Queensland Health

Enhancing Foodborne Disease Surveillance Across Australia

OzFoodNet Queensland
2025 Annual Report

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Enhancing Foodborne Disease Surveillance Across Australia: OzFoodNet Queensland 2025 Annual Report

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- Public Health Microbiology and Virology laboratories, Public and Environmental Health Reference Laboratory (PEHRL)
- Food Safety Standards and Regulation Unit
- Communicable Diseases Branch
- Safe Food Production Queensland
- Local government authorities.

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Report Summary

This report summarises surveillance and outbreak response activities for enteric diseases in Queensland as part of national foodborne disease surveillance efforts. The report draws on notifiable disease data collated by the Public Health Intelligence Branch, Queensland Health, together with surveillance and investigation activities undertaken in collaboration with Queensland Public Health Units, the Public and Environmental Health Reference Laboratory, the Food Safety Standards and Regulation Unit, the Communicable Diseases Branch, Safe Food Production Queensland, and local government authorities.

In 2025, 15,766 notifications were recorded across sixteen enteric diseases in Queensland. *Campylobacter* remained the most frequently notified pathogen, with 9,536 cases and a notification rate of 168.2 per 100,000 population. *Salmonella* was the second most notified pathogen, with a notification rate of 68.9 per 100,000 population, comparable with 2024 and the five-year average. *Cryptosporidium* notifications declined markedly to 704 cases (12.4 per 100,000 population) following record-high levels in 2024 (6,178 cases, notification rate 110.6 per 100,000 population).

Typhoid and hepatitis A virus infection were mainly travel-associated, with 30 of 32 typhoid cases and 39 of 44 hepatitis A cases acquired overseas. Outbreak investigations covered foodborne, environmental, waterborne, and person-to-person transmission events. Person-to-person (or otherwise unknown) transmission accounted for 987 of 1,004 gastrointestinal outbreaks (98%) in 2025, with these events occurring mainly in childcare centres and residential aged care facilities.

Multi-jurisdictional outbreak investigations included hepatitis A with an unknown source, hepatitis E associated with pork liver products, *Salmonella* Enteritidis associated with trekking in Tasmania, and *Salmonella* Havana linked to contaminated alfalfa sprouts, with 23 Queensland cases identified across these four investigations.

These findings highlight the continuing burden of enteric disease in Queensland and the importance of coordinated surveillance, laboratory analysis and multi-agency outbreak investigation to detect trends, identify sources, and support timely public health action.

Introduction

OzFoodNet, established in 2000 by the Commonwealth Department of Health, 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 conducts national and local investigations into foodborne disease, strengthening Australia's understanding of its epidemiology and providing critical intelligence to guide public health action aimed at reducing disease incidence. Recent Australian studies estimate that around 4.67 million cases of foodborne disease occur each year, costing A$2.44 billion annually.

Enhanced communication and cooperation among network members have strengthened Australia's capacity to detect and respond to emerging foodborne diseases and multijurisdictional outbreaks that cross state and territory borders. In 2025, the network's coverage included the entire Australian population, estimated at 27,724,744 as of 30 September 2025.

OzFoodNet Queensland works collaboratively across the public health system to strengthen the detection, management and prevention of foodborne disease. This includes coordinated efforts with state and territory health departments, Queensland Public Health Units, Queensland Health Food Safety Standards and Regulation, public health laboratories, biosecurity agencies and local councils. OzFoodNet is a member of the Communicable Diseases Network Australia (CDNA), Australia's peak body for communicable disease control.

This report is based on statutory notification data, which capture only infections identified through healthcare presentation and diagnostic testing. Notification data provide an important indicator of disease trends but represent only a fraction of infections occurring in the community, as they rely on individuals seeking healthcare and undergoing diagnostic testing. The COVID-19 pandemic (2020-2022) affected notification numbers, with changes in healthcare-seeking behaviour and reduced pathology testing likely influencing disease detection and reporting.

This report provides an overview of the surveillance, epidemiological and outbreak response activities undertaken by OzFoodNet Queensland during 2025. These activities were undertaken in collaboration with Queensland Public Health Units, the Food Safety Standards and Regulation Unit, and the Public and Environmental Health Reference Laboratory.

Results

Overview of Enteric Conditions Notified in 2025

Total enteric conditions: 15,766 (Table 1).

Campylobacter was the most frequently notified enteric pathogen in 2025 (9,536 cases) followed by *Salmonella* (3,907 cases).

Cryptosporidium notifications fell sharply in 2025 to 704 cases, a 63% decrease compared with the 2020-2024 annual average (1,890 cases), following a record-high year in 2024 (6,178 cases).

Yersinia enterocolitica notifications decreased by 26% in 2025, from 1,101 cases in 2024 to 819 cases. Among typed *Yersinia* isolates, biotype 1A remained the predominant subtype, accounting for 74% of isolates.

Vibrio parahaemolyticus infections became a notifiable condition in Queensland on 3 May 2025.

Table 1. Foodborne pathogen notification numbers and crude rates per 100,000 population, Queensland, 2025, 2024 and 5-year (2020-2024) mean

Pathogen	2025		2024		5-year mean (2020-2024)	
	Number	**Rate**	**Number**	**Rate**	**Number**	**Rate**
BACTERIAL						
Clostridium botulinum (Botulism)	0	0.0	1	0.0	0	0.0
Campylobacter	9,536	168.2	9016	161.5	9,128	171.5
Listeria monocytogenes (Listeriosis)	6	0.1	9	0.2	9	0.2
Salmonella (non-typhoidal)	3907	68.9	3899	69.8	3696	69.5
Salmonella Typhi (Typhoid)	32	0.6	29	0.5	21	0.4
Salmonella Paratyphi (Paratyphoid)	6	0.1	15	0.3	6	0.1
STEC[a]	54	1.0	56	1.0	39	0.7
Shigella	620	10.9	501	9.0	304	5.7
Vibrio cholerae (Cholera)	1	0.0	1	0.0	0	0.0
Vibrio parahaemolyticus[c]	19	-	-	-	-	-
Yersinia enterocolitica	819	14.4	1101	19.7	775	14.6
PARASITIC						
Cryptosporidium	704	12.4	6178	110.6	1890	35.5
VIRAL						
Hepatitis A	44	0.8	30	0.5	25	0.5
Hepatitis E	2	0.0	3	0.1	3	0.1
OTHER						
Ciguatera poisoning	14	0.2	6	0.1	11	0.2
HUS[b]	2	0.0	3	0.1	3	0.1
Total	**15,766**	**-**	**20,848**	**-**	**15,910**	**-**

[a] STEC: Shiga toxin-producing *Escherichia coli;* [b] HUS: Haemolytic Uraemic Syndrome; [c] Vibrio parahaemolyticus became notifiable In QLD on 3 May 2025. Previous years data unavailable.

Total gastrointestinal disease outbreaks reported: 1,008

Foodborne / probable foodborne outbreaks: 13 (109 cases, 11 hospitalisations).

Multi-jurisdictional foodborne outbreaks: 4 outbreaks: 133 cases nationally, 23 (17%) cases among QLD residents.

Waterborne outbreaks: 1 (16 cases, 1 hospitalisation)

Environmental / Probable environmental outbreaks: 3 (55 cases, 5 hospitalisations).

Zoonotic outbreaks: 0

Non-foodborne outbreaks: 987 (9,732 cases, 139 hospitalisations).

Culture independent diagnostic testing among frequently notified bacterial pathogens:

68% of *Campylobacter* notifications in 2025 were detected by PCR only (Table 2).

9% of *Salmonella* notifications in 2025 were detected by PCR only.

79% of *Shigella* notifications in 2025 were detected by PCR only.

66% of *Yersinia* notifications in 2025 were detected by PCR only.

Table 2. Notifications for selected pathogens by diagnostic test type (PCR and Culture) 2025

Pathogen	Culture only		PCR Only		Culture and PCR		Total
	Number	**%**	**Number**	**%**	**Number**	**%**	
Campylobacter	373	4	6,507	68	2,656	28	9,536
Salmonella	626	16	370	9	2,911	75	3,907
Shigella	5	1	488	79	127	20	620
Yersinia enterocolitica	15	2	537	66	267	33	819
Total	**1,019**	**7**	**7,902**	**53**	**5,961**	**40**	**14,882**

Enteric disease notifications among First Nations peoples

During 2025, the proportion of notifications among First Nations peoples for the five most frequently reported enteric pathogens in Queensland were comparable to their respective 5-year means (2020-2024), (Table 3).

Shigella contributed the highest proportion of infections among First Nations peoples (14%).

Table 3. Notifications for selected pathogens by First Nations status, 2025

Pathogen	First Nations		Non-First Nations		Unknown Status	Total Notifications
	2025	**5-year mean (2020-2024)**	**2025**	**5-year mean (2020-2024)**		
Campylobacter	365 (6%)	335 (5%)	6,219 (94%)	6,794 (95%)	2,952	9,536
Cryptosporidiosis	40 (8%)	88 (6%)	434 (92%)	1270 (94%)	230	704
Salmonella	213 (8%)	217 (7%)	2,613 (92%)	2,814 (93%)	1,081	3,907
Shigella spp	81 (14%)	38 (13%)	514 (86%)	254 (87%)	25	620
Yersinia enterocolitica	17 (3%)	17 (3%)	503 (97%)	545 (97%)	299	819

Salmonella

Total notifications: 3,907
Notification rate per 100,000: 68.9
Median age: 25 years (range <1-100 years)
Sex: 1,991 (51%) female
Outbreaks/clusters investigated:

- 4 outbreaks (46 cases, 13 hospitalisations)
- 10 clusters (75 cases)

Other key information:

- 3,513 isolates serotyped (90% notified cases).
- 159 different serotypes reported in 2025 (69 were associated with single notifications).
- 370 (9%) detections via PCR only (Table 2).

Changes in incidence

Salmonella notifications remained stable in 2025, with 3,907 cases and a rate of 68.9 per 100,000, consistent with 2024 and the five-year mean (69.5 per 100,000). (Table1, Figure 1).

Rates have been steady since the decline observed in 2016-2018, and Queensland continued to report higher rates than Australia overall, with the 2025 rate 1.6 times the national rate (44 per 100,000 (Figure 2).

Groups with highest notification rate

Age: Highest rates were observed in the 0-4 year age group (33% of notifications, 421.2 cases per 100,000 population); children aged <1 year (notification rate 1086.0 per 100,000) and those aged above 70 years (79.8 per 100,000), (Table 4, Figure 3).

HHS: Areas outside of South-East Queensland had the highest rates, notably Central West, South West, Central Queensland and Torres and Cape (101.4 to 213.2 per 100,000), (Table 5).

Seasonality

Notifications typically peak in warmer months, particularly between January and April each year (Figure 4).

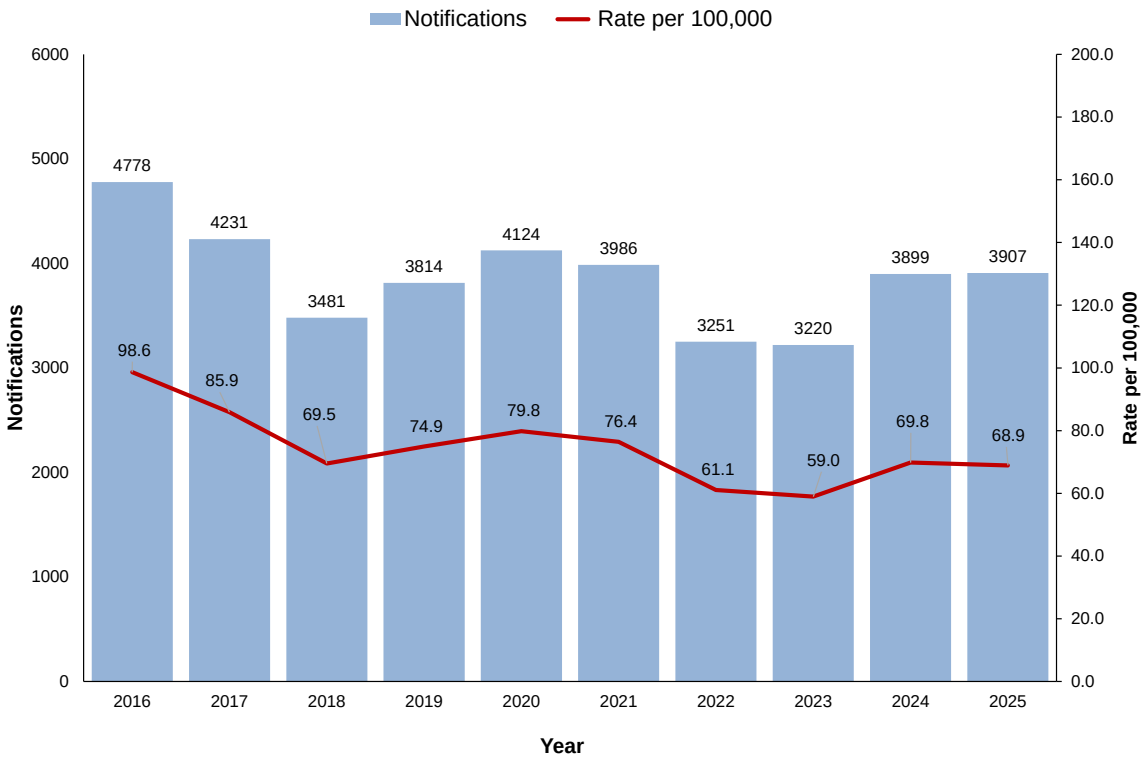


Figure 1. Salmonella notifications and rate per 100,000 population by year, Queensland, 2016-2025

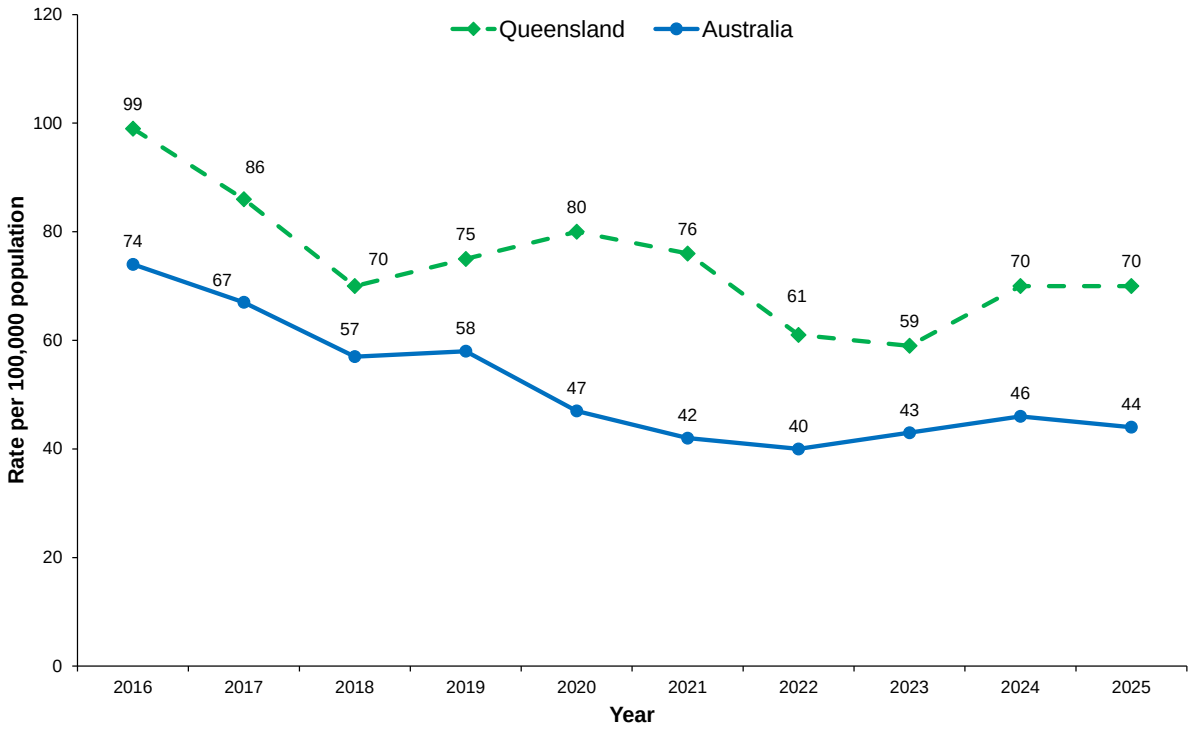


Figure 2. Salmonella notification rate by year in Queensland and Australia (sourced from the National Notifiable Diseases Surveillance System), 2016-2025

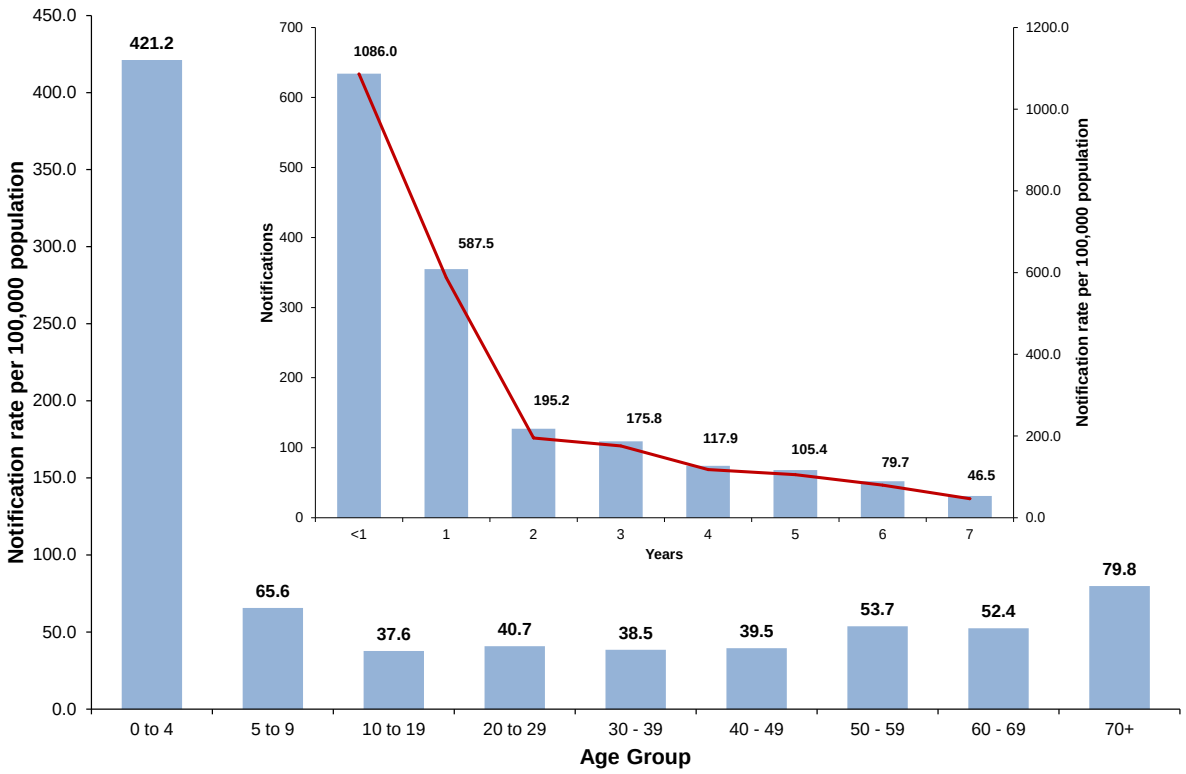


Figure 3. Salmonella notifications and rate per 100,000 population by age group, Queensland, 2025

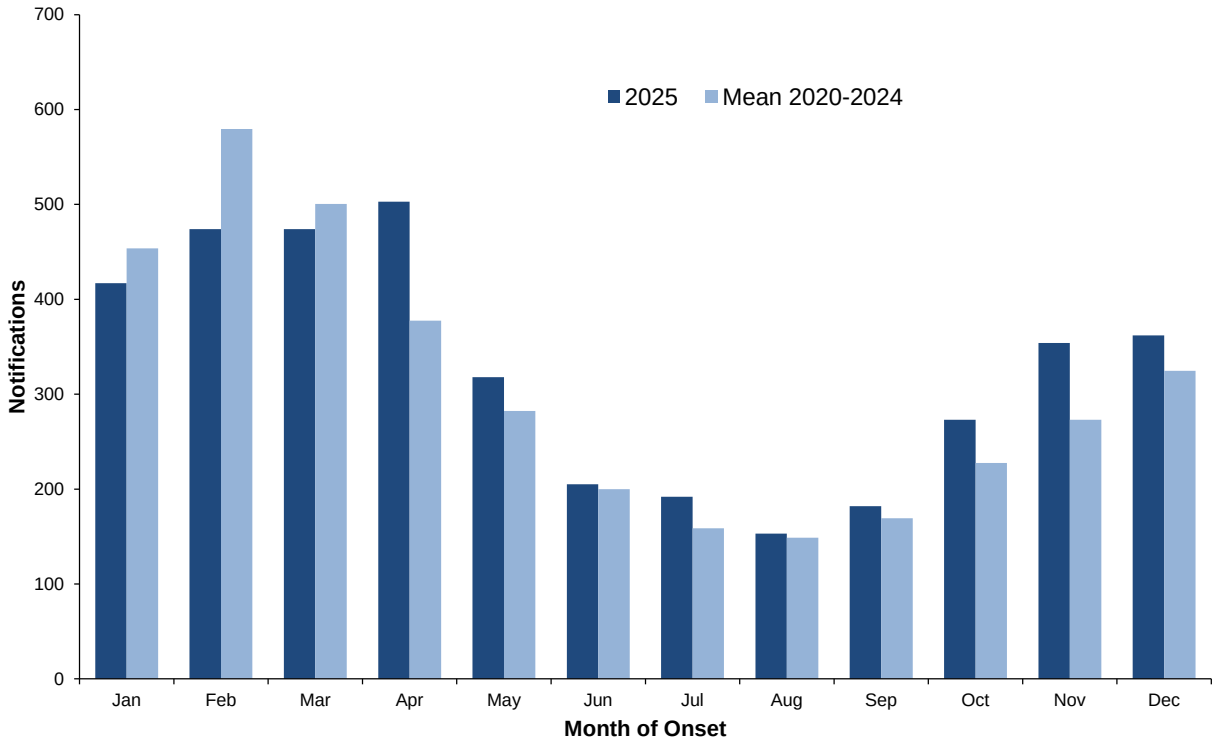


Figure 4. Salmonella notifications by month of onset, Queensland, 2025

Table 4. Salmonella notifications and rate per 100,000 population by age group and sex, Queensland, 2025

Age Group (years)	Male		Female		Total	
	Number	**Rate**	**Number**	**Rate**	**Number**	**Rate**
0-4	687	433.9	613	407.8	1300	421.2
5-9	116	67.1	104	63.9	220	65.6
10-19	159	42.8	113	32.2	272	37.6
20-29	145	37.9	163	43.6	308	40.7
30-39	124	32.0	179	44.9	303	38.5
40-49	126	36.1	156	42.8	282	39.5
50-59	161	48.1	205	59.1	366	53.7
60-69	128	43.9	187	60.4	315	52.4
70 +	270	85.0	271	75.2	541	79.8
All ages	**1,916**	**69.3**	**1,991**	**70.6**	**3,907**	**68.9**

Table 5. Salmonella notifications and rate per 100,000 population by Hospital and Health Service, Queensland, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	**5-year mean***	**2025**	**5-year mean**
Cairns and Hinterland	148	160	53.9	60.1
Central Queensland	236	244	101.4	108.1
Central West	23	19	213.2	176.6
Darling Downs	194	174	63.6	58.7
Gold Coast	493	416	70.6	62.7
Mackay	191	187	99.3	100.4
Metro North	640	622	55.9	57.4
Metro South	736	703	56.1	56.9
North West	26	37	90.4	127.8
South West	31	32	126.5	130.7
Sunshine Coast	398	363	80.9	77.4
Torres and Cape	27	29	102.5	112.9
Townsville	248	263	98.5	107.5
West Moreton	291	227	84.1	69.9
Wide Bay	225	220	91.7	93.8
Total	**3,907**	**3,696**	**68.9**	**69.5**

* 5-year mean (2020-2024)

Serotypes*Salmonella* Typhimurium

Salmonella Typhimurium remained the most frequently reported *Salmonella* serovar in Queensland.

Notifications in 2025 (467) were comparable to those reported in 2024 (468).

The 2025 notification rate (8.2 per 100,000 population) was 41% lower than the five-year annual average for 2020-2024 (720 cases; 13.9 per 100,000 population).

All human *Salmonella* Typhimurium isolates are routinely genotyped in Queensland using a PCR-based technique termed 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[6] and Gilbert[7].

MLVA profile results were available for 449 (96%) notifications.

173 different MLVA profiles were reported among the 449 notifications; 61% of profiles were associated with single notifications.

The most frequently reported MLVA profile in 2025 was 03-11-13-09-523 (66 cases, Table 7).

No outbreaks were reported among the top 10 MLVA genotypes in 2025.

Seven *Salmonella* Typhimurium cluster investigations were conducted in 2025 where no common exposure or mode of transmission was identified. Five of these were among the top 10 MLVA genotypes (refer to Cluster Investigations).

Table 7. Top 10 Salmonella Typhimurium MLVA profiles by year, Queensland, 2021-2025

Rank	2021	2022	2023	2024	2025
1	03-13-07-09-523 (88)	03-13-07-09-523 (93)	03-13-09-11-523 (26)	03-12-09-12-523 (35)	03-11-13-09-523 (66)
2	03-14-09-08-523 (58)	03-11-10-08-523 (34)	03-13-07-09-523 (23)	03-11-13-09-523 (22)	03-11-11-09-523 (23)
3	03-14-10-08-523 (44)	03-11-13-09-523 (26)	03-15-13-10-523 (15)	03-16-10-08-523 (21)	06-14-17-12-490 (16)
4	03-11-10-08-523 (38)	03-11-11-09-496 (25)	03-15-10-13-523 (14)	03-14-10-08-523 (17)	03-11-14-09-523 (16)
5	03-15-10-13-523 (22)	03-12-10-12-523 (24)	03-11-10-08-523 (13)	03-11-10-08-523 (15)	03-13-07-09-523 (13)
6	03-16-09-11-523 (22)	03-15-10-13-523 (23)	04-15-11-00-490 (12)	03-11-11-09-496 (11)	03-15-10-13-523 (12)
7	03-15-11-10-523 (19)	03-14-10-08-523 (20)	03-12-09-12-523 (12)	03-13-07-09-523 (11)	03-12-09-12-523 (12)
8	03-12-10-12-523 (17)	03-09-07-13-523 (18)	03-14-10-08-523 (9)	03-22-12-09-523 (8)	03-13-13-09-523 (10)
9	06-11-16-10-490 (13)	03-11-13-07-523 (17)	03-16-10-08-523 (7)	03-11-12-09-496 (8)	03-11-10-08-523 (9)
10	05-11-15-10-490 (11)	03-16-09-11-523 (15)	03-11-12-09-496 (7)	03-15-10-13-523 (7)	03-15-09-10-523 (7)

* Colour code indicates same MLVA profile

Salmonella Enteritidis

155 notifications reported in 2025, compared to 154 notifications in 2024 (Table 8).

Epidemiological information was collected on 81 cases:

65 (80%) cases were likely overseas acquired infections (Table 9).

- 64 isolates were designated Clade B on sequencing:
    - Travel to Indonesia was reported by 30 cases (47%).
    - South Africa (2 cases) and Malaysia (2 cases) were the next most frequently reported travel destinations.
    - 6 cases reported travel to multiple overseas locations prior to illness.
    - Single cases reported travel to: China, Cook Islands, Japan, New Zealand, Philippines, Samoa, Singapore, Spain, USA and Vietnam.
    - Overseas travel destinations were unspecified for 14 cases.
    - 1 case designated Clade A was likely acquired in the Solomon Islands.
- 16 (20%) cases did not report recent overseas travel (locally acquired):
    - One case was associated with a multijurisdictional outbreak investigated in April among persons who had travelled to Tasmania for a walking excursion.
        - 10 outbreak cases were identified following whole genome sequencing (VIC (5), NSW (3), WA (1) and QLD (1).
        - *Salmonella* Enteritidis detected in rainwater tank samples from a hut on a walking track was genomically highly related to the case isolates.
    - 6 case isolates were designated as Clade A on sequencing, 7 were designated as Clade B and 2 cases were Clade C. (Table 9).
    - No common exposures or source of infection were identified among these 15 remaining locally acquired cases.

Travel information was unknown for 74 cases (Table 9).

Table 8. Salmonella Enteritidis notifications and case reported travel, 2020-2025

Year	Locally acquired	Overseas Travel	No travel information	Total
2020	17	21	54	92
2021	8	0	58	66
2022	28	28	57	113
2023	12	72	93	177
2024	7	62	85	154
2025	16	65	74	155

Table 9. Salmonella Enteritidis whole genome sequencing analysis (grouped as Clade A, B or C) with epidemiological information on travel, 2025

SNP Clade	Locally acquired	Overseas Travel	No Travel information	Total	%
A	6	1	24	31	20
B	7	64	40	111	72
C	2	0	6	8	5
Not done	1	0	4	5	3
Total	**16**	**65**	**74**	**155**	**100**

Salmonella Saintpaul

327 notifications in 2025 compared with 285 notifications in 2024 and a 5-year (2020-2024) annual mean of 348 cases.

Median age 21 years (range <1-86 years); 160 (49%) were female.

Notifications were widespread across the state with the proportion of notifications highest in Wide Bay HHS (13%) and Sunshine Coast HHS (12%).

Cluster analysis via whole genome sequencing was conducted on 308 (94%) case isolates:

177 (57%) isolates did not cluster genomically and were considered sporadic.

131 cases (43%) were among 59 genomic clusters reported in 2025 that were related to one or more cases (from either 2025 or previous years).

One outbreak of *Salmonella* Saintpaul infection was investigated in November:

24 cases identified among persons who resided in or had travelled to the same Darling Downs town prior to symptom onset.

All case isolates were highly related genomically.

Epidemiological investigations did not identify any foods or venues that were common to cases.

All water samples collected during the investigation tested negative for *E. coli* and *Salmonella*.

A source of infection was unable to be identified.

Please refer to 'Non-foodborne Bacterial Outbreaks' section for further information.

Campylobacter

Total notifications: 9,536
Notification rate per 100,000: 168.2
Median age: 43 years (range <1-99 years)
Sex: 5116 (54%) male
Outbreaks/clusters: 0 investigated
Other key information:

- 6,507 (68%) detected through PCR only (Table 2).
- Notification rates among males were higher than females, most notably among children 0-4 years and those aged 60+ (Figure 5, Table 10).

Changes in incidence

2025 notification counts (9,536) increased by 6% compared with 2024 (9,016), (Table 1).

The 2025 notification rate (168.2 per 100,000) was slightly lower than the 5-year (2020-2024) annual mean (171.5 per 100,000).

Consecutive annual declines in incidence appear to have slowed with the first annual incidence increase reported since 2021 (Figure 6).

Notification rates in Queensland continue to remain higher in comparison to Australian (national) notification rates (Figure 7).

Groups with highest notification rate

Age: Highest rates were observed in the 0-4 year age group (254.3 per 100,000) and 70+ age group (238.3 per 100,000) (Table 10).

Sex: Males (185.0 per 100,000), (Table 10).

HHS: South West (<1% of cases – 248.9 per 100,000), followed by Darling Downs (6% of cases – 197.7 per 100,000) (Table 11).

Seasonality

Campylobacter notifications increase during spring and remain elevated during summer.

In 2025, monthly notification counts were generally comparable to 5-year monthly means (Figure 8).

Table 10. Campylobacter notifications and rate per 100,000 population by age group and sex in Queensland, 2025

Age Group (years)	Male		Female		Total	
	Number	**Rate**	**Number**	**Rate**	**Number**	**Rate**
0-4	447	282.3	338	224.9	785	254.3
5-9	192	111.1	167	102.6	359	107.0
10-19	457	122.9	292	83.2	750	103.8
20-29	701	183.4	604	161.5	1307	172.9
30-39	616	158.9	619	155.1	1236	157.1
40-49	534	152.9	563	154.4	1098	153.8
50-59	630	188.4	552	159.3	1182	173.6
60-69	656	225.0	547	176.6	1203	200.1
70 +	883	278.1	733	203.3	1616	238.3
All ages	**5116**	**185.0**	**4415**	**156.6**	**9536**	**168.2**

Table 11. Campylobacter notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	5-year mean*	2025	5-year mean
Cairns and Hinterland	394	410	143.5	154.1
Central Queensland	417	390	179.1	172.5
Central West	14	17	129.8	161.5
Darling Downs	603	594	197.7	200.5
Gold Coast	1,225	1,075	175.5	162.0
Mackay	331	306	172.1	164.4
Metro North	1935	1,911	169.1	176.3
Metro South	2,097	2,048	159.9	165.6
North West	40	34	139.1	118.1
South West	61	56	248.9	231.7
Sunshine Coast	917	852	186.4	182.0
Torres and Cape	40	26	151.8	100.5
Townsville	475	493	188.6	201.3
West Moreton	578	516	167.0	158.6
Wide Bay	409	400	166.7	170.7
QLD Total	**9,536**	**9,128**	**168.2**	**171.5**

* 5-year mean (2020-2024)

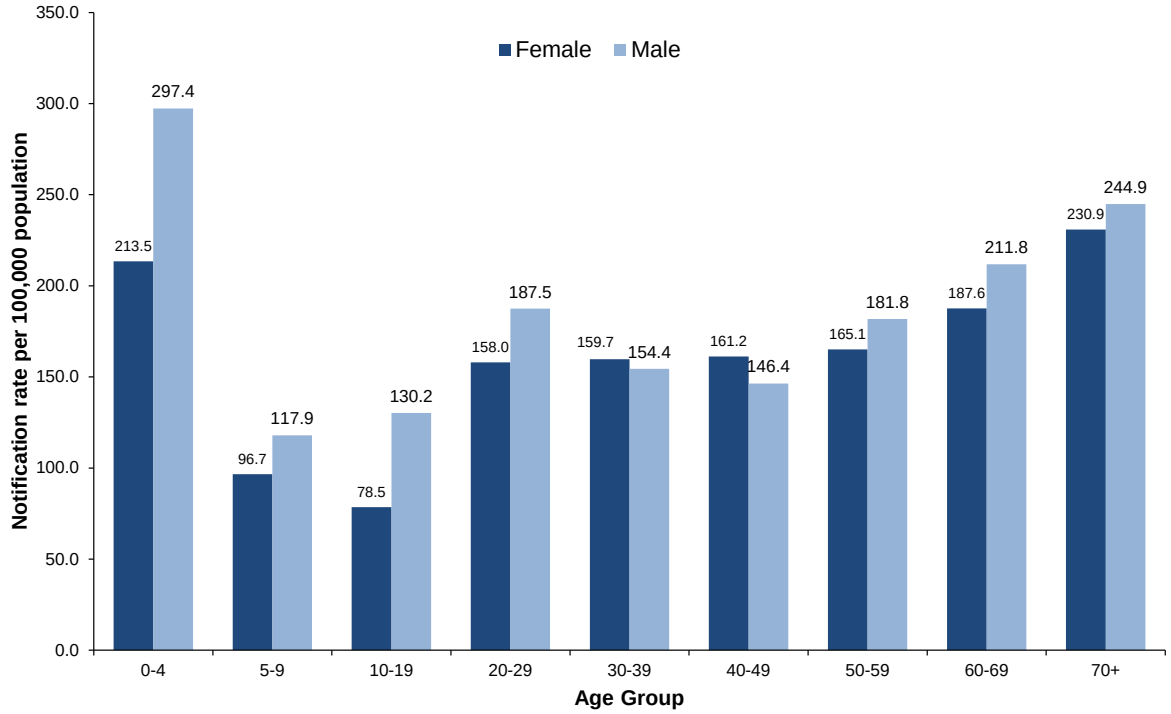


Figure 5. Campylobacter notification rates per 100,000 population by age group and sex, Queensland, 2025

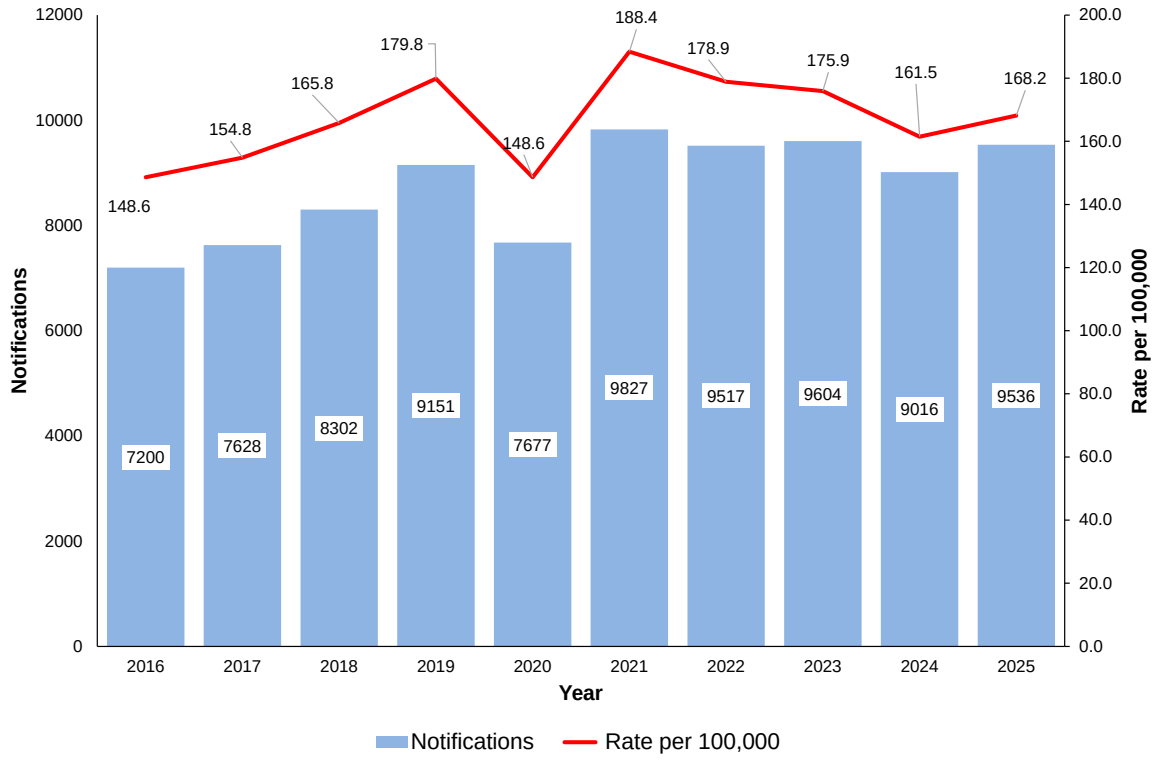


Figure 6. Campylobacter notifications and rate per 100,000 population by year, Queensland, 2016-2025

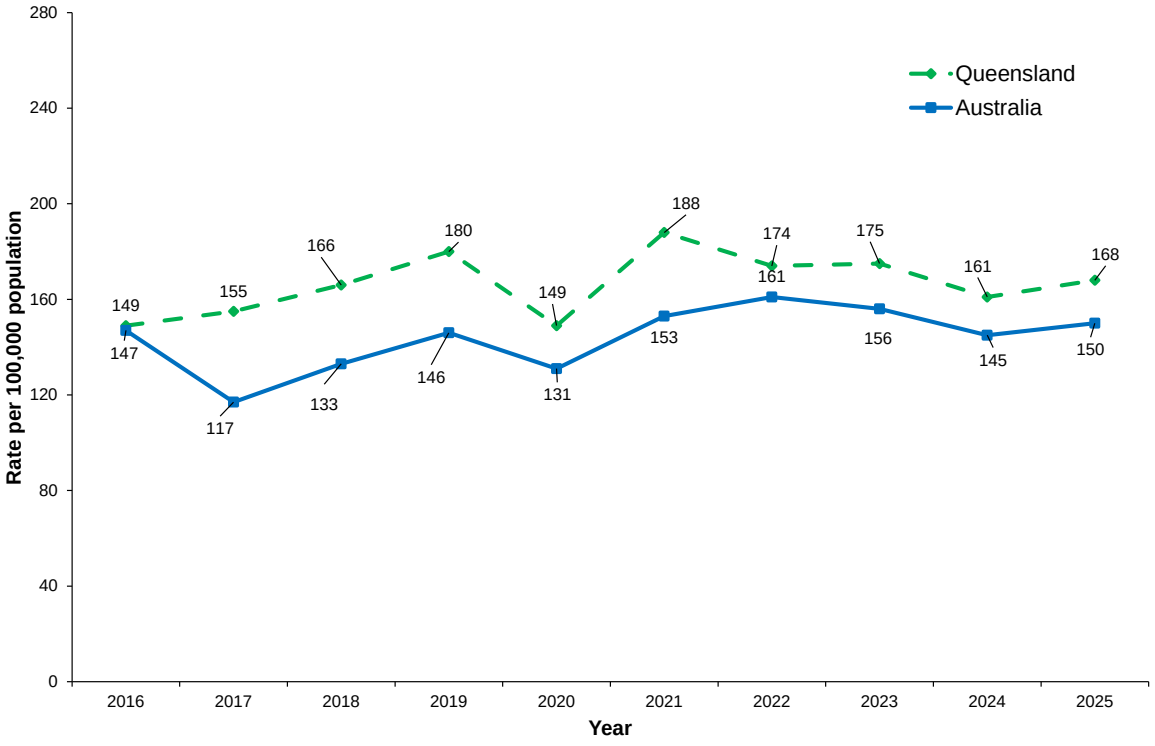


Figure 7. Campylobacter notification rates by year, for Queensland and Australia, 2016-2025 (source NNDSS)

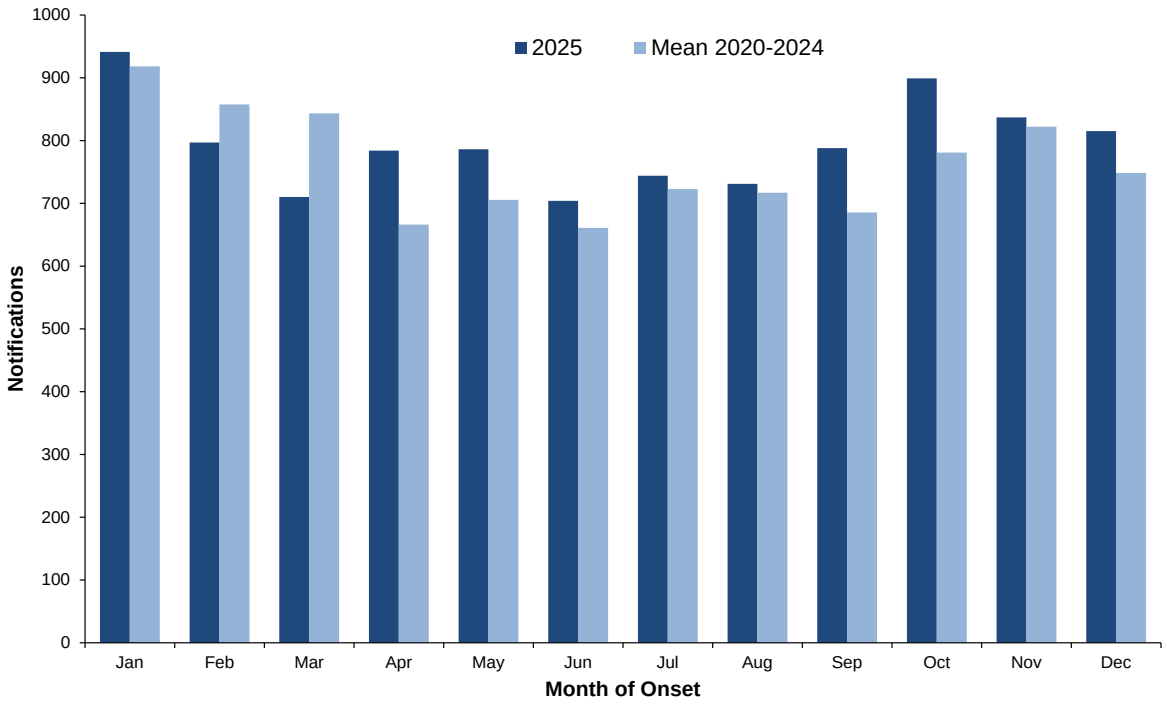


Figure 8. Campylobacter notifications by month of onset in 2025 compared to the mean number of notifications by month, Queensland, 2020-2024

Cryptosporidium

Total notifications: 704

Notification rate per 100,000: 12.4

Median age: 26 years (range <1-97 years)

Sex: 381 (54%) females

Outbreaks investigated: 3 outbreaks (2 aquatic facilities and 1 school)

Other key information:

- *Cryptosporidium* is a parasitic infection transmitted via animal-to-person or person-to-person contact or through ingestion of contaminated water and less commonly food.
- Genotyping to identify species and subtypes is not routinely undertaken in Queensland.

Changes in incidence

Notification counts and rates in 2025 (704) decreased markedly from the record figures reported during 2024 (6178) (Table 1, Figure 9).

Groups with highest notification rate

Age: Highest rates were observed in the 0-4 year age group (19% of cases – 43.4 per 100,000), (Table 12).

Disparity in rates of notification was most obvious in the 30-39 age group with female rates (22.3 per 100,000) twice that of males (10.3 per 100,000) (Figure 10).

Overall, female notification rates (13.5 per 100,000) were slightly above those of males (11.7 per 100,000).

HHS: South West reported the highest annual notification rate (6 cases, 24.5 per 100,000) while Metro South had the highest number of notifications (158 cases, 12.0 per 100,000) (Table 13).

Seasonality

Notification counts were highest during the summer months of January (94 cases) and February (90 cases) and lowest during August (24 cases). A subsequent rise in cases was observed during Spring (Figure 11).

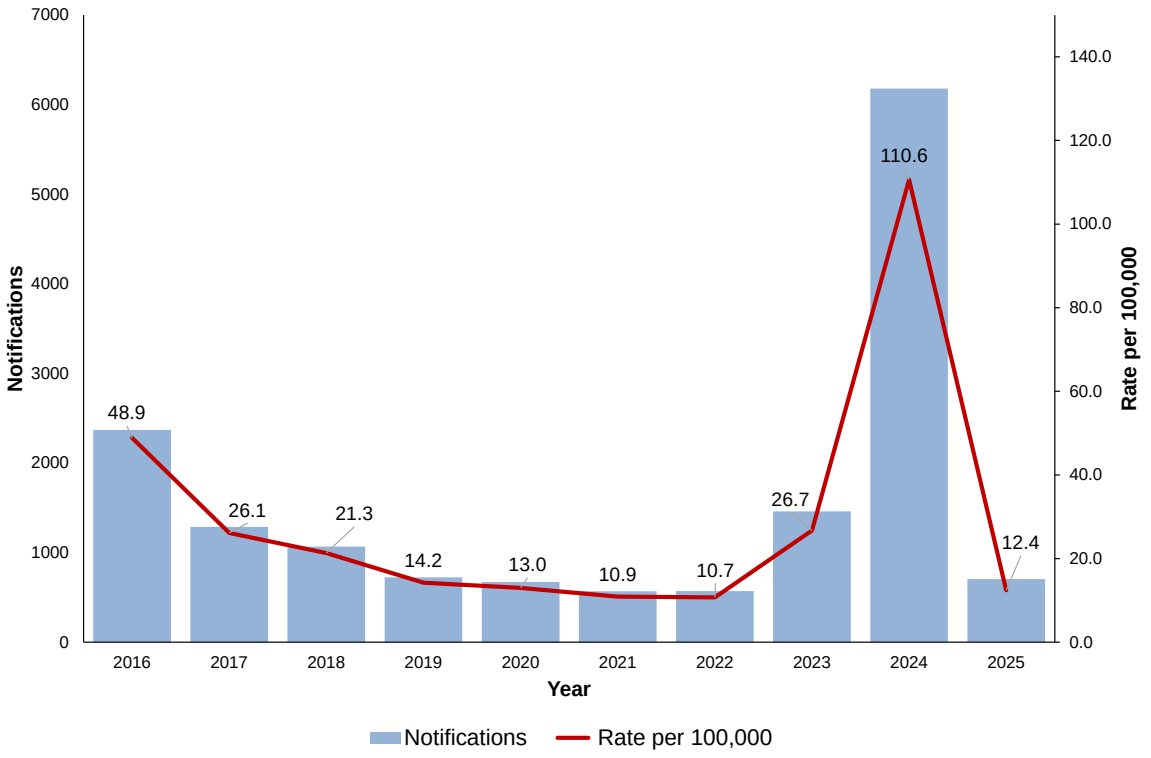


Figure 9. Cryptosporidium notifications and rate per 100,000 population by year, Queensland, 2016-2025

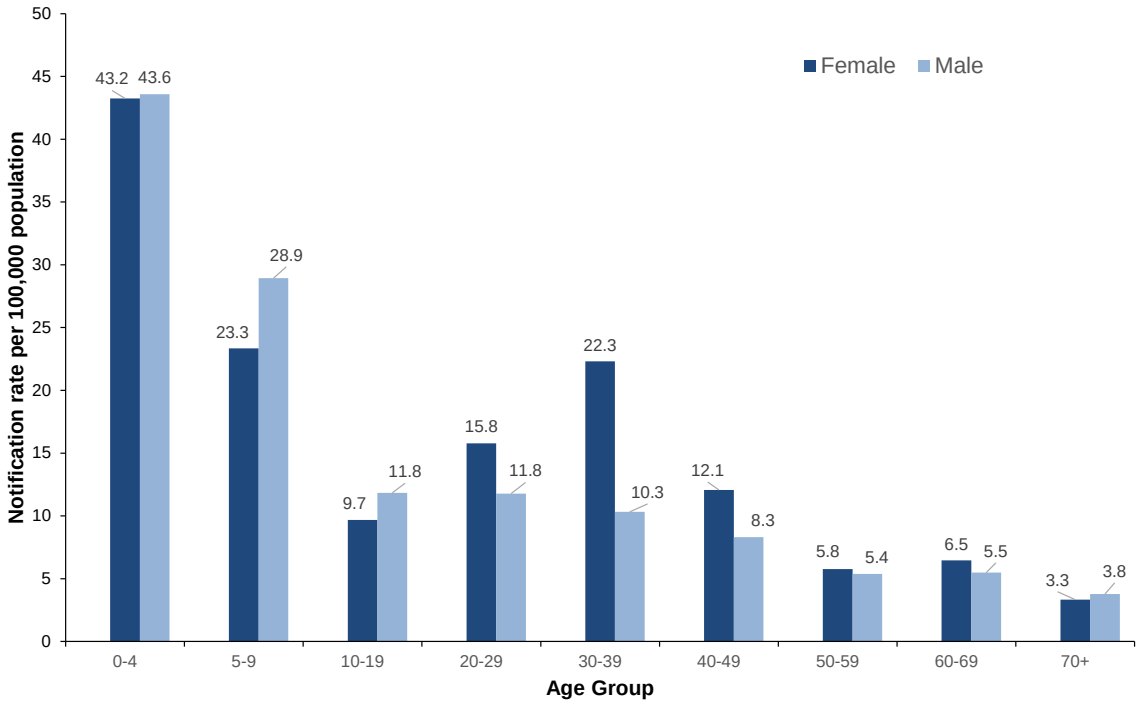


Figure 10. Cryptosporidium notification rates per 100,000 population by age group and sex, Queensland, 2025

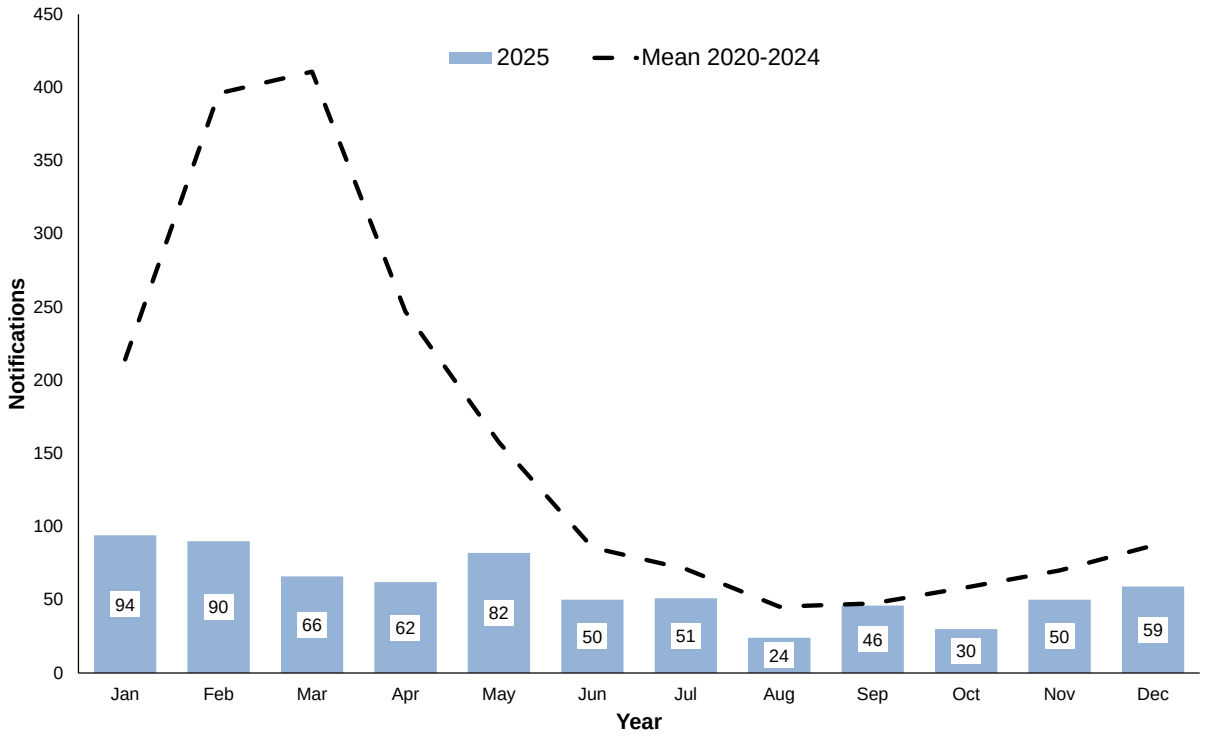


Figure 11. Cryptosporidium notifications in 2025 and previous 5-year mean by month, Queensland

Table 12. Cryptosporidium notifications and rate per 100,000 population by age group and sex, Queensland, 2025

Age Group (years)	Male		Female		Total	
	Number	**Rate**	**Number**	**Rate**	**Number**	**Rate**
0-4	69	43.6	65	43.2	134	43.4
5-9	50	28.9	38	23.3	88	26.2
10-19	44	11.8	34	9.7	78	10.8
20-29	45	11.8	59	15.8	104	13.8
30-39	40	10.3	89	22.3	129	16.4
40-49	29	8.3	44	12.1	73	10.2
50-59	18	5.4	20	5.8	38	5.6
60-69	16	5.5	20	6.5	36	6.0
0 +	12	3.8	12	3.3	24	3.5
All ages	**323**	**11.7**	**381**	**13.5**	**704**	**12.4**

Table 13. Cryptosporidium notifications and rate per 100,000 population by Hospital and Health Service, Queensland, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	**5-year mean***	**2025**	**5-year mean**
Cairns and Hinterland	18	75	6.6	28.3
Central Queensland	34	114	14.6	50.3
Central West	2	4	18.5	35.7
Darling Downs	45	106	14.8	35.8
Gold Coast	77	204	11.0	30.7
Mackay	28	74	14.6	40.0
Metro North	113	413	9.9	38.1
Metro South	158	411	12.0	33.2
North West	4	8	13.9	27.1
South West	6	15	24.5	63.7
Sunshine Coast	83	161	16.9	34.4
Torres and Cape	0	3	0.0	11.6
Townsville	19	121	7.5	49.5
West Moreton	46	134	13.3	41.1
Wide Bay	71	47	28.9	20.0
QLD Total	**704**	**1890**	**12.4**	**35.5**

* 5-year mean (2020-2024)

Listeria monocytogenes

Total notifications: 6

Notification rate per 100,000: 0.1

Median age: 76 years (range 33-83 years)

Gender: 4 (67%) female

Outbreaks investigated: 1 outbreak

Other key information:

1 perinatal case (miscarried at 13 weeks gestation).

Serotyping and sequencing:

- 3 serotype 4b, 4d, 4e – all were different genomic subtypes and unrelated on phylogenetic analysis.
- 2 serotype 1/2a, 3a – both part of a foodborne outbreak that also included a non-notified QLD case (urine isolate) and a NSW case (diagnosed in QLD). All four cases were serotype 1/2a, 3a and were highly related genomically on phylogenetic analysis. Commercially distributed ready-to-eat chicken meat was the implicated food vehicle (refer to Significant Foodborne Outbreaks section).
- 1 serotype 1/2b, 3b, 7 – did not cluster genomically and was considered a sporadic infection.

Changes in incidence

6 cases reported in 2025 compared to 9 cases in 2024, (Table 1).

Annual notification counts have varied between 6 and 18 cases per year (median 12 cases) during the past 10-year period (Figure 12).

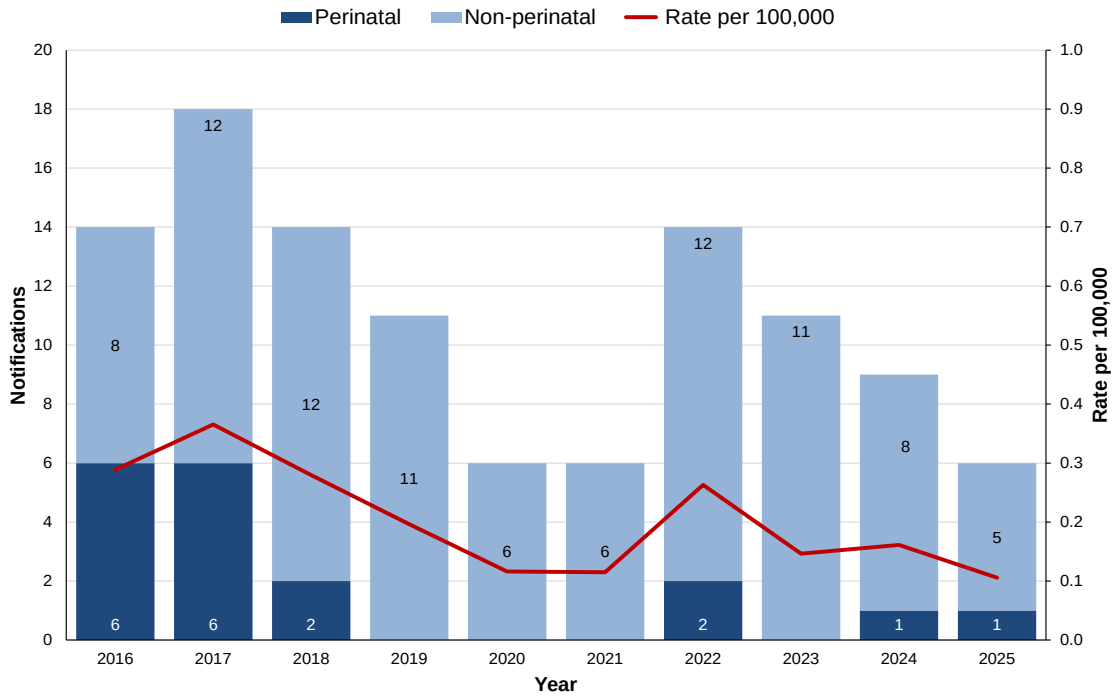


Figure 12. Invasive Listeria monocytogenes notifications and rate per 100,000 population by year, Queensland, 2016-2025

Shigella

Total notifications: 620
Notification rate per 100,000: 10.9
Median age: 38.5 years (range <1-85 years)
Sex: 329 (53%) male
Outbreaks investigated: 1 outbreak (12 cases)
Other key information:
Of 114 confirmed cases with enhanced surveillance information available:

- 55 (48%) reported overseas travel during exposure period
- 50 (44%) were multi-drug resistant (MDR/XDR).

Changes in incidence

Notifications received in 2025 (620) were 24% higher than notifications received in 2024 (501), (Table 1).

The annual notification rate in 2025 (10.9 per 100,000) was 1.7 times higher than the 5-year annual mean (5.7 per 100,000), (Table 1).

Culture-positive annual notification rate in 2025 (2.3 per 100,000) was 28% higher than 2024 (1.8 per 100,000) (Figure 14).

Groups with highest notification rate

Age: Highest rates were observed in the 0-4 year age group (17.1 per 100,000) and 5-9 years (16.6 per 100,000), (Figure 15, Table 15).

HHS: Torres and Cape (26 cases – 99.5 per 100,000) (Table 16). Compares with 34.8 per 100,000 in 2024 and the 5-year mean 12.4 per 100,000 population. All 26 cases were First Nations peoples from multiple communities.

Other key information

132 (21%) confirmed cases (culture positive); 488 probable cases (PCR only) (Table 2).

93/132 (70%) confirmed cases were male.

81/595 (14%) notifications were First Nations peoples, with the status unknown for 25 cases.

Annual notification rate among First Nations peoples (28.3 per 100,000) was 2.6 times higher than the overall Queensland notification rate (10.9 per 100,000).

No risk factor information was collected from probable cases.

55/114 (48%) confirmed cases reported overseas travel during exposure period (18 unknown). *Shigella sonnei* biotype g was the most frequently reported strain acquired overseas (Table 17).

34/81 (42%) confirmed male cases (aged 18 years and older) reported MSM as a risk factor.

131/132 (99%) culture positive cases were speciated (Table 14, Figure 13):

- 74 (56%) *Shigella sonnei*
- 53 (41%) *Shigella flexneri*
- 3 (2%) *Shigella dysenteriae*
- 1 (<1%) *Shigella boydii*

Antimicrobial resistance

50/114 (44%) were multi-drug resistant (MDR/XDR) [1]

- Antimicrobial susceptibility profiles unknown for 18 cases.

2/50 were MDR but were not resistant to third-generation cephalosporins

- No reported overseas travel
- No other risk factors identified.

48/50 were XDR:

- Serogroups: 38 *S. sonnei* (89% biotype g), 6 *S. flexneri*, 2 *S. dysenteriae*, 1 *S. boydii*, 1 *Shigella sp*.
- 42 (88%) were among males.
  - 39/42 (93%) were adult males (aged 18+ years).
  - 21/39 (54%) adult males reported MSM as a risk factor.
- 14 (33%) reported overseas travel during their exposure period.
  - Overseas travel unknown for 6 cases.
  - 1 case who travelled overseas also reported MSM as a risk factor.
- 3 (6%) were First Nations peoples.

Outbreaks

One reported outbreak of 12 cases of shigellosis at a remote community in North Queensland.

All cases were PCR positive (species unknown). Suspected person to person transmission.

[1] **MDR**: isolate **phenotypically** resistant to 3 or more of the following combinations: ampicillin/amoxicillin, ciprofloxacin/norfloxacin, co-trimoxazole, ceftriaxone/cefotaxime/ceftazidime or azithromycin.

XDR: isolate that is phenotypically resistant to any third-generation cephalosporin (e.g. ceftriaxone/cefotaxime/ceftazidime) **or** with genotypic detection of an ESBL gene.

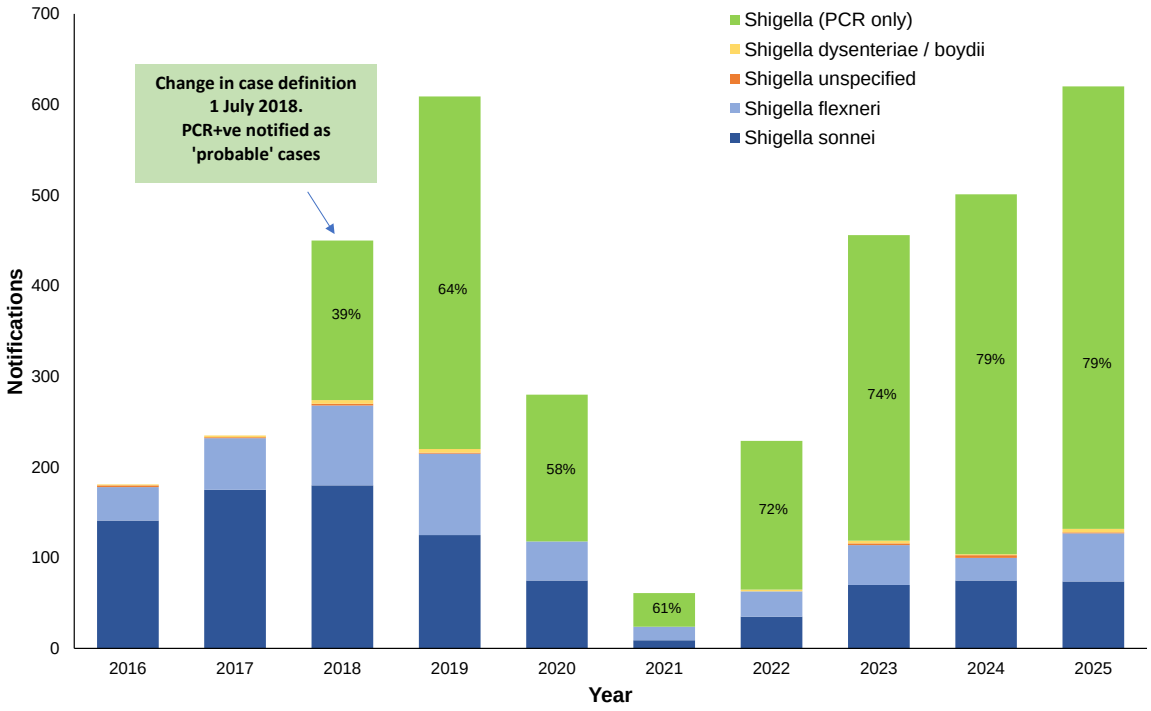


Figure 13. Shigella notifications in Queensland by species, 2016-2025

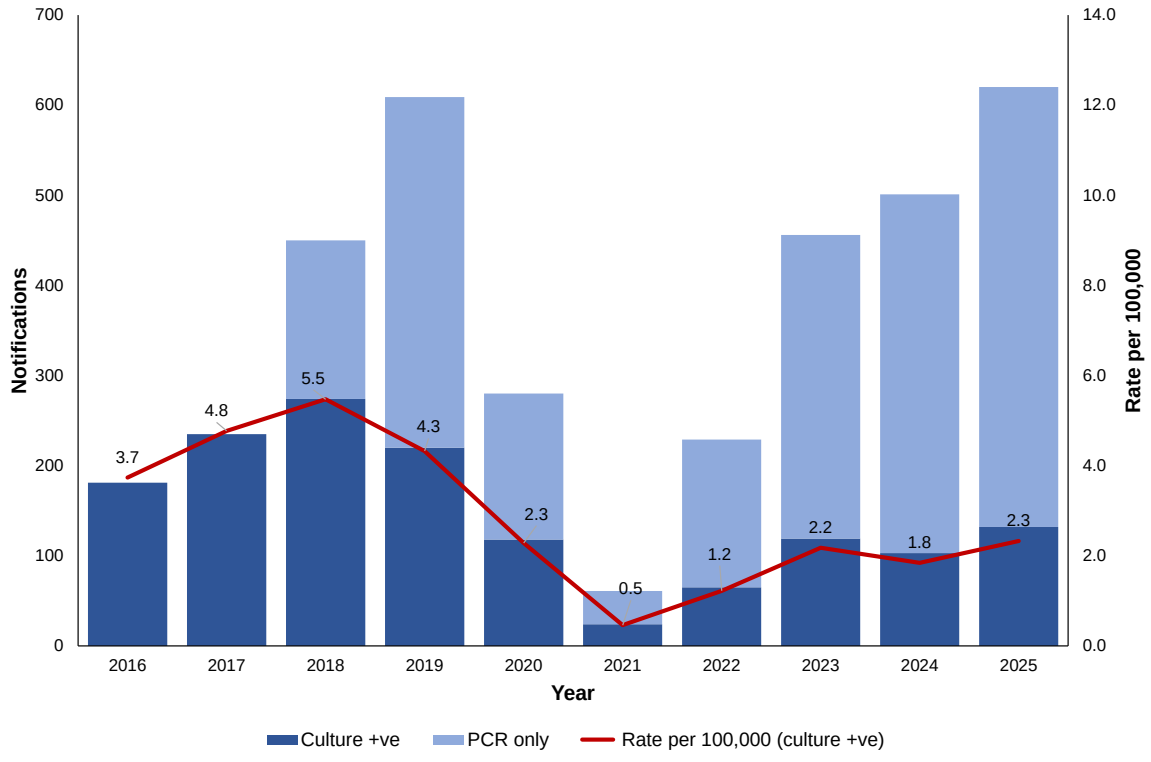


Figure 14. Shigella notifications by method of diagnosis and culture-positive rate per 100,000 population, Queensland 2016-2025

Table 15. Shigella notifications and rate per 100,000 population by age group and sex, Queensland 2025

Age Group (years)	Male		Female		Total	
	Number	Rate	Number	Rate	Number	Rate
0-4	32	20.1	21	14.0	53	17.1
5-9	31	18.1	24	14.9	55	16.6
10-19	20	5.3	15	4.2	35	4.8
20-29	29	7.4	37	9.7	66	8.5
30-39	66	16.7	44	10.8	110	13.7
40-49	52	14.6	50	13.4	102	14.0
50-59	39	11.6	44	12.6	83	12.1
60-69	33	11.2	35	11.2	68	11.2
70+	27	8.2	21	5.6	48	6.9
All ages	**329**	**11.7**	**291**	**10.2**	**620**	**10.9**

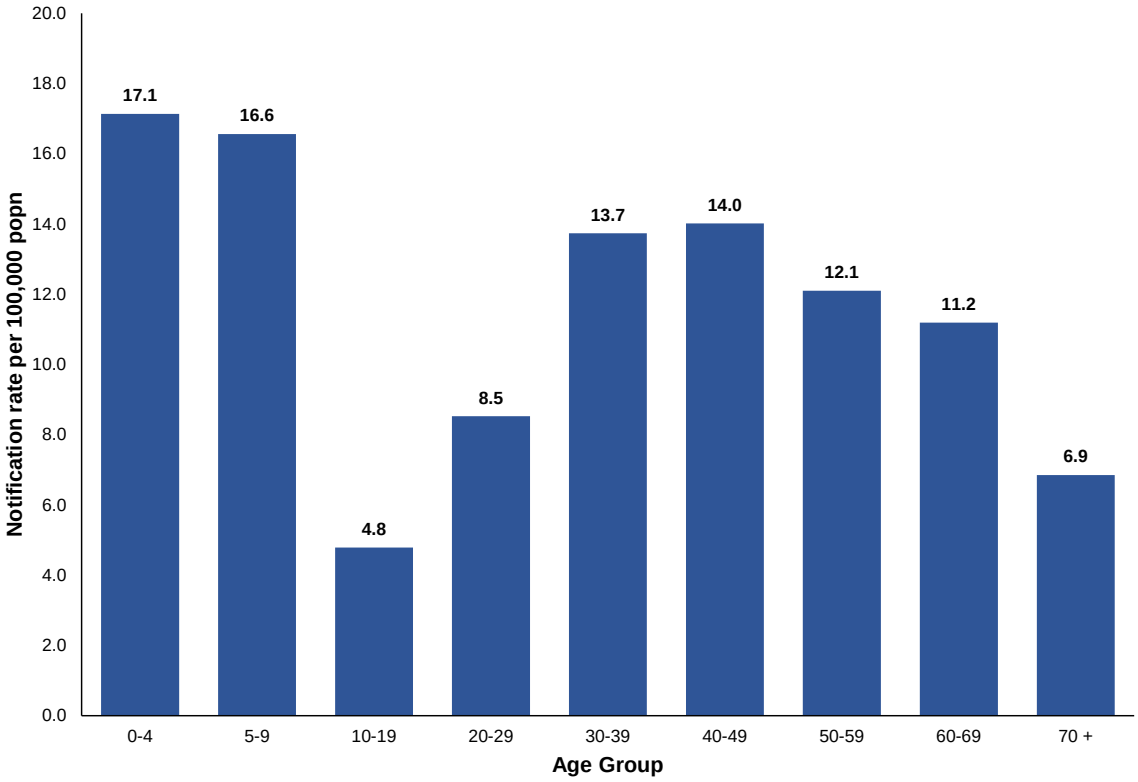


Figure 15. Shigella notification rates per 100,000 population by age group, in Queensland, 2025

Table 16. Shigella notifications and rate per 100,000 population in Queensland by Hospital and Health Service, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025**	**5-year mean***	**2025**	**5-year mean**
Cairns and Hinterland	39	25	14.4	9.5
Central Queensland	15	12	6.5	5.1
Central West	1	0.4	9.3	3.8
Darling Downs	21	7	7.0	2.4
Gold Coast	67	37	9.8	5.5
Mackay	9	4	4.7	1.9
Metro North	149	77	13.3	7.1
Metro South	189	74	14.8	6.0
North West	6	8	20.8	27.1
South West	1	1	4.1	4.1
Sunshine Coast	47	27	9.8	5.8
Torres and Cape	26	3	99.5	12.4
Townsville	14	13	5.6	5.4
West Moreton	30	10	8.9	3.1
Wide Bay	3	5	1.2	2.0
QLD Total	**620**	**304**	**10.9**	**5.7**

* 5-year mean (2020-2024); ** 3 cases were overseas residents

Table 17. Reported risk factors among Shigella biotypes & serotypes, 2025 (confirmed cases)

Species	Bio / serotype	Count	O/S travel	First Nations	MSM	MDR	XDR
S. sonnei	Biotype a	10	6	1	0	1	1
	Biotype f	3	2	0	0	1	1
	Biotype g	57	24	3	18	31	34
	Not reported	4	2	2	1	2	2
S. flexneri	1b	5	1	1	1	1	2
	2a	14	5	5	0	2	1
	2 var	1	1	0	0	0	0
	3a	19	4	2	12	1	2
	3b	5	0	0	2	1	1
	4	1	0	0	0	0	0
	6	1	1	0	0	0	0
	var X	2	1	0	0	0	0
	var Y	1	0	0	0	0	0
	Untypeable	3	2	0	0	0	0
	Not reported	1	1	0	0	0	0
S. boydii	-	1	1	0	0	0	1
S. dysenteriae	-	3	3	0	0	2	2
S. unspecified	-	1	1	0	0	1	1
Totals		**132**	**55**	**14**	**34**	**43**	**48**

travel information unknown for 18 cases, ∞ MSM status unknown for 33 adult males, * First Nations status unknown for 3 culture-positive cases

MDR: isolate phenotypically resistant to 3 or more of the following combinations: ampicillin/amoxicillin, ciprofloxacin/norfloxacin, co-trimoxazole, ceftriaxone/cefotaxime/ceftazidime or azithromycin.

XDR: isolate that is phenotypically resistant to any third-generation cephalosporin (e.g. ceftriaxone/cefotaxime/ceftazidime) or with genotypic detection of an ESBL gene.

Yersinia enterocolitica

Total notifications: 819

Notification rate per 100,000: 14.4

Median age: 46 years (range <1-97 years)

Gender: 497 (61%) females

Outbreaks investigated: 0 outbreaks

Other key information:

- 282 (34%) culture positive; 537 (66%) cases detected through PCR only.
- 271 (96%) culture positive isolates were biotyped.
- Biotype: 1a – 208 cases (74%) was the most frequently reported strain (Table 18, Figure 16).

Changes in incidence

26% decrease in the 2025 notifications (819) compared to 2024 (1,101), (Table 1).

Yersinia annual notification rate in 2025 (14.4 per 100,000) was comparable to the 5-year (2020-2024) annual mean (14.6 per 100,000), (Table 1).

Culture positive rate in 2025 (5.0 per 100,000) was comparable to 2024 (5.0 per 100,000), (Figure 17).

Groups with highest notification rate

Age: Highest rates were observed in the 70+ years age group (21% of cases – 25.1 per 100,000), (Table 19).

HHS: Central West (<1% of cases – 37.1 per 100,000) and Mackay HHS (<5% of cases – 19.2 per 100,000), (Table 20).

Notification rate among females was noticeably higher than the notification rate among males for all age groups apart from the 0-4 years group, (Figure 18).

Seasonality

Notifications typically peak during the warmer months. Higher than expected counts were reported in January and March 2025 when compared with 5-year monthly means, (Figure 19).

Table 18. Yersinia enterocolitica notifications by biotype, serotype in Queensland, 2025

Biotype/serotype	Count	%
Biotype 1a, non-typeable	208	74
Biotype 3, non-typeable	20	7
Biotype 3, serotype O:3	1	<1
Biotype 4, serotype O:3	42	15
Untyped	11	4
Total	**282**	**100**

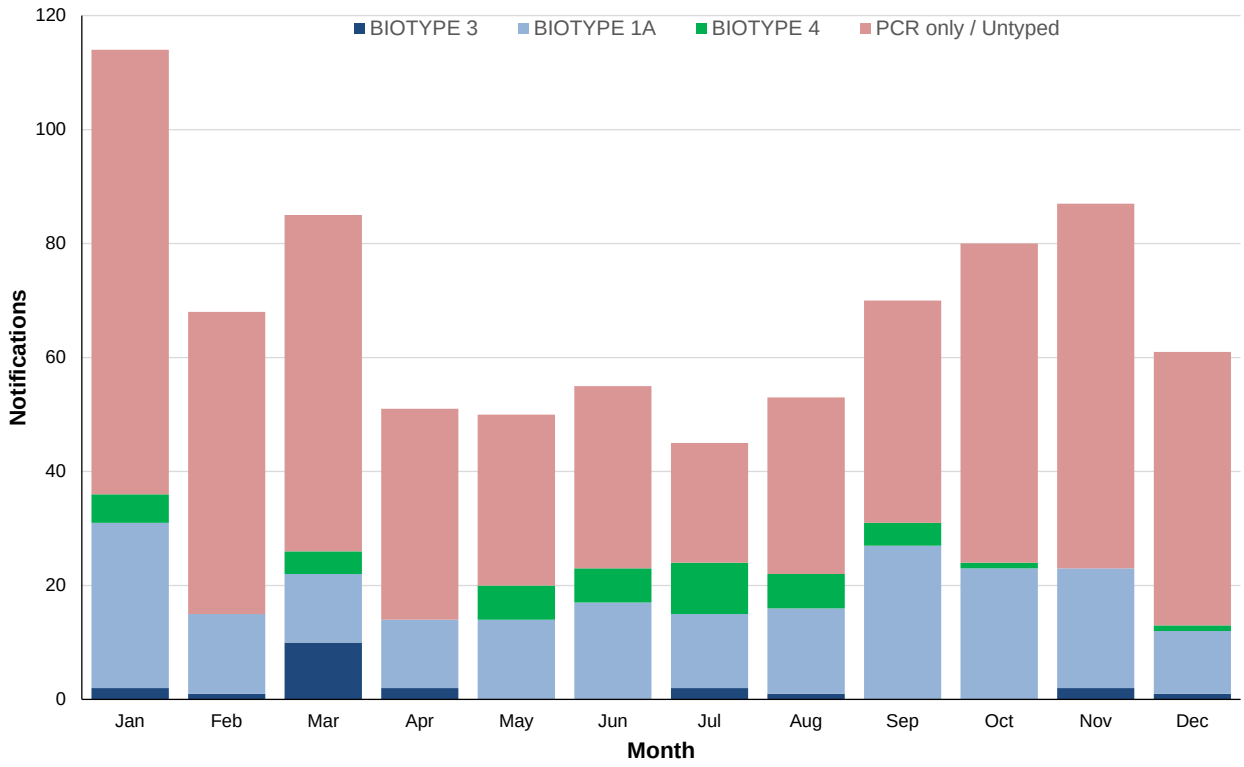


Figure 16. Yersinia enterocolitica notifications by month of onset and biotype, Queensland, 2025

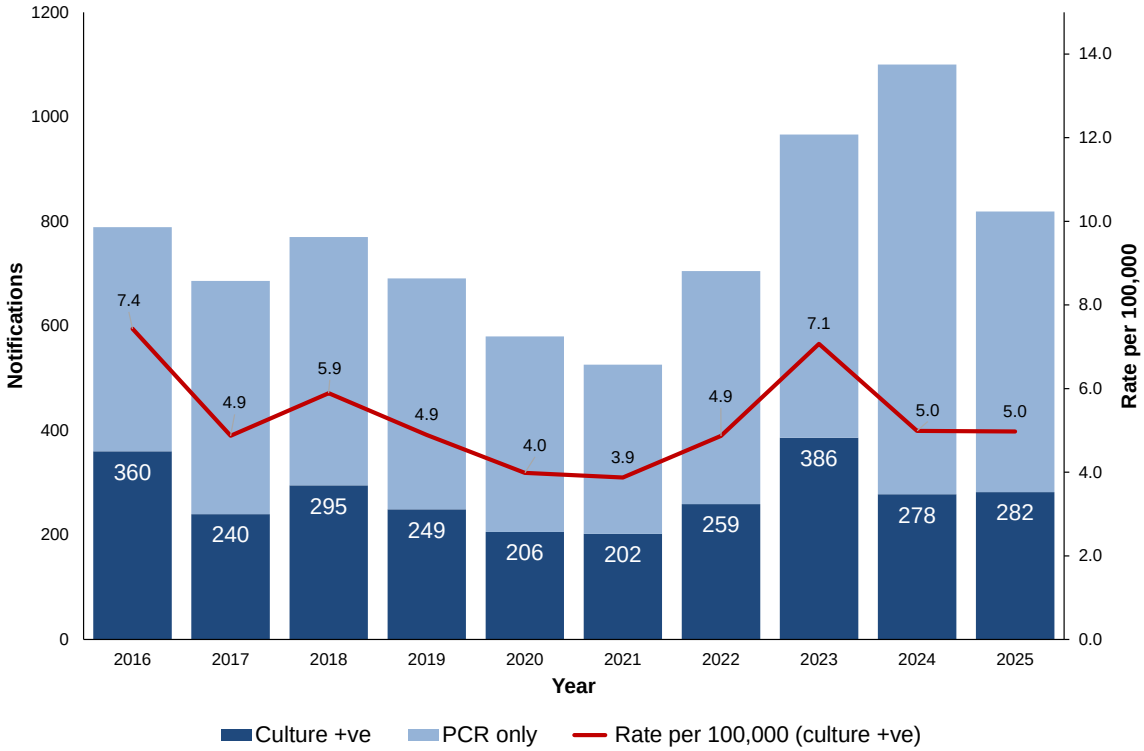


Figure 17. Yersinia enterocolitica notifications and culture positivity rate per 100,000 population by year, Queensland, 2016-2025

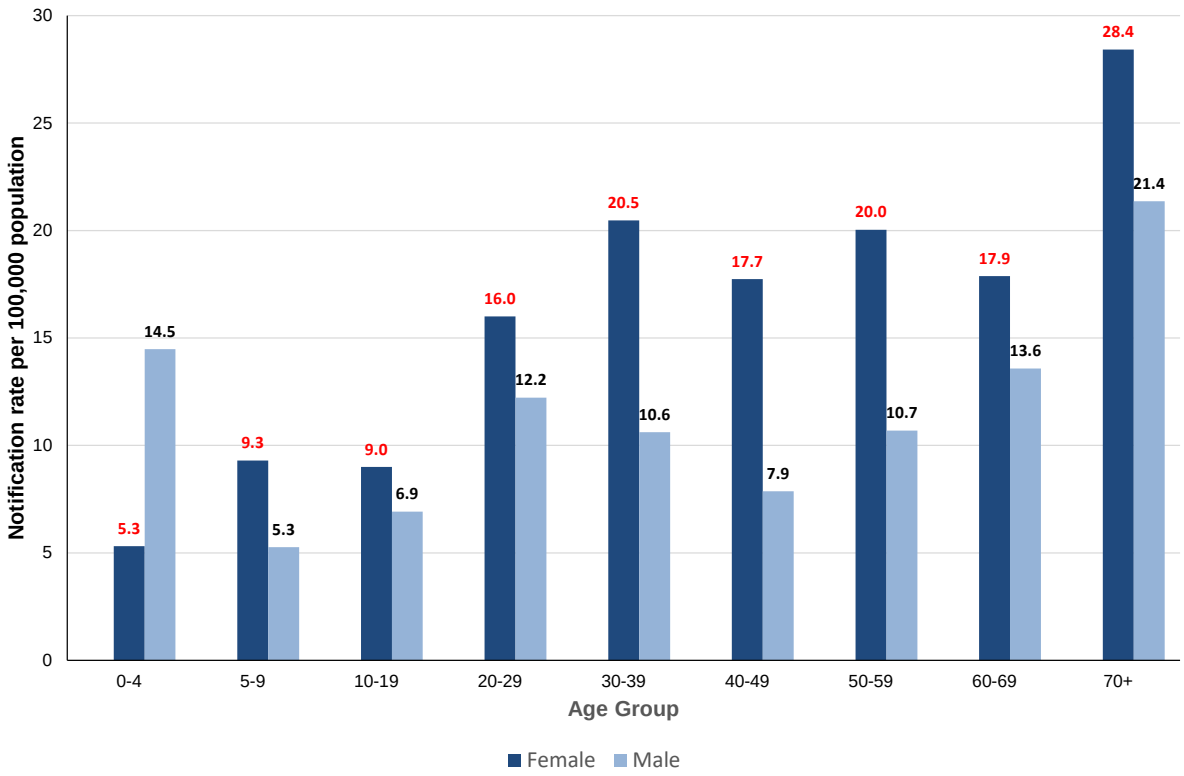


Figure 18. Yersinia enterocolitica notification rates per 100,000 population by age group and sex, Queensland, 2025

Table 19. Yersinia enterocolitica notifications and rate per 100,000 population by age group and sex, Queensland, 2025

Age Group (years)	Male		Female		Total	
	Number	**Rate**	**Number**	**Rate**	**Number**	**Rate**
0-4	23	14.5	8	5.3	31	10.0
5-9	9	5.3	15	9.3	24	7.2
10-19	26	6.9	32	9.0	58	7.9
20-29	48	12.2	61	16.0	109	14.1
30-39	42	10.6	83	20.5	125	15.6
40-49	28	7.9	66	17.7	94	12.9
50-59	36	10.7	70	20.0	106	15.5
60-69	40	13.6	56	17.9	96	15.8
70+	70	21.4	106	28.4	176	25.1
All ages	**322**	**11.5**	**497**	**17.4**	**819**	**14.4**

Table 20. Yersinia enterocolitica notifications and rate per 100,000 population by Hospital and Health Service, Queensland, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	5-year mean*	2025	5-year mean
Cairns and Hinterland	40	42	14.6	15.8
Central Queensland	29	29	12.5	12.8
Central West	4	1	37.1	9.4
Darling Downs	51	38	16.7	12.8
Gold Coast	94	105	13.5	15.8
Mackay	37	27	19.2	14.5
Metro North	182	176	15.9	16.2
Metro South	190	179	14.5	14.5
North West	0	2	0.0	6.9
South West	4	3	16.3	12.4
Sunshine Coast	89	75	18.1	16.0
Torres and Cape	0	0	0.0	0.0
Townsville	47	37	18.7	15.1
West Moreton	24	30	6.9	9.2
Wide Bay	28	32	11.4	13.6
QLD Total	**819**	**775**	**14.4**	**14.6**

* 5-year mean (2020-2024)

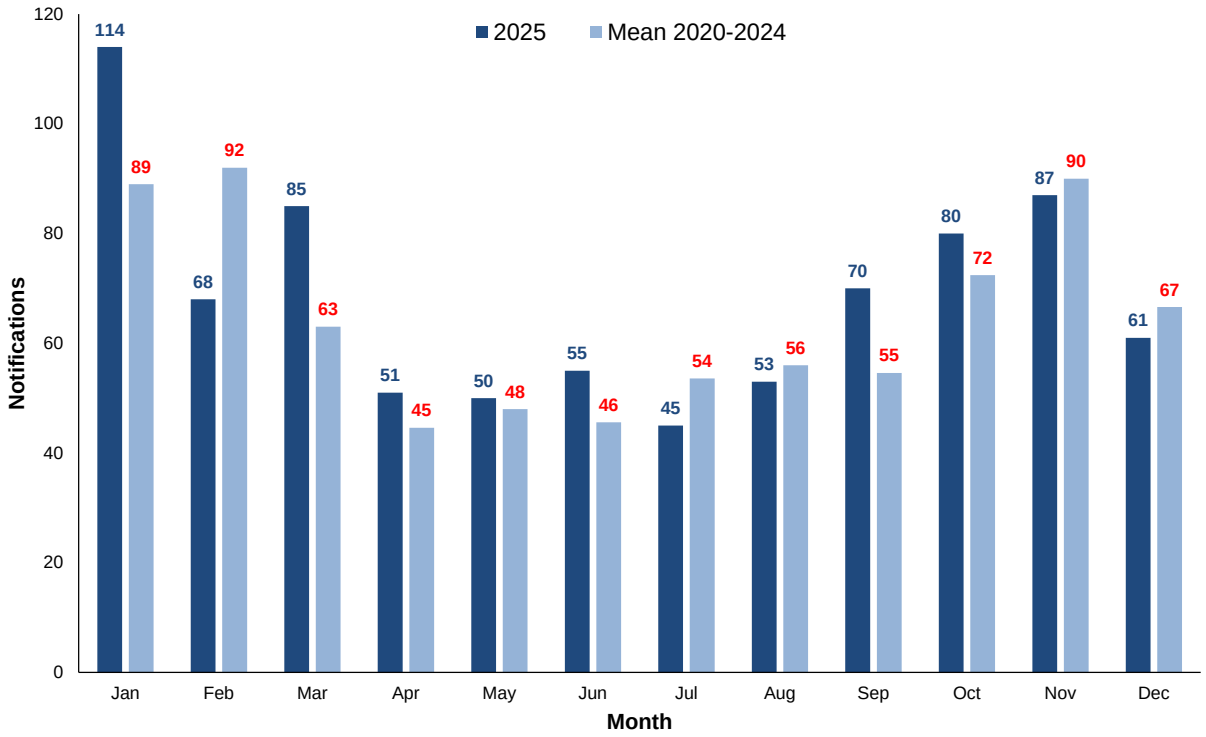


Figure 19. Yersinia enterocolitica notifications in 2025 by month of onset, and mean monthly notifications for the five-year period, 2020-2024, Queensland

Shiga toxin-producing E. coli (STEC)

Total notifications: 54

Notification rate per 100,000: 1.0

Median age: 33 years (range 1-87 years)

Gender: 31 (57%) female

Outbreaks investigated: 1

Other key information:

- Acute diarrhoeal illness was reported by 19 (35%) cases, including one case who developed HUS.
- 35 cases did not report an acute illness (referred by alternative health practitioner for faecal testing).

Changes in incidence

Annual notification rates have slowly increased since 2021 (Figure 20). These increases primarily relate to increased faecal testing by a single diagnostic pathology laboratory that provides services to alternative health practitioners.

Only 35% cases in 2025 reported an acute diarrhoeal illness.

Groups with highest notification rate

Gender: Female (57% of cases – 1.1 per 100,000), (Table 21).

Age: Females aged 20-29 years (11 cases – 2.9 per 100,000).

HHS: Mackay (7 cases – 3.6 per 100,000), (Table 22).

Seasonality

23 cases (43%) were reported during the 4th quarter (October – December) period.

Other key information

STEC target genes:

- 17 cases (31%) were PCR positive for stx1 gene only.
- 19 cases (35%) were PCR positive for stx2 gene only.
- 15 cases (28%) were PCR positive for both stx1 and stx2 genes.
- 3 cases with stx target genes detected but stx type not specified.
- 24/53 (45%) cases with culture positive stools (culture was not performed for 1 case).

14 different serogroups were detected among 27 cases, either by culture or multiplex PCR.

The most frequently reported serogroups were O26 (5 cases), O157 (4), O128 (3).

Acute diarrhoeal illness was reported by 19/54 (35%) cases:

- 15/19 (79%) reported bloody diarrhoea.
- 11/19 (58%) hospitalised (median 2 days; range 1-11 days).
- One case developed HUS (refer to HUS section).

- No deaths reported.
- 4/19 cases were overseas acquired infections: Indonesia (3) and El Salvador (1).
- No confirmed source of infection among these cases.

35 cases did not report an acute illness:

- 33/35 non-acute cases were referred by an alternative health practitioner for faecal testing.
- 2 cases were referred by a clinician.

The most frequently reported risk factors among cases with acute illness included overseas travel (4 cases), exposure to a rural environment (2 cases), and exposure to farm animals (2 cases).

Two cases in December 2025 and 1 case notified in January 2026 were serotype O145:H28 and highly related on whole genome sequencing. Exposure to kangaroo meat was reported by two cases. A confirmed source of infection was not identified.

No cases were reported among First Nations peoples.

Table 21. STEC notifications and rate per 100,000 population by age group and sex, Queensland, 2025

Age Group (years)	Male		Female		Total	
	Number	**Rate**	**Number**	**Rate**	**Number**	**Rate**
0-4	1	0.6	1	0.7	2	0.6
5-9	3	1.7	0	0.0	3	0.9
10-19	3	0.8	1	0.3	4	0.6
20-29	3	0.8	11	2.9	14	1.9
30-39	3	0.8	3	0.8	6	0.8
40-49	5	1.4	4	1.1	9	1.3
50-59	1	0.3	3	0.9	4	0.6
60-69	3	1.0	5	1.6	8	1.3
70+	1	0.3	3	0.8	4	0.6
All ages	**23**	**0.8**	**31**	**1.1**	**54**	**1.0**

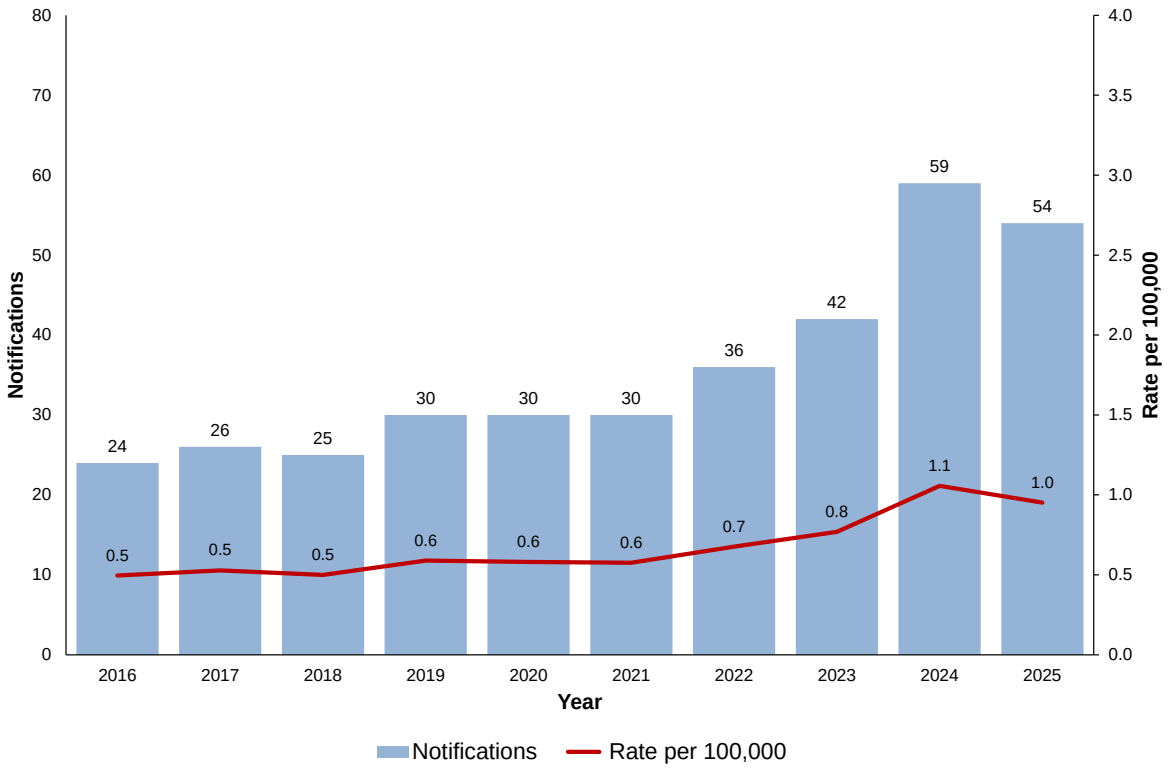


Figure 20. STEC notifications and rate per 100,000 population by year, Queensland, 2016-2025

Table 22. STEC notifications and rate per 100,000 population by Hospital and Health Service, Queensland, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	**5-year mean***	**2025**	**5-year mean**
Cairns and Hinterland	2	1	0.7	0.4
Central Queensland	0	3	0.0	1.3
Central West	1	1	9.3	9.4
Darling Downs	4	3	1.3	1.0
Gold Coast	7	6	1.0	0.9
Mackay	7	2	3.6	1.1
Metro North	10	6	0.9	0.6
Metro South	6	6	0.5	0.5
North West	0	0	0.0	0.0
South West	0	0	0.0	0.0
Sunshine Coast	6	4	1.2	0.9
Torres and Cape	0	0	0.0	0.0
Townsville	2	1	0.8	0.4
West Moreton	4	1	1.2	0.3
Wide Bay	5	4	2.0	1.7
QLD Total	**54**	**39**	**1.0**	**0.7**

* 5-year mean (2020-2024)

Haemolytic Uraemic Syndrome (HUS)

Total notifications: 2

Notification rate per 100,000: <0.1

Other key information:

- 1 case associated with STEC infection.

Changes in incidence

2025 notifications (2) compared with 3 cases in 2024 and the 5-year annual mean of 3 cases, (Table 1).

There were no deaths reported among the two cases.

Case summaries

Case 1 – associated with a prior STEC infection:

- Young adult female.
- Faecal specimen PCR positive for stx2, eaeA and ehxA genes. Serogroup O157 detected on PCR.
- No environmental exposures were identified other than regular care of domestic pets.
- Food history included handling and consumption of beef.
- No source of infection was identified.

Case 2 – associated with a prior Enteropathogenic *E. coli* (EPEC) infection:

- Adult male.
- Faecal specimen tested negative for both stx1 and stx2 genes.
- Case reported their household dog was unwell at the same time with bloody diarrhoea.
- Food history not obtained.
- No source of infection identified.

Typhoid Fever

Total notifications: 32
Notification rate per 100,000: 0.6
Median age: 23 years (range <1-88 years)
Gender: 19 (59%) female
Outbreaks investigated: 0
Other key information:

- 30 (94%) were overseas acquired.

Changes in incidence

32 notified cases in 2025 compared with 29 cases in 2024 and a the 5-year (2020-2024) annual mean of 21 cases (Table 1, Figure 21).

Groups with highest notification rate

Gender: Female (59% of cases – 0.7 per 100,000).

Age: 5-9 years (16% of cases – 1.5 per 100,000).

Place of acquisition

Overseas acquired: 30 (94%): India (23 cases), Bangladesh (2), Indonesia (1), Pakistan (1), Samoa (1), Afghanistan (1), multiple countries (India and Indonesia) visited (1).

Locally acquired: 1 (3%): No history of overseas travel reported during exposure period, immunocompromised.

Unknown: 1 (3%): Elderly case, hospitalised for approximately one month prior to their diagnosis, and likely asymptomatic carrier who returned a positive faecal result while being investigated for Norovirus gastroenteritis.

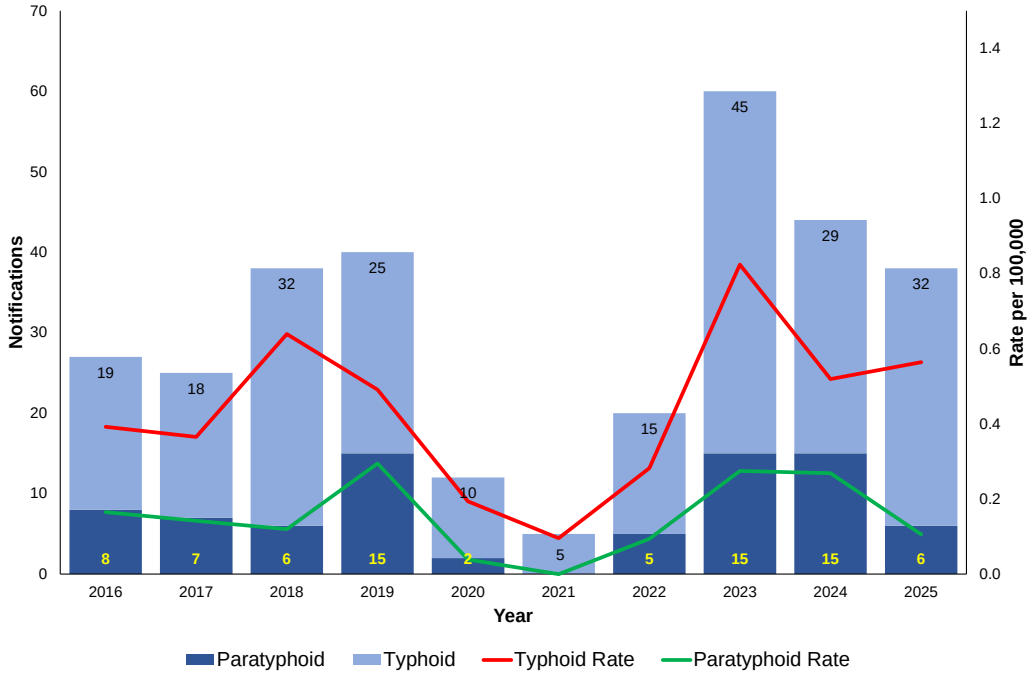


Figure 21. Typhoid/Paratyphoid notifications and rate per 100,000 population by year, Queensland, 2016-2025

Paratyphoid Fever

Total notifications: 6
Notification rate per 100,000: 0.1
Median age: 37.5 years (range 11-55 years).
Gender: 3 (50%) female
Outbreaks investigated: 0
Other key information:

- 5 (83%) were overseas acquired, and 1 was a household contact of returning traveller.

Changes in incidence

6 notified cases in 2025 compared with 15 cases in 2024 and a 5-year (2020-2024) annual mean of 6 cases, (Table 1, Figure 21).

Paratyphoid fever A (6 cases).

No cases of paratyphoid fever B were reported.

Groups with highest notification rate

Not reported - insufficient notifications.

Place of acquisition

Overseas acquired: 5 cases:

- All 5 cases had travelled from India.

Locally acquired: 1 case:

- Likely acquired from a close household contact who had returned from India with a clinically compatible illness but was not tested.

Hepatitis A

Total notifications: 44

Notification rate per 100,000: 0.8

Median age: 24 years (range 3-63 years)

Gender: 26 (59%) female

Outbreaks investigated: 1

Other key information:

- 39 (87%) were overseas acquired.

Changes in incidence

2025 notifications (44) were 47% higher than the number of notifications received in 2024 (30) and 76% higher in comparison to the 5-year (2020-2024) annual mean (25), (Table 1, Figure 22).

Groups with highest notification rate

Age: 20-29 years (41% of cases – 2.3 per 100,000), (Table 24).

HHS: Metro North and Metro South (combined 68% of cases – each 1.2 per 100,000), (Table 25).

Place of acquisition

39 likely overseas acquired infections:

- India (20), Fiji (4), Overseas (cruise ship) (3), Vanuatu (3), Afghanistan (1), Iran (1), Laos (1), Nauru (1), Nepal (1), North-East Asia (1), Pakistan (1), Papua New Guinea (1), and Syria (1).

5 locally acquired infections (no overseas travel reported):

- 2 cases were close contacts of confirmed cases with recent overseas exposure.
- 3 cases had an unknown source of infection.

Other key information

32/44 (73%) hospitalised.

32/34 (94%) were unvaccinated (10/44 cases had an unknown vaccination status).

First Nations peoples: 0 cases

41/44 (93%) infections were genotyped (Table 23).

- Genotype IA was identified in 16 cases.
- Genotype IB was identified in 1 case.
- Genotype IIIA was identified in 24 cases.

3 outbreak-associated cases were reported among staff members from the same cruise ship (genotype IA). The cruise ship had previously travelled to both New Caledonia and Vanuatu.

Table 23. Hepatitis A notifications by genotype, Queensland, 2025

Genotype	Locally acquired infections	Overseas acquired infections	Total
IA	3	13	16
IB	0	1	1
IIIA	2	22	24
Not typed	0	3	3
Total	**5**	**39**	**44**

Table 24. Hepatitis A notifications and rate per 100,000 population by age group and sex, Queensland, 2025

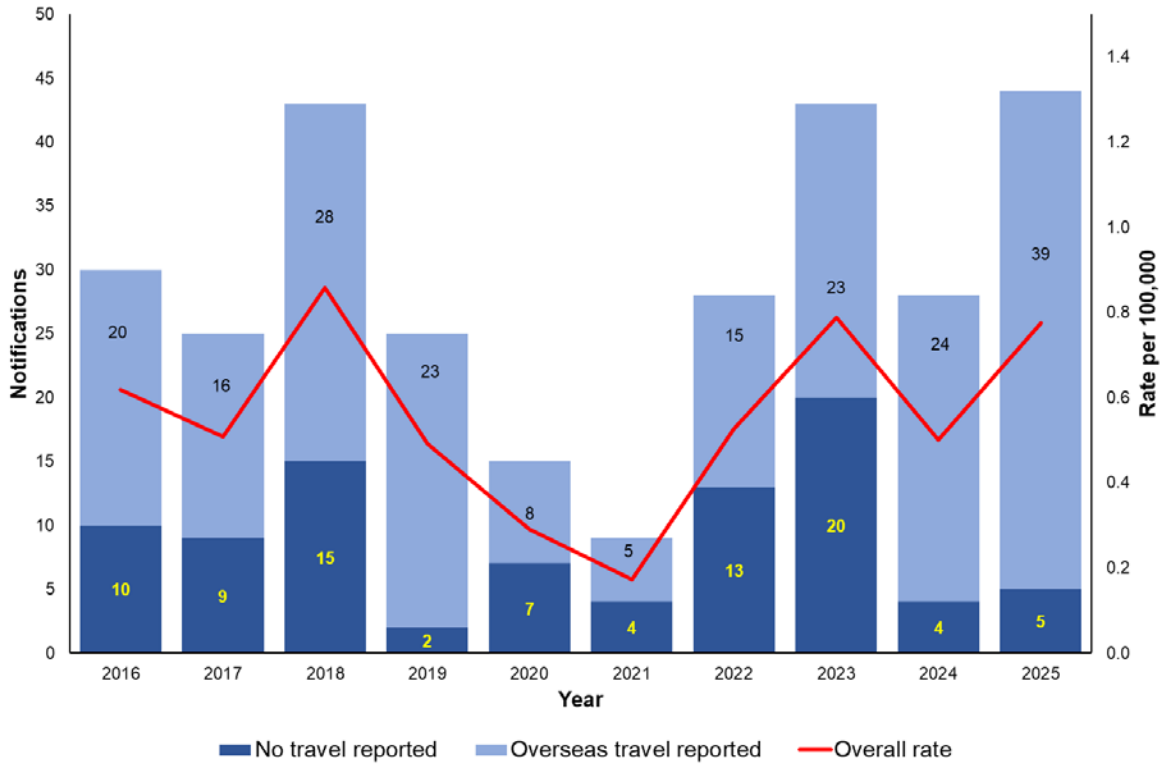
Age Group (years)	Male		Female		Total	
	Number	**Rate**	**Number**	**Rate**	**Number**	**Rate**
0-4	2	1.3	1	0.7	3	1.0
5-9	3	1.7	2	1.2	5	1.5
10-19	1	0.3	6	1.8	7	1.0
20-29	9	2.3	9	2.4	18	2.3
30-39	1	0.3	5	1.3	6	0.8
40-49	0	.0.0	3	0.8	3	0.4
50-59	0	0.0	0	0.0	0	0.0
60-69	2	0.7	0	0.0	2	0.3
70+	0	0.0	0	0.0	0	0.0
All ages	**18**	**0.7**	**26**	**1.0**	**44**	**0.8**

Table 25. Hepatitis A notifications and rate per 100,000 population by Hospital and Health Service, Queensland, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	**5-year mean***	**2025**	**5-year mean**
Cairns and Hinterland	0	1	0.0	0.4
Central Queensland	2	1	0.9	0.4
Central West	0	0	0.0	0.0
Darling Downs	1	2	0.3	0.7
Gold Coast	8	5	1.1	0.8
Mackay	0	0	0.0	0.0
Metro North	14	3	1.2	0.3
Metro South	16	7	1.2	0.6
North West	0	0	0.0	0.0
South West	0	0	0.0	0.0
Sunshine Coast	1	4	0.2	0.9
Torres and Cape	0	0	0.0	0.0
Townsville	0	1	0.0	0.4
West Moreton	2	2	0.6	0.6
Wide Bay	0	0	0.0	0.0

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	5-year mean*	2025	5-year mean
Total	**44**	**25**	**0.8**	**0.5**

* 5-year mean (2020-2024)



* 2 cases had an unidentified place of acquisition in 2025

Figure 22. Hepatitis A notifications by reported travel and overall rate per 100,000 population by year, Queensland, 2016-2025*

Hepatitis E

Total notifications: 2

Notification rate per 100,000: <0.1

Other key information: Both cases were locally acquired infections.

Changes in incidence

2 cases notified in 2025, compared with 3 cases in 2024 and a five-year (2020-2024) annual mean of 3 cases (Table 1).

Eleven of the past 12 notified cases in Queensland between 2022 and 2025 have been locally acquired infections (Figure 23).

Case summaries

Case 1:

- Reported consumption of oysters, pork meat and kangaroo meat during their exposure period.
- Confirmed with genotype 3 (HEV-3) and clustered (on partial genome sequencing) with seven previous, locally acquired infections notified between 2022 and 2024 who all reported consumption of the same brand of liverwurst

Case 2:

- Diagnosed by seroconversion (no RNA detected).
- Was pregnant at the time of infection, no adverse complications were reported.
- Source of infection was unable to be confirmed.

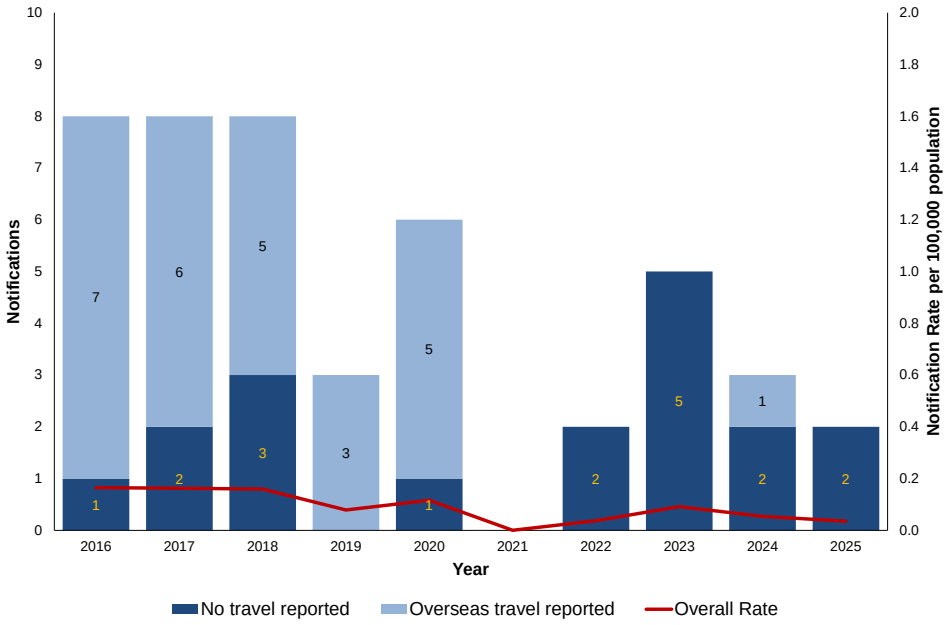


Figure 23. Hepatitis E notifications by reported travel and overall rate per 100,000 population by year, Queensland, 2016-2026

Ciguatera

Total notifications: 14

Notification rate per 100,000: 0.2

Median age: 43 years (range 7-68 years)

Gender: 7 male, 6 female, 1 case with unknown sex

Outbreak investigated: 4 (9 cases)

Other key information:

- All ciguatera notifications are based on clinical diagnoses.

Changes in incidence

14 cases reported in 2025 compared with 6 cases in 2024. Notifications in 2025 were comparable to the 5-year (2020-2024) annual mean of 11 cases, (Figure 24).

Groups with highest notification rate

Age: 40-49 years (36% of cases).

HHS: Cairns and Hinterland (29% of cases – 1.5 per 100,000 population), (Table 26).

Other key information

All cases reported neurological symptoms.

13/14 cases reported gastrointestinal symptoms: cramps (85%), diarrhoea (54%), vomiting (15%).

Median incubation period: 6.5 hours (range 1-14 hours).

9/14 notified cases were outbreak related; 5 cases were sporadic intoxications.

Implicated fish included coral trout, red throat emperor, red bass (snapper), Spanish mackerel, green jobfish, and barracuda.

Ciguatoxin was detected in left-over fish collected during three outbreak investigations (7 cases).

No left-over fish was available for testing for 1 outbreak (2 cases) or the 5 sporadic cases.

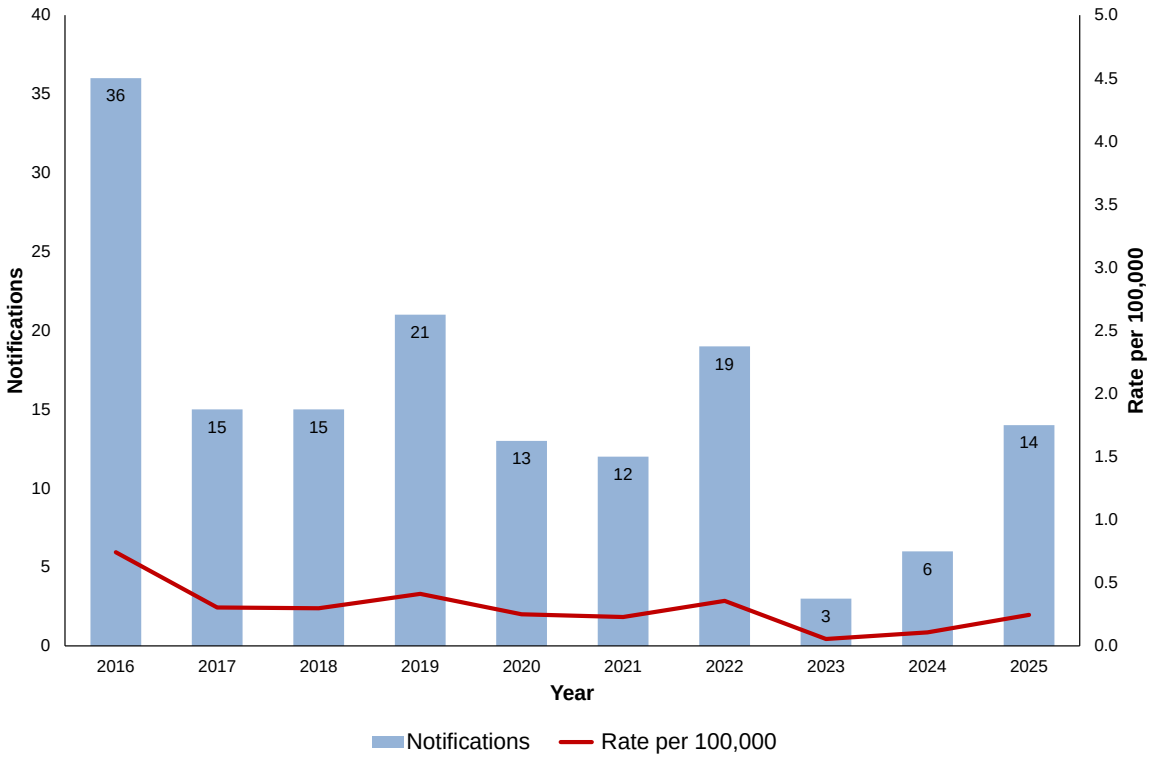


Figure 24. Ciguatera notifications and rate per 100,000 population by year, Queensland, 2016-2025

Table 26. Ciguatera notifications and rate per 100,000 population by Hospital and Health Service, Queensland, 2025

Hospital and Health Service	Notification Count		Notification Rate per 100,000	
	2025	5-year mean*	2025	5-year mean
Cairns and Hinterland	4	4	1.5	1.5
Central Queensland	0	0	0.0	0.0
Central West	0	0	0.0	0.0
Darling Downs	0	0	0.0	0.0
Gold Coast	2	1	0.3	0.2
Mackay	0	0	0.0	0.0
Metro North	3	0	0.3	0.0
Metro South	3	3	0.2	0.2
North West	0	0	0.0	0.0
South West	0	0	0.0	0.0
Sunshine Coast	0	0	0.0	0.0
Torres and Cape	0	0	0.0	0.0
Townsville	0	1	0.0	0.4
West Moreton	0	0	0.0	0.0
Wide Bay	2	0	0.8	0.0
QLD Total	**14**	**11**	**0.2**	**0.2**

* 5-year mean (2020-2024)

Vibrio cholerae (cholera)

Total notifications: 1

Notification rate per 100,000: <0.1

Other key information:

- The case was overseas acquired.

Case summary

Confirmed as toxigenic *Vibrio cholerae* serogroup 01 Ogawa infection.

History of recent travel to Bangladesh.

Onset of illness on date of arrival in Australia. Developed acute diarrhoea and vomiting and subsequently hospitalised.

No other cases detected among household contacts.

Vibrio parahaemolyticus

Total notifications: 19

Notification rate per 100,000: (incomplete annual data)

Median age: 57 years (range 28-80 years)

Sex: 12 (63%) male

Other key information:

- *Vibrio parahaemolyticus* became notifiable in QLD on 3 May 2025.

Case summaries

10 cases were gastrointestinal infections (positive faecal specimen).

7 cases were wound infections, and 2 cases were ear infections.

Routine follow-up is not conducted.

Gastrointestinal Illness Outbreaks

Table 27. Outbreaks by mode of transmission, Queensland, 2025

Mode of transmission*	No. of Outbreaks	No. ill	No. hospitalised
Foodborne / probable foodborne	13	109	11
Environmental / probable environmental	3	55	5
Waterborne	1	16	1
Person-to-person	699	7,709	113
Unknown	288	2,023	26
Total	**1,004**	**9,912**	**156**

*See Appendices: Definitions

Table 28. Outbreaks by mode of transmission and aetiology, Queensland, 2025

Mode of transmission	Aetiology	No. of Outbreaks	No. ill	No. hospitalised
Foodborne / probable foodborne	Chemical - copper	1	19	0
	Ciguatera	4	9	1
	Clostridium perfringens	1	5	0
	Hepatitis E+	1	1	0
	Histamine	1	2	2
	Listeria monocytogenes	1	4	4
	Salmonella Chester	1	3	1
	Salmonella Havana+	1	17	2
	Unknown	2	49	1
	Sub Total	**13**	**109**	**11**
Environmental / probable environmental	Cryptosporidiosis	2	53	3
	Salmonella Wangata	1	2	2
	Sub Total	**3**	**55**	**5**
Waterborne	Cryptosporidiosis	1	**16**	**1**
Person-to-person	Adenovirus	1	17	0
	Hepatitis A	1	3	3
	Norovirus	54	1254	37
	Rotavirus	2	18	0
	Sapovirus	3	37	1
	Shigella (unspecified)	1	12	9
	Mixed aetiologies^	9	209	6
	Unknown	628	6159	57
	Subtotal	**699**	**7709**	**113**
Unknown	Adenovirus	2	6	0
	Giardia	1	3	0
	Norovirus	6	86	0
	Salmonella Saintpaul	1	24	8
	STEC O145:H28	1	3	2
	Unknown	277	1901	16
	Subtotal	**288**	**2023**	**26**
Total		**1,004**	**9,912**	**156**

^ 9 outbreaks with mixed aetiologies: norovirus detected in 6/9, rotavirus in 4/9, adenovirus in 2/9, sapovirus in 2/9, giardia in 2/9, astrovirus in 1/9, campylobacter in 1/9.

+ QLD case associated with an ongoing MJOI.

Foodborne disease outbreaks

Total outbreaks: 13

Total cases: 109 (30 laboratory confirmed)

Hospitalisations: 11 (10% of cases)

No deaths reported.

13 foodborne outbreaks investigated in Queensland associated with 109 cases of illness and 11 hospitalisations (Tables 27, 28, 29).

- 4 (31%) outbreaks had a bacterial aetiology (Table 29): *Listeria monocytogenes* (1), *Salmonella* Chester (1), *Salmonella* Havana (1) and *Clostridium perfringens* (1).
- 5 (38%) outbreaks were associated with marine toxins: Ciguatera (4), Histamine (1).
- A likely food vehicle was identified in 11 (85%) outbreaks.
- Outbreak settings (where food was consumed) included: private residences (5), schools (2), community (2), hospital (1), bakery (1), restaurant (1) and a catered function (1).

Salmonella was the confirmed aetiological agent in 2 outbreaks:

- One multi-jurisdictional outbreak of *Salmonella* Havana was epidemiologically and genomically linked to the consumption of contaminated alfalfa sprouts. A total of 102 cases were linked to this outbreak nationally, with specimen collection dates between 7 October and 29 December 2025. 17/102 cases were reported from QLD.
- One outbreak of *Salmonella* Chester (3 cases) was linked to the consumption of pork banh mi that was produced and sold from a bakery.

4 outbreaks (9 cases) were associated with eating fish containing ciguatoxins.

1 outbreak of histamine poisoning (2 cases) was associated with the consumption of tuna patties purchased from a seafood market. Issues around temperature and shelf life were identified.

1 outbreak of *L. monocytogenes* infection (4 cases) was investigated that was associated with the consumption of contaminated ready to eat chicken meat.

1 outbreak of suspected copper poisoning occurred among primary school students.

1 outbreak due to *Clostridium perfringens* (5 cases) was investigated in November associated with the consumption of birria tacos.

2 outbreaks of probable foodborne transmission were investigated where an aetiological agent and food vehicle was unable to be determined.

- One outbreak was associated with food consumed from a boarding school cafeteria (34 cases).
- One outbreak was associated with food consumed at a catered funeral wake (15 cases).

2 multi-jurisdictional outbreak investigations (MJOIs) were investigated during 2025 that included residents from QLD.

- Hepatitis E virus (1 case) - ongoing in 2026.
- *Salmonella* Havana (17 cases) were the causative agents of these outbreaks.

Table 29. Foodborne or probable foodborne outbreaks, Queensland, 2025

No.	Month	Aetiology	Total cases	Lab confirmed	Vehicle	Likely source	Setting	Evidence†
Bacterial								
1	Jul	*Listeria monocytogenes*	4	4	Chicken meat	Unknown	Hospital	M
2	Aug	*Salmonella* Chester	3	3	Pork Banh Mi	Unknown	Bakery	D
3	Oct	*Salmonella* Havana^	17	17	Alfalfa	Unknown	Community	M
4	Nov	*Clostridium perfringens*	5	5	Birria tacos	Meat	Restaurant	M
Chemical								
5	May	Copper toxicity	19	0	Cupcakes with gold dust icing	Copper	School	M
Marine Toxins								
6	May	Ciguatera	2	0	Red Throat Emperor	Fish	Private Residence	M
7	Jun	Ciguatera	2	0	Red Bass	Fish	Private Residence	M
8	Aug	Ciguatera	3	0	Green Jobfish	Fish	Private Residence	M
9	Nov	Ciguatera	2	0	Red Throat Emperor	Fish	Private Residence	D
10	Nov	Histamine	2	0	Tuna patties	Fish	Private Residence	M
Viral								
11	Oct	Hepatitis E^	1	1	Pork meat	Pork	Community	DM
Unknown								
12	Feb	Unknown	34	0	Unknown	Unknown	School	D
13	Jul	Unknown	15	0	Unknown	Unknown	Function	D

† D – Descriptive evidence implicating the suspected vehicle or suggesting foodborne transmission. M – Microbiological confirmation in suspect vehicle.

^ QLD cases associated with an ongoing MJOI.

Outbreak Spotlight: Chemical copper poisoning

An outbreak of gastrointestinal illness was reported in May among an early primary school class group. The children developed gastrointestinal symptoms including vomiting, abdominal cramps and nausea within ten minutes following the consumption of cupcakes that were provided to the group by a parent.

Eighteen children (median age 7 years) and 1 staff member who all consumed the cupcakes became unwell. Four children who did not consume the cupcakes remained well. The reported duration of symptoms was short (~ 15-30 minutes). No cases were hospitalised.

Two faecal specimens collected during the investigation tested negative for bacterial pathogens.

The cupcakes were prepared by a hobbyist who used gold dust sparkle icing as decoration. It was noted on inspection, that an excessive amount of gold dust icing had been applied to the cupcakes, though there were no clear product use instructions provided on the packaging. Eight initial samples were collected, which comprised both left-over food samples and ingredients from the hobby cupcake maker's

home (5 samples), and 3 control samples from retail. All samples underwent both microbiological and chemical testing.

Copper and zinc were detected within a gold dust sample collected from the household with concentrations found to be 20 times (copper) and 10 times (zinc) higher than a similar sample obtained from retail.

A further 16 retail samples were collected consisting of multiple varieties of metallic cake decoration including gold, copper, bronze and spumante colours. Chemical testing revealed variable results in terms of percentage copper by weight. Four metallic gold dust samples were considered to have high concentrations of copper detected (ranging 13.2%-47.7% w/w).

Toxicology results and reported symptoms suggested copper ingestion was the probable cause of illness among cases in this outbreak.

Inadequate product labelling and instructions for use were considered as contributing factors for this outbreak.

Outbreak Spotlight: *Listeria monocytogenes*

Three cases of invasive listeriosis and one case of non-invasive *Listeria* infection were reported from South-East Queensland during July-October 2025. *Listeria monocytogenes* (Lm) serotype 1/2a,3a, binary gene type 58, MLST 321 was detected in blood cultures from two cases, a placental swab for one case and a urine specimen for the 4th case. The Lm isolates from these specimens were genomically highly related on whole genome sequence phylogenetic analysis.

All four cases had recent admissions to three different private hospitals during their respective exposure periods. Review of hospital food histories showed consumption of chicken sandwiches and/or chicken salad was frequently reported among these cases. A specific food manufacturer in Queensland was identified as supplying ready-to-eat cooked chicken meat to two of the three hospitals. This manufacturer supplied a range of meat products to multiple food businesses, hospitals, wholesale distributors and other businesses in South-East Queensland and Northern NSW.

Food and environmental sampling were conducted at the hospital kitchens and the manufacturer. A total of 28 samples (12 foods, 16 environmental swabs) collected from two hospitals and from the manufacturer tested positive for Lm. Seven food isolates (including two samples from unopened ready-to-eat chicken meat) were sequenced and found to be genomically highly related to the case isolates.

Investigation of the manufacturer identified multiple food safety issues relating to hygiene, maintenance, lack of record keeping, temperature checks and production processes. The business's food licence was temporarily suspended with consumer and trade level recalls conducted during this period.

Outbreak Spotlight: Ciguatera Poisoning

Four outbreaks of ciguatera poisoning were investigated in 2025 which resulted in 9 cases of illness and one hospitalisation. Two to three individuals were affected in each outbreak with incubation periods ranging from 1 to 12 hours (median 7 hours).

The implicated fish species included red throat emperor (2 outbreaks), red bass (1 outbreak) and green jobfish (1 outbreak). The fish were purchased from seafood vendors in three outbreaks, one of which was an overseas market in Fiji where the fish was frozen and brought into Australia (red bass).

Ciguatoxin was detected in left-over fish collected from all three of these outbreaks. The remaining outbreak was a private catch. No left-over fish was available for toxin analysis.

Multi-jurisdictional outbreak investigations

Total outbreaks: 4

Total cases: 133 nationally, 23 (17%) from QLD

Hospitalisations: 38 (29% of cases) nationally

No deaths reported.

Queensland participated in 4 multi-jurisdictional outbreak investigations (MJOI) in 2025 (Table 30).

Table 30. Multi-jurisdictional outbreaks investigated during 2025

	Organism	National		Queensland		
		Cases	Hospitalised	Cases	Hospitalised	Deaths
MJOI 2025-001	Hepatitis A	6	4	1	1	0
MJOI 2025-002	Hepatitis E^	15	13	4	2	0
MJOI^ (Tasmania)	*Salmonella* Enteritidis	10	1	1	1	0
MJOI 2025-003	*Salmonella* Havana	102	20	17	2	0
TOTAL		**133**	**38**	**23**	**6**	**0**

^ includes all outbreak cases from Dec 2024-Mar 2026

Outbreak Spotlight: *Salmonella* Havana MJOI

A multi-jurisdictional outbreak investigation was commenced in November, identifying 102 cases of genomically related *S*. Havana infection across seven jurisdictions. Initial investigations commenced in Queensland following a local increase in *S*. Havana notifications in October, with interviews showing a higher-than-expected consumption of alfalfa sprouts among cases.

PHUs commenced retail sampling of alfalfa sprouts across Queensland, while at this same time other jurisdictions, notably NSW, began to report increases in *S*. Havana counts. The MJOI was endorsed by CDNA on 10 November 2025, with Queensland Health as lead agency.

Cases were reported from NSW (41), VIC (34), QLD (17), SA (4), ACT (2), NT (2) and TAS (2), with dates of specimen collection recorded between 07 October and 29 December 2025. The median age of a confirmed case was 54 years (range, <1-100 years) and 64% were female. The reported hospitalisation rate was 20%. No deaths were reported.

S. Havana was isolated from 12/26 Queensland retail alfalfa samples collected between 3 and 6 November. These positive retail samples had been grown and packaged by an interstate sprout producer. Interstate regulators undertook a site inspection, including extensive sampling of alfalfa seeds, alfalfa sprouts, and irrigation water, and swabbing of the production environment.

In total, 12 environmental samples, 1 alfalfa husk sample and 1 composite irrigation water sample tested positive for *S.* Havana. Phylogenetic analysis showed a high degree of genomic similarity between clinical isolates from around Australia, isolates from the alfalfa production environment and those from retail samples collected in Queensland.

Regulators issued a prohibition order following isolation of *Salmonella* from the production environment. Once clearance testing had determined the facility was clear of contamination, the prohibition order was lifted and a mandated test and hold clearance program was instituted.

No further detections were reported, with the clearance protocol ceasing on 31 January 2026. Additional traceback of the implicated seed batch identified it had been supplied to the sprout producer from an interstate supplier. The alfalfa producer was reported to be the sole recipient of this seed batch, with remnant seed quarantined at the time of the investigation being returned to the seed supplier.

In support of the investigation, both consumer and trade level recalls were initiated for a variety of alfalfa products produced by the sprout producer, in addition to the delivery of coordinated public health messaging.

Non-foodborne disease outbreaks

Total outbreaks: 991

Total cases: 9,803

Hospitalisations: 145 (1.5% of cases)

Waterborne transmission: 1 (16 cases)

Environmental / probable environmental transmission: 3 (55 cases).

Excluding waterborne and environmental transmission events, there were 987 non-foodborne related outbreaks comprising at least 9,732 cases with 139 hospitalisations (transmission by person to person or unknown).

Aetiology identified in 85 (8.5%) outbreaks (Table 31):

- 77/85 (91%) with viral aetiologies
- 4 (5%) with parasitic aetiologies
- 4 (5%) with bacterial aetiologies

Most frequently reported outbreak settings:

Childcare centres: 832 (84%):

- Frequently reported throughout the year, with peaks observed in both February and November (Figure 25).
- Number of reported outbreaks among childcare settings has been steadily increasing during the past decade (Figure 26).

Aged care facilities: 125 (13%).

Schools: 5 (<1%).

The median number of cases per outbreak was 10 cases (range 2-107 cases):

- Childcare centres: median 6 cases (range 2-72 cases).
- Aged care facilities: median 10 cases (range 2-107 cases).
- Schools: median 16 cases (range 4-40 cases).

Table 31. Non-foodborne / waterborne / environmental transmission outbreaks by aetiology and setting 2025

Aetiology	Setting	No. of outbreaks	No. ill	No. hospitalised
Bacterial				
Salmonella Saintpaul	Community	1	24	8
Salmonella Wangata	Hospital	1	2	2
Shigella spp	Community	1	12	9
STEC O145:H28	Community	1	3	2
Parasitic				
Cryptosporidiosis	Aquatic facility	2	53	3
	School	1	16	1
Giardia	Child care	1	3	0
Viral				
Adenovirus	Child care	3	23	0
Hepatitis A	Cruise ship	1	3	3
Norovirus	Aged care	42	1,066	30
	Camp	1	19	0
	Catered function	2	43	0
	Child care	9	127	6
	Hospital	3	24	0
	Correctional facility	1	24	1
	Resort	1	20	0
	Restaurant	1	17	0
Rotavirus	Aged care	1	6	0
	Child care	1	12	0
Sapovirus	Aged care	1	10	1
	Child care	2	27	0
Mixed viral*	Aged care	2	56	0
	Child care	6	146	3
Unknown				
	Aged care	79	781	18
	Camp	1	3	0
	Child care	810	7,075	54
	Function	1	40	0
	Hospital	2	9	0
	Other	5	48	1
	Resort	1	5	
	Restaurant	1	9	0
	School	4	77	0
	School camp	1	13	0
Mixed (bacterial, viral, parasitic)	Community	1	7	3
Total		**991**	**9,803**	**145**

**2 outbreaks norovirus and adenovirus; 2 outbreaks with norovirus and rotavirus; 1 outbreak with norovirus and astrovirus; 1 outbreak with norovirus and sapovirus; 1 outbreak with astrovirus and sapovirus; and 1 outbreak with rotavirus and giardia.*

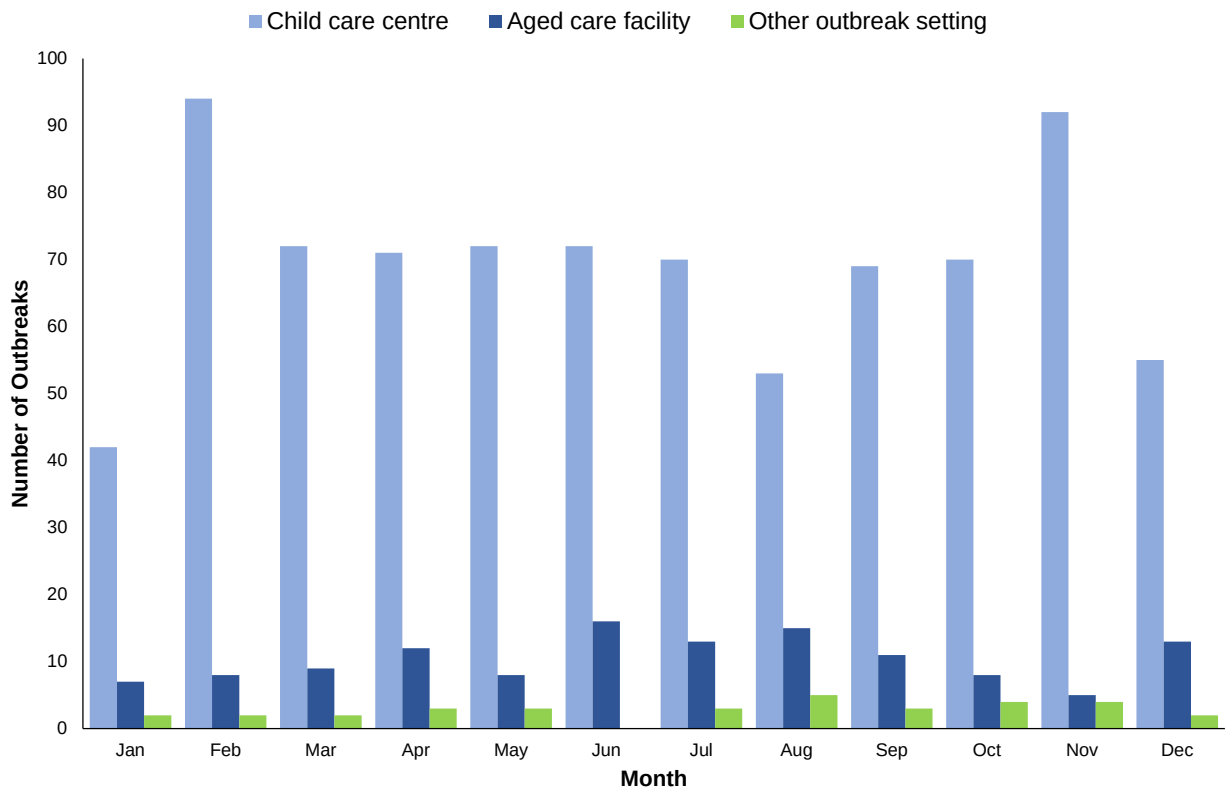


Figure 25. Non-foodborne outbreaks reported by month of onset of index case and setting, Queensland, 2025

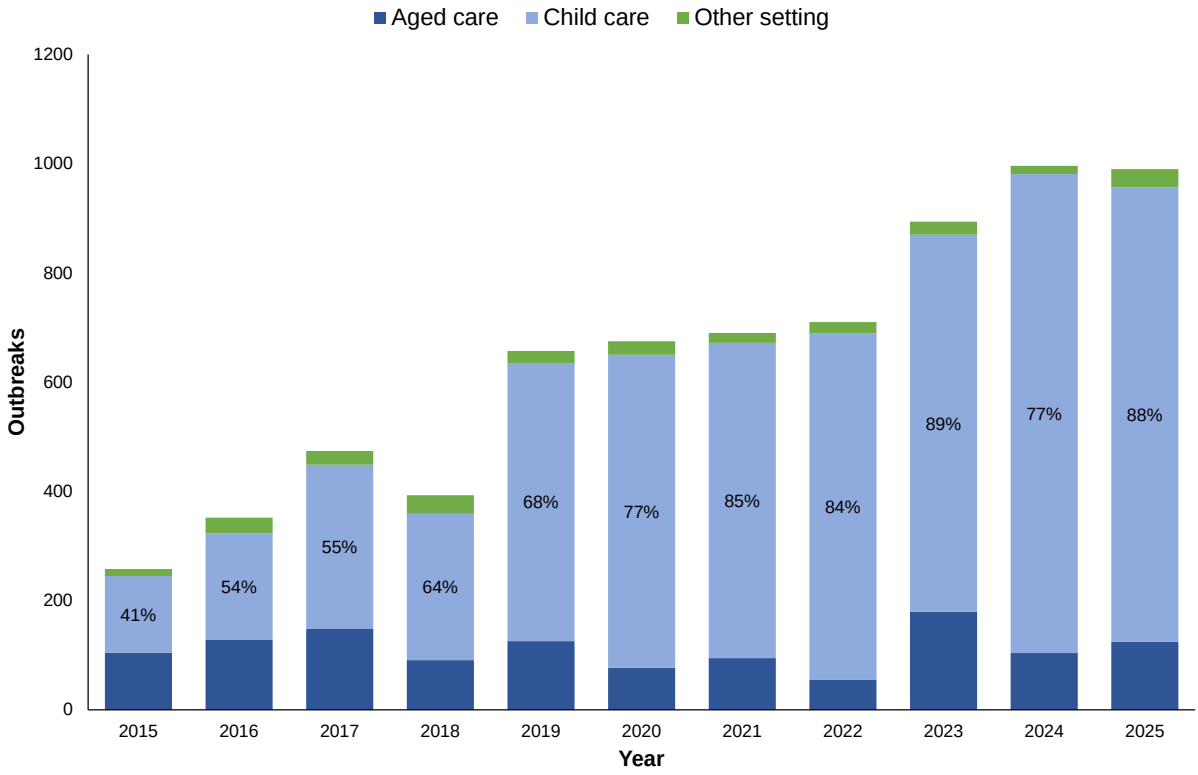


Figure 26. Non-foodborne outbreaks by setting and year, Queensland, 2015-2025

Environmental transmission outbreaks

3 outbreaks of environmental / probable environmental transmission comprising 55 cases of illness.

- 2 outbreaks of cryptosporidiosis comprising 53 cases (6 laboratory confirmed) were associated with aquatic facilities.
- 1 outbreak of *Salmonella* Wangata infection was associated with 2 hospital inpatients: Isolates from both cases and from a sample of vacuum cleaner dust collected from the room of one case were highly related on whole genome sequencing.

Waterborne Outbreaks

1 outbreak due to waterborne transmission was investigated comprising 16 cases of illness (see below)

Outbreak Spotlight: *Cryptosporidium*

An outbreak of cryptosporidiosis was investigated in September 2025, linked to a school (including an associated early learning centre).

Sixteen laboratory confirmed infections were reported. These comprised 8 eight students (5 males, 3 females, median age 11 years, range 3-14 years), 7 staff and 1 parent (median age 28 yrs, range 24-53 years). Dates of illness onset ranged between 30 August and 25 September. School attendance data suggested many additional cases may have occurred within the student cohort. One confirmed case was hospitalised.

An environmental health inspection with sampling was undertaken. This focused on water treatment and supply as rainwater tanks were used to hold drinking water. Eleven water samples were collected from sites around the school. These samples comprised both treated and untreated rainwater, bore water and dam water.

Cryptosporidium oocysts were identified in samples from 2 rainwater tanks. The first was a treated potable rainwater sample that supplied drinking fountains near the school tuck shop and the second was a treated (non-potable) water sample used for garden irrigation and toilet flushing. Review of the water filtration system showed it was inadequate to remove *Cryptosporidium* oocysts, with residual chlorine in potable water sources below recommended levels.

The school followed public health advice to disconnect the reticulated water system and switch to the use of bottled water until such time as the system could be remedied. An independent water consultant undertook a comprehensive review, providing an action plan for the school. Following an upgrading of the school's water system, repeat sampling identified no further detections of *Cryptosporidium*.

Outbreak Spotlight: *Salmonella* Saintpaul

A community-wide outbreak investigation was commenced in November following a significant increase in notified cases of *Salmonella* Saintpaul in a rural local government area.

A total of 24 cases of *S.* Saintpaul with specimen collection dates between 11 November 2025 and 10 January 2026 were reported. The median age was 18.5 years (range <1-69 years) and 63% were female. All 24 case isolates were genomically highly related on phylogenetic analysis.

Cases were interviewed with a specifically developed questionnaire that included a wide range of fruit and vegetables as well as the standard risk factor information for *Salmonella*. The epidemiological investigation did not identify any foods, food venues or other potential exposures that were common to

cases. However, it was noted that cases were either residents or recent visitors to a particular town within the local government area.

Given the rural environment and ongoing reporting of cases, multiple water samples were collected from pump stations and end point taps for microbiological testing. All samples tested negative for *E. coli* and *Salmonella*. Review of residual chlorine records during the outbreak period did not identify any aberrant levels in the reticulated water system.

No food sampling was conducted as no potential food vehicles were identified from the epidemiological investigation.

The source of infection was unable to be identified. *S.* Saintpaul notifications in this region returned to usual background levels in January 2026.

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Appendices

Abbreviations

CDNA	Communicable Diseases Network Australia
cgMLST	core genome multi-locus sequence type
FSANZ	Food Standards Australia New Zealand
HEV-3	Hepatitis E Virus genotype 3
HHS	Hospital Health Service
HUS	Haemolytic Uraemic Syndrome
MDU	Microbiological Diagnostic Unit, Doherty Institute for Infection and Immunity
MDR	Multi-drug resistant
MJOI	Multijurisdictional outbreak investigation
MLVA	Multilocus Variable Number Tandem Repeats Analysis
MLST	Multilocus sequence type
MSM	Men who have sex with men
NOCs	Notifiable Conditions System
NNDSS	National Notifiable Diseases Surveillance System
PCR	Polymerase chain reaction (nucleic acid amplification)
PEHRL	Public and Environmental Health Reference Laboratories
PHLN	Public Health Laboratory Network
SNP	Single Nucleotide Polymorphism
STEC	Shiga toxin-producing E. coli
WGS	Whole genome sequencing
XDR	Extensively drug resistant

Data Sources and Methods

Incidence data are derived from statutorily notified cases of infection collated by the Public Health Intelligence 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 sixteen 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, Haemolytic Uraemic Syndrome (HUS) and *Vibrio parahaemolyticus*.

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 2025 and 31 December 2025. Notifications were collated and analysed using Microsoft Excel for Office 365. National data was sourced from the National Notifiable Diseases Surveillance System (NNDSS)[3]. Notification data extracted for this report may have been adjusted since the time of extraction. However, any subsequent minor changes to the notification numbers would not substantially affect the overall trends and patterns.

Crude notification rates were calculated using data derived from the Australian Bureau of Statistics mid-year estimated resident population figures for a single year between 2016 and 2025 as the denominator[2,4,5]. The mid-year estimated resident population for 2022 was used to calculate crude notification rates associated with 5-year (2020-2024) means.

Serotype and genotype data were obtained from the Public and Environmental Health Reference Laboratory, Queensland Health. Outbreak data were obtained from the OzFoodNet Gastrointestinal Illness Outbreak Register, Public Health Intelligence Branch, Queensland Department of Health.

Definitions

Cluster: 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.

Outbreak: 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.

Foodborne outbreak: The occurrence of two 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, invasive listeriosis).

Probable foodborne outbreak: An incident where two 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).

Waterborne outbreak: The occurrence of two or more cases of a similar illness after consumption of water from a common source and analytical epidemiological evidence and/or microbiological evidence implicates the drinking water supply as the source of illness. This does not include outbreaks associated with accidental consumption of water during recreational water exposures (environmental transmission).

Probable waterborne outbreak: The occurrence of two or more cases of a similar illness after consumption of water from a common source and compelling descriptive epidemiological evidence implicates the drinking water supply as the source of illness. This does not include outbreaks associated with accidental consumption of water during recreational water exposures (environmental transmission).

Zoonotic outbreak: The occurrence of two or more cases of a similar illness after exposure to an animal(s) and analytical epidemiological evidence and/or microbiological evidence implicates the animal(s) as the source of illness.

Environmental outbreak: An incident where two or more persons experience a similar illness following exposure to a contaminated environment and epidemiological evidence and/or microbiological evidence implicates a specific environmental source as the cause of illness. Includes recreational exposure to water.

Probable Environmental outbreak: An incident where two or more persons experience a similar illness following exposure to a contaminated environment and compelling descriptive epidemiological evidence identifies a specific environmental source as the suspected cause of illness, but the exact source of contamination is unknown. Includes recreational exposure to water.

Annual notifications of foodborne pathogens

Table A1. Annual notifications of potential foodborne pathogens/conditions, Queensland, 2016-2025 by year of onset

Pathogen/Condition	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
Botulism	0	0	0	0	0	0	0	0	1	0
Campylobacter	7,200	7,628	8,302	9,151	7677	9,826	9,517	9603	9,016	9,536
Cholera	0	0	0	0	0	0	1	0	1	1
Ciguatera	38	15	15	21	13	12	19	3	6	14
Cryptosporidium	2,368	1,288	1,068	724	672	569	571	1459	6,178	704
Hepatitis A	30	26	43	25	15	9	28	43	30	44
Hepatitis E	8	8	8	3	6	0	2	5	3	2
HUS*	4	3	4	3	4	1	5	4	3	2
Listeria	14	18	14	10	6	6	14	11	9	6
Paratyphoid	8	7	6	15	2	0	5	8	15	6
Salmonella	4,780	4,231	3,482	3,815	4124	3988	3251	3218	3,899	3,907
Shigella	181	235	450	609	280	61	229	456	501	620
STEC**	24	26	25	30	30	30	36	42	56	54
Typhoid	19	18	32	25	10	5	16	45	29	32
*V.parahaemolyticus****	-	-	-	-	-	-	-	-	-	19
*Yersinia*****	790	686	770	691	580	526	704	964	1,101	819

* HUS: Haemolytic uraemic syndrome ** STEC: Shiga toxin producing *Escherichia coli*

*** *Vibrio parahaemolyticus* became notifiable in May 2025 **** *Y. enterocolitica*

Table A2. Crude notification rates per 100,000 population for potential foodborne pathogens/conditions by year of onset, Queensland, 2016-2025

Pathogen/Condition	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
Botulism	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Campylobacter	148.6	154.8	165.8	179.8	148.6	188.4	178.9	175.9	161.5	168.2
Cholera	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ciguatera	0.8	0.3	0.3	0.4	0.3	0.2	0.4	0.1	0.1	0.2
Cryptosporidium	48.9	26.1	21.3	14.2	13.0	10.9	10.7	26.7	110.6	12.4
Hepatitis A	0.6	0.5	0.9	0.5	0.3	0.2	0.5	0.8	0.5	0.8
Hepatitis E	0.2	0.2	0.2	0.1	0.1	0.0	0.0	0.1	0.1	0.0
HUS*	0.1	0.1	0.1	0.1	0.1	0.0	0.1	0.1	0.1	0.0
Listeria	0.3	0.4	0.3	0.2	0.1	0.1	0.3	0.2	0.2	0.1
Paratyphoid	0.2	0.1	0.1	0.3	0.0	0.0	0.1	0.1	0.3	0.1
Salmonella	98.7	85.9	69.5	75.0	79.8	76.5	61.1	58.9	69.8	68.9
Shigella	3.7	4.8	9.0	12.0	5.4	1.2	4.3	8.4	9.0	10.9
STEC**	0.5	0.5	0.5	0.6	0.6	0.6	0.7	0.8	1.0	1.0
Typhoid	0.4	0.4	0.6	0.5	0.2	0.1	0.3	0.8	0.5	0.6
*Yersinia****	16.3	13.9	15.4	13.6	11.2	10.1	13.2	17.7	19.7	14.4

* HUS: Haemolytic uraemic syndrome ** STEC: Shiga toxin producing *Escherichia coli* *** *Y. enterocolitica*