurium outbreak cases and 130 *Campylobacter* cases (control group) were enrolled in the study. All variables that showed a statistically significant association with illness in the univariate analyses were selected for consideration to be included in the multivariable analyses.

The multivariable analysis indicated that cases were significantly more likely to have eaten a *bagged/packaged salad product* during the 5 day exposure period compared to the control group [Odds ratio (OR) = 9.2, 95% CI (3.6, 23.1)]. When adjusted for age, sex and other potential risk factors, this item remained independently significant with a strong estimate of effect [adjusted OR = 6.1, 95% CI: 2.3, 16.2]. No other variables were independently associated with illness. Given the strong association with bagged/packaged salad products, a separate multivariable model was run for individual bagged/packaged products. *Asian style salad bowl* was the only product that was independently associated with illness [aOR = 19.3, 95% CI (2.3, 160.4)].

A total of 1,021 food samples and 103 environmental samples were collected nationally during the course of the investigation (447 QLD, 313 NSW, 178 VIC and 83 SA). None of these samples tested positive for the outbreak strain of *Salmonella* Typhimurium. Despite the wide variety of salad products tested, the *Asian style salad bowl* was not one of the products sampled during the investigation.

Although lacking microbiological evidence, the epidemiological evidence (based on both the binomial probability analysis and the case-case study) strongly supported the hypothesis that a *bagged/packaged salad product* was the likely cause of this outbreak. However, the case-case study was unable to establish an epidemiological link to an individual salad item or brand. An ingredient in the *Asian style salad bowl* may have been a possible source of infection given the very high odds ratio for this food vehicle.

The outbreak was declared over on 30 July 2020.

# Non-foodborne disease outbreaks

## Summary 2020

- Total outbreaks: 675
- Total cases: 12,470
- Hospitalisations: 156 (1% of cases)

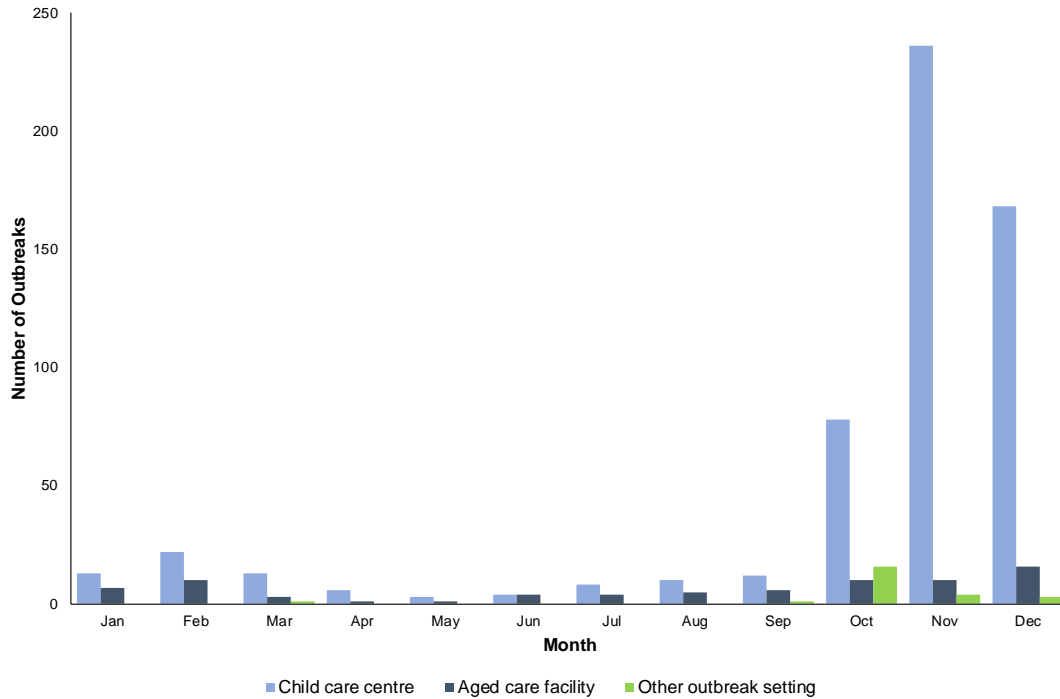
## Other Key Information

- Aetiology identified in 61 (9%) outbreaks
  - 57 (93%) with viral aetiologies (Table 30):
    - Adenovirus (2 outbreaks, 78 cases, 1 hospitalised)
    - Hepatitis A (1 outbreak, 7 cases, 1 hospitalised)
    - Norovirus (53 outbreaks, 1,298 cases, 17 hospitalised)
    - Sapovirus (1 outbreak, 11 cases)
  - 4 (<1%) with bacterial aetiologies:
    - Blastocystis hominis (1 outbreak, 3 cases)
    - Clostridium difficile (1 outbreak, 9 cases, 2 hospitalised)
    - Shigellosis (2 outbreaks, 14 cases, 9 hospitalised)
- Most frequently reported outbreak settings:
  - Childcare centres: 573 (85%)
  - Aged care facilities: 77 (11%)
  - Schools: 16 (2%)
- The average number of cases per outbreak was 14 (range 2–180 cases).
  - Childcare centres: average 18 cases (range 2–68 cases)
  - Aged care facilities: average 13 cases (range 2–37 cases)
  - Schools: average 62 cases (range 14–180 cases)
- Hospitalisations were more frequent among cases in aged care outbreaks (23/970; 2.4%) than cases in childcare outbreaks (117/10,401; 1.1%)

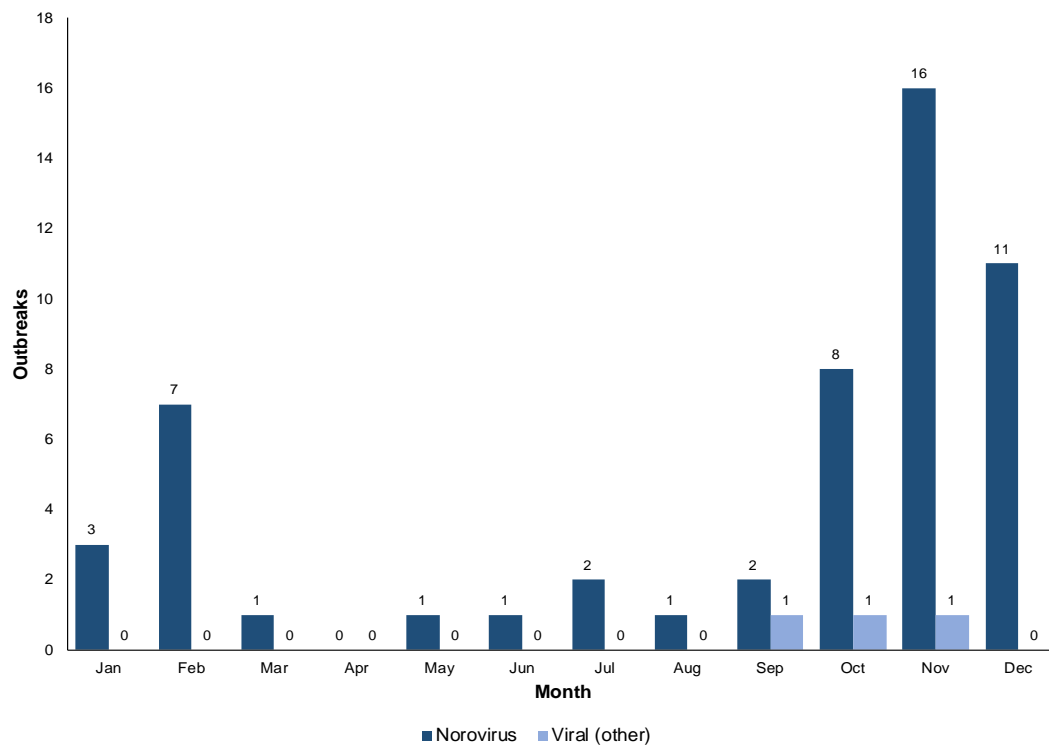
- A surge in reported childcare centre outbreaks occurred during the last quarter of 2020 (October–December):
  - There were 482 reported childcare outbreaks during the last quarter of 2020 compared to 91 childcare outbreaks during the January to September period (Figure 26)
- Laboratory confirmed viral outbreaks were more frequently reported between October and December (Figure 27)
- Two outbreaks of shigellosis were investigated in 2020 within North Queensland Indigenous communities, both with suspected person to person transmission:
  - *Shigella flexneri* 2b (9 cases, 4 hospitalisations)
  - *Shigella sonnei* biotype a (5 hospitalised cases)
- One outbreak of *Clostridium difficile* occurred at a health service facility (9 cases, 2 hospitalisations). Four cases were confirmed with the organism. No ribotyping performed. No environmental swabs taken.
- An outbreak of 7 cases of hepatitis A (genotype 1B) infection was investigated with cases reported across 2 households with no reported social interaction.
  - Specimen collection dates ranged from 30 March 2020 to 1 May 2020
  - All cases were locally acquired infections
  - The first household included 5 children (aged 2–9 years) with hepatitis A infection (1 symptomatic, 4 asymptomatic); 2 cases were identified in the second household (32-year-old symptomatic female and a 5-year-old asymptomatic child)
- Both households had children who attend the same primary school:
  - 4-year-old symptomatic case from household 1 and a 5-year-old asymptomatic case from household 2 (attend same prep class)
  - A 9-year-old case from household 1 attends the same school (year 4)
- While a source of infection was not identified, the children attend a multicultural school where there are a significant number of migrants who may travel to or have visitors from hepatitis A endemic areas
- A vaccination clinic was setup at the school for all students, staff, and their families/households

**Table 30.** Non-foodborne illness outbreaks by aetiology and setting 2020

Aetiology	Setting	No. of outbreaks	No. ill	No. hospitalised
<b>BACTERIAL</b>				
<i>Blastocystis hominis</i>	Aged care	1	3	0
<i>Clostridium difficile</i>	Health service	1	9	2
<i>Shigella flexneri</i> 2b	Community	1	9	4
<i>Shigella sonnei</i> biotype a	Community	1	5	5
<b>VIRAL</b>				
Adenovirus	Childcare	2	78	1
Hepatitis A	Other	1	7	1
Norovirus	Aged care	20	389	7
	Childcare	31	869	10
	Restaurant	1	25	0
	School	1	15	0
Sapovirus	Childcare	1	11	0
<b>UNKNOWN</b>				
	Aged care	56	578	16
	Camp	1	4	0
	Childcare	539	9,443	107
	Institution	2	42	0
	Other	1	4	0
	School	15	979	3
<b>Total</b>		<b>675</b>	<b>12,470</b>	<b>156</b>



**Figure 26.** Non-foodborne outbreaks reported in Queensland, 2020 by month of onset of index case and setting



**Figure 27.** Non-foodborne viral outbreaks reported in Queensland, 2020 by month of onset of index case

# Cluster Investigations

## Summary 2020

- Total clusters: 3
- Total cases: 33
- Hospitalisations: 4

## Other Key Information

- *Salmonella* Typhimurium was the confirmed aetiological agent in 2 clusters (18 cases, 3 hospitalisations), and cryptosporidiosis in one cluster (15 cases, 1 hospitalisation), (Table 31).

**Table 31.** Cluster investigations by aetiology and setting 2020

No.	Month	Aetiology	Cases in cluster	Setting
1	May	<i>Salmonella</i> Typhimurium MLVA 03-12-12-09-523	12	Community
2	May	Cryptosporidiosis	15	Community
3	Oct	<i>Salmonella</i> Typhimurium MLVA 03-11-10-08-523	6	Community

# Appendix A

## Annual Notifications of Foodborne Pathogens

**Table A1.** Annual notifications of foodborne pathogens/conditions, Queensland, 2011 to 2020 by year of onset

Pathogen/Condition	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Botulism	0	0	0	1	0	0	0	0	0	0
<i>Campylobacter</i>	5,129	4,176	3,832	6,227	7,554	7,203	7,628	8,302	9,152	7660
Cholera	5	1	0	0	0	0	0	0	0	0
Ciguatera	18	7	25	68	11	36	15	15	21	13
Cryptosporidium	464	1,373	769	667	1,314	2,368	1,288	1,068	724	670
Hepatitis A	26	34	47	44	33	30	26	43	25	15
Hepatitis E	6	6	2	7	1	8	11	8	4	6
HUS*	1	4	2	3	2	4	3	4	3	4
<i>Listeria</i>	10	5	9	17	8	14	18	13	11	6
Paratyphoid	7	8	6	8	7	8	7	6	15	2
<i>Salmonella</i>	2,834	2,719	3,161	4,802	5,368	4,778	4,231	3,483	3,815	4131
<i>Shigella</i>	63	82	72	170	145	181	235	450	609	280
STEC**	16	27	83	28	32	24	27	25	29	30
Typhoid	22	15	24	17	24	19	18	32	25	10
<i>Yersinia</i> ***	35	59	133	533	736	790	686	770	691	579
<b>Total</b>	<b>8,636</b>	<b>8,516</b>	<b>8,165</b>	<b>12,592</b>	<b>15,235</b>	<b>15,463</b>	<b>14,193</b>	<b>14,219</b>	<b>15,124</b>	<b>13,406</b>

\* HUS: Haemolytic uraemic syndrome

\*\* STEC: Shiga toxin producing Escherichia coli

\*\*\*Y. enterocolitica



**Table A2.** Crude notification rates per 100,000 population for foodborne pathogens/conditions by year of onset, Queensland, 2011 to 2020

Pathogen/Condition	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020
Botulism	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<i>Campylobacter</i>	114.6	91.4	82.4	131.9	158.1	148.7	154.8	165.7	179.6	150.4
Cholera	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ciguatera	0.4	0.2	0.5	1.4	0.2	0.7	0.3	0.3	0.4	0.3
Cryptosporidium	10.4	30.1	16.5	14.1	27.5	48.9	26.1	21.3	14.2	13.2
Hepatitis A	0.6	0.7	1.0	0.9	0.7	0.6	0.5	0.9	0.5	0.3
Hepatitis E	0.1	0.1	0.0	0.1	0.0	0.2	0.2	0.2	0.1	0.1
HUS*	0.0	0.1	0.0	0.1	0.0	0.1	0.1	0.1	0.1	0.1
<i>Listeria</i>	0.2	0.1	0.2	0.4	0.2	0.3	0.4	0.3	0.2	0.1
Paratyphoid	0.2	0.2	0.1	0.2	0.1	0.2	0.1	0.1	0.3	0.0
<i>Salmonella</i>	63.3	59.5	67.9	101.7	112.4	98.6	85.9	69.5	74.9	81.1
<i>Shigella</i>	1.4	1.8	1.5	3.6	3.0	3.7	4.8	9.0	12.0	5.5
STEC**	0.4	0.6	1.8	0.6	0.7	0.5	0.5	0.5	0.6	0.6
Typhoid	0.5	0.3	0.5	0.4	0.5	0.4	0.4	0.6	0.5	0.2
<i>Yersinia</i> ***	0.8	1.3	2.9	11.3	15.4	16.3	13.9	15.4	13.6	11.4
<b>Total</b>	<b>192.9</b>	<b>186.4</b>	<b>175.5</b>	<b>266.8</b>	<b>318.9</b>	<b>319.1</b>	<b>288.0</b>	<b>283.8</b>	<b>296.9</b>	<b>263.1</b>

\* HUS: Haemolytic uraemic syndrome

\*\* STEC: Shiga toxin producing Escherichia coli

\*\*\*Y. enterocolitica

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