CIPARS Human Surveillance Component

Salmonella and *Campylobacter* AMR – 2025 Results

Presented by Kathryn McDonald, MPH

World Antimicrobial Resistance Awareness Week

November 19, 2026

Agenda

- Background
- *Salmonella*
- *Campylobacter*
- Questions

Methods for AMR evaluation

Primary Method

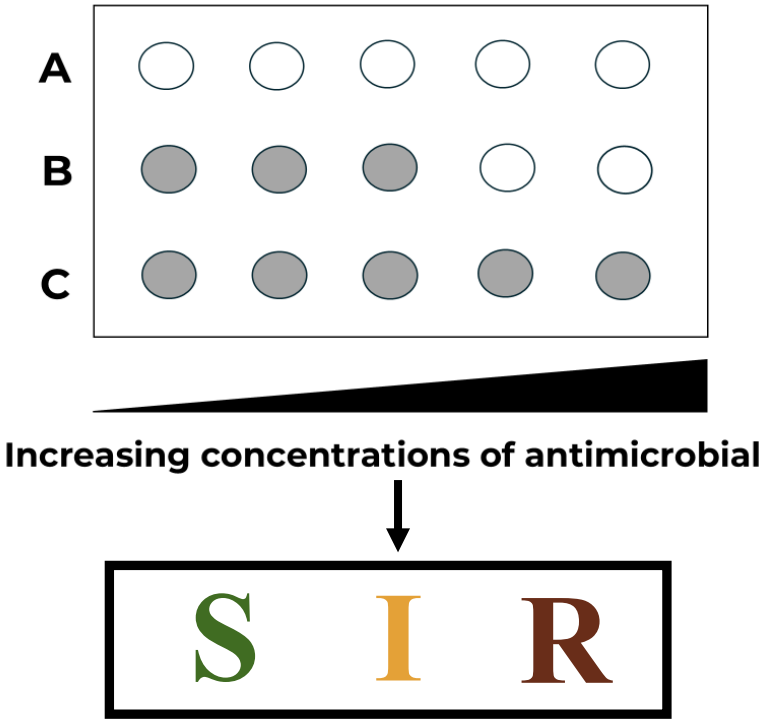
Whole Genome Sequencing (WGS)



Predicted phenotypes based on the resistance genes and/or mutations detected

Supplementary Method

Broth Microdilution



Methods for AMR Interpretation

AMR Data

(obtained from WGS or Broth Microdilution)

For **CIPROFLOXACIN,** genotypic AMR prediction cannot discriminate between resistant and intermediate using the resistance isolates based on detected resistance genes and mutations.

Report as not susceptible

I/R

For **ALL OTHER VALIDATED ANTIMICROBIALS,** genotypic AMR prediction can distinguish susceptible/intermediate from resistant isolates based on detected resistance genes and mutations.

Report as resistant

R

NOTE: “not susceptible to ciprofloxacin” is referred to as “resistant to ciprofloxacin” for the remainder of the presentation

AMR descriptions and colour gradient used throughout presentation

Description	Resistance (%)	Gradient
20 or fewer isolates	Any %	
Rare	< 0.1%	
Very low	0.1% to 1%	
Low	>1% to 10%	
Moderate	>10% to 20%	
High	>20% to 50%	
Very High	>50% to 70%	
Extremely High	>70%	

https://www.efsa.europa.eu/en/efsajournal/pub/7867

AMR reporting definitions

- Multidrug Resistant (MDR)
  - Resistance to three or more classes of antimicrobials

- Extensive Drug Resistant (XDR)*
  - Typhoidal *Salmonella*:
    - Resistance to:
      - Ceftriaxone
      - Ciprofloxacin
      - Trimethoprim-sulfamethoxazole
      - Ampicillin
  - Non-typhoidal *Salmonella*:
    - Resistance to:
      - Azithromycin
      - Ceftriaxone
      - Ciprofloxacin
      - Trimethoprim-sulfamethoxazole
      - Ampicillin

*XDR measures are only reported for *Salmonella* AMR data

Human *Salmonella*

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

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Most non-typhoidal *Salmonella* infections do NOT require treatment with antimicrobials.

- Non-typhoidal *Salmonella* have an animal reservoir and typhoidal *Salmonella* do not
- Non-typhoidal *Salmonella* infections most commonly cause self-limiting diarrhea
  - Treatment with antimicrobials is not required or recommended
- Treatment with antimicrobials is considered:
  - When clinical signs are severe or prolonged
    - >6 diarrheal episodes/day, bloody diarrhea, diarrhea lasting >1 week, persistent fever
  - When patient is immunocompromised
  - When patient is at increased risk for invasive infection
  - Culture and susceptibility testing directed treatment options include ciprofloxacin, ceftriaxone, azithromycin, trimethoprim-sulfamethoxazole or amoxicillin

bugsanddrugs.org/CFF1EDAF-526D-4B32-852A-25E3E7F1872E
IDSA 2017 Clinical Practice Guidelines for the Diagnosis and Management of Infectious Diarrhea

Invasive *Salmonella* infections require treatment with antimicrobials.

- Typhoidal *Salmonella* infections most commonly cause bloodstream infections
- Invasive infections including bloodstream infections can occur with non-typhoidal *Salmonella* infections, but are less common than gastrointestinal infections
  - Treatment with antimicrobials is required
  - Culture and susceptibility testing directed treatment options include ceftriaxone, ciprofloxacin, azithromycin, ampicillin or trimethoprim-sulfamethoxazole

bugsanddrugs.org/67b9e5cb-60f4-4b35-8581-374bd4c4cdbb
IDSA 2017 Clinical Practice Guidelines for the Diagnosis and Management of Infectious Diarrhea

Salmonella **has the highest incidence rate of the enteric pathogens tracked by NESP.**

- Incidence rates of Canadians with *Salmonella* in 2025

	2025 Incidence Rates* (cases/100,000 population)
Total *Salmonella*	16.64
Non-typhoidal *Salmonella*	15.34
Typhoidal *Salmonella*	1.18

*2025 incidence rates are preliminary and subject to change with final validation of the data

Source of data – National Enteric Surveillance Program (NESP) - Canada.ca

CIPARS enhanced passive human *Salmonella* surveillance reports temporal and regional variation in the frequency of AMR.

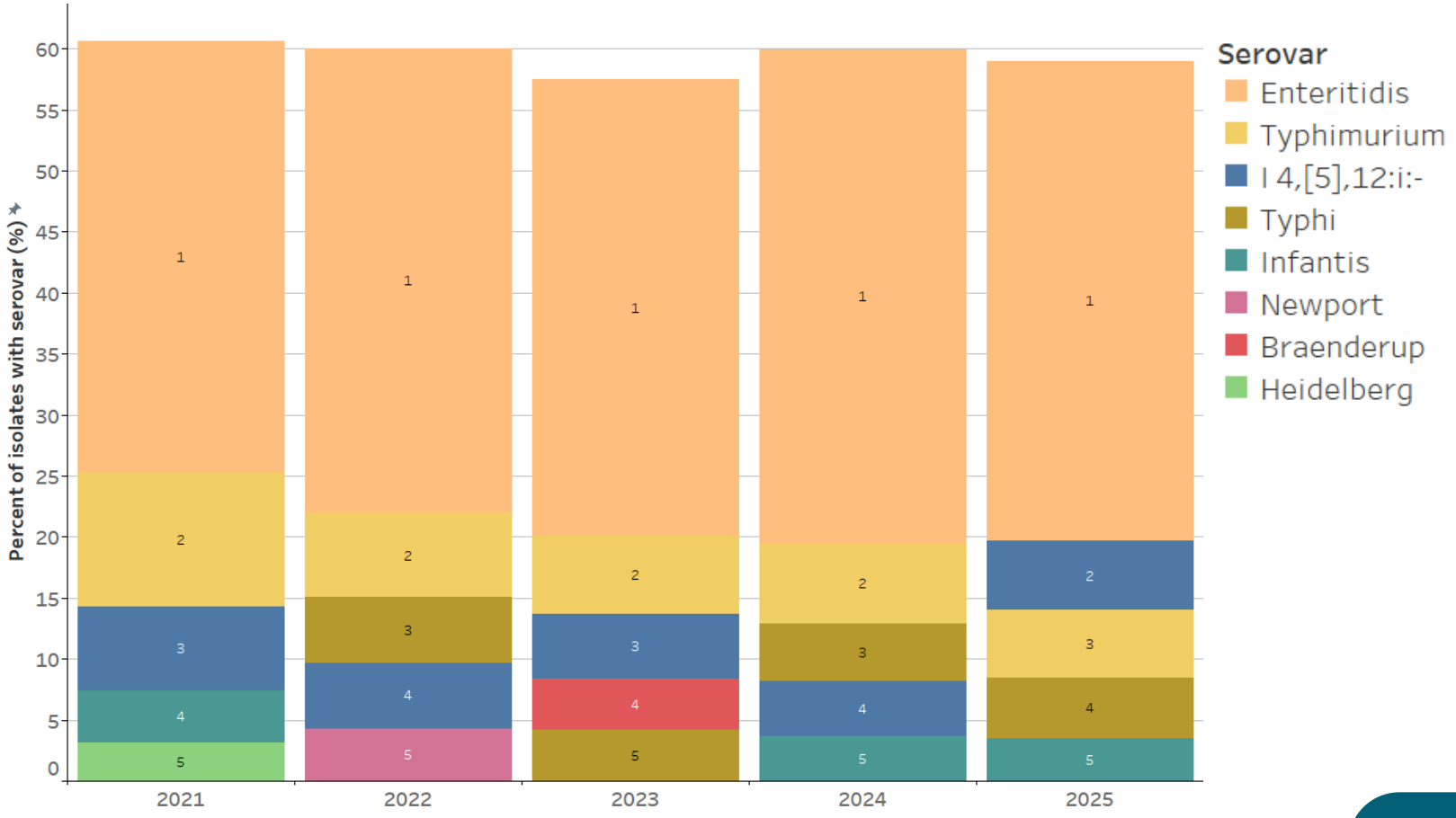
- Reporting of *Salmonella* infections is mandatory through laboratory notification of reportable diseases to the National Notifiable Disease Reporting System
  - However, forwarding of *Salmonella* isolates to provincial reference laboratories is voluntary and passive

- Isolates undergo whole genome sequencing
  - Predictive serotyping with SISTR
  - AMR prediction using StarAMR
    - Validated for 14 antimicrobials in 11 antimicrobial classes (2021 to present)

- Data from 2021-2025 are presented

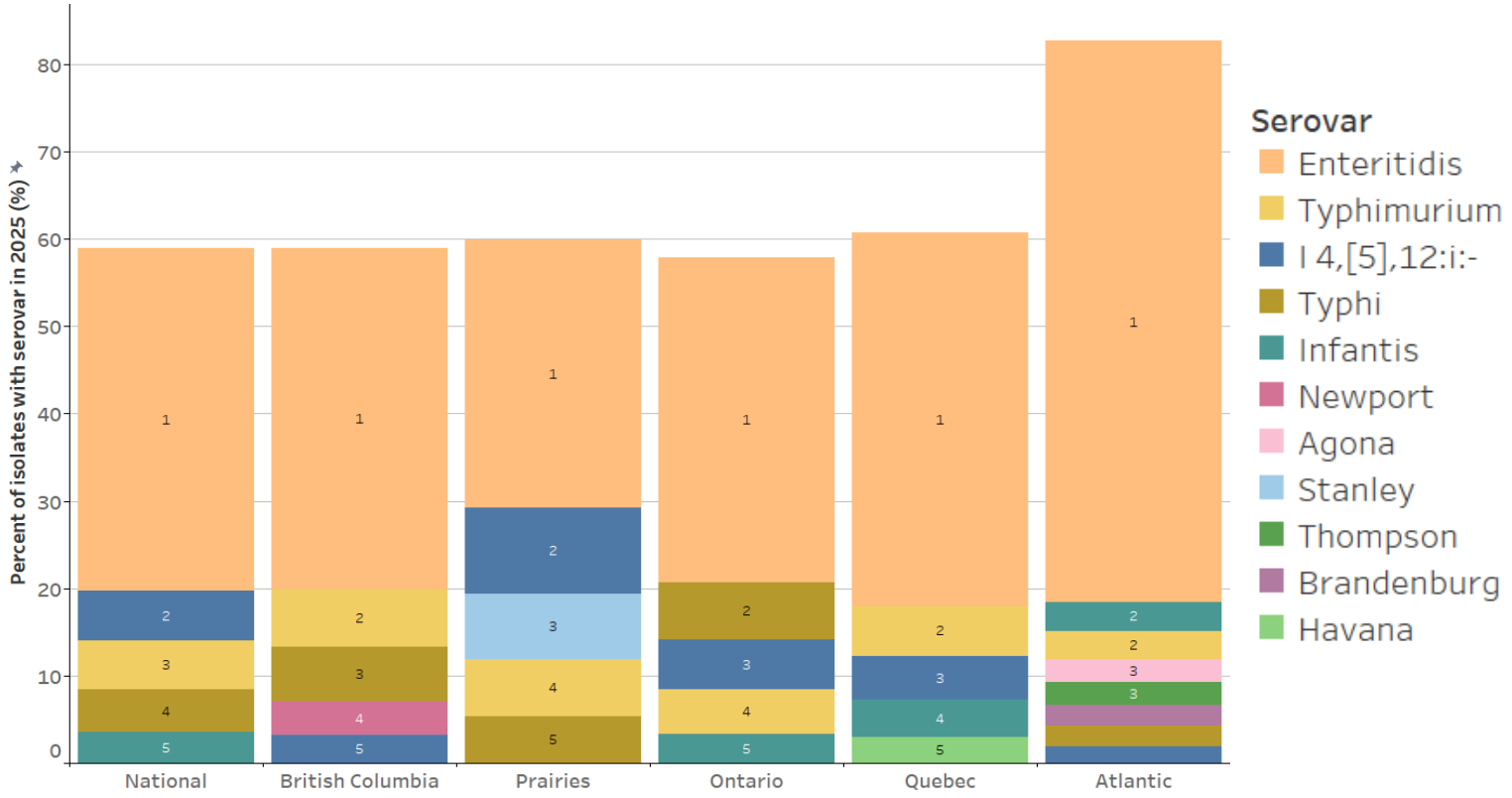
S. Enteritidis has been the top serovar nationally since 2005; ranking of other serovars varied from year to year.

- In 2025, 39% of the isolates were *S.* Enteritidis
- There are temporal differences in the frequency of serovars



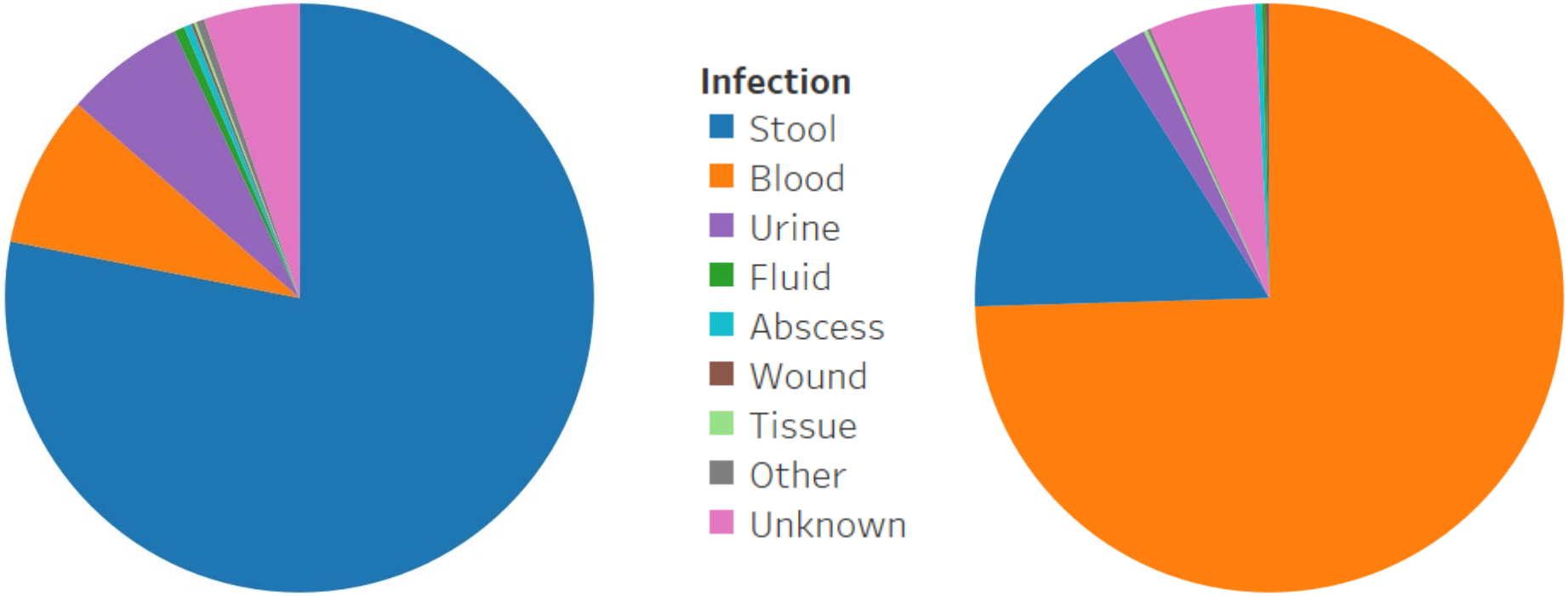
S. Enteritidis was consistently the top serovar in all regions in 2025; ranking of other serovars varied from region to region.

- *S.* Enteritidis was the top serovar in all regions in 2025
- There are regional differences in the frequency of serovars



Non-typhoidal *Salmonella* are generally from non-invasive infections, whereas typhoidal *Salmonella* are generally from invasive infections.

- Non-typhoidal *Salmonella* predominantly from gastrointestinal infections (78% stool in 2025)
- Typhoidal *Salmonella* predominantly from bloodstream infections (75% blood in 2025)



More *Salmonella* invasive blood stream infections in males than females.

Distribution of sex and sample types in human *Salmonella* cases from 2025

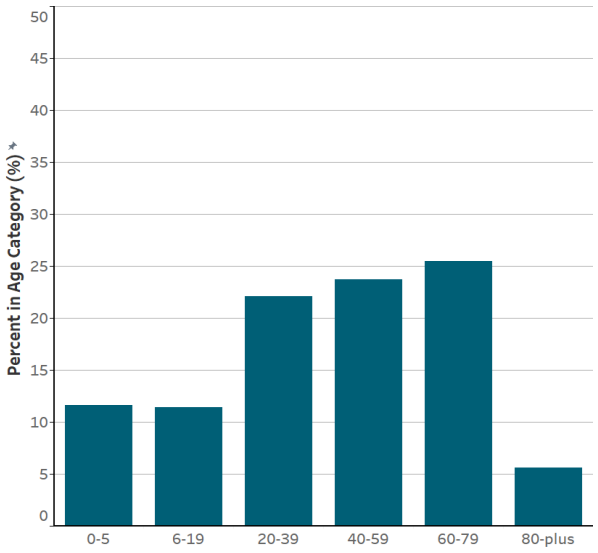
Salmonella	Sex	Sample Types			
		All samples	Stool	Blood	Urine
Non-typhoidal	All cases	93%	78%	8%	7%
	Female	53%	53%	40%	73%
	Male	46%	46%	59%	26%
Typhoidal	All cases	7%	17%	75%	2%
	Female	45%	45%	47%	30%*
	Male	54%	55%	52%	70%*

Note – unknown and other sample types, and unknown sexes are not shown
* - Less than 20 isolates

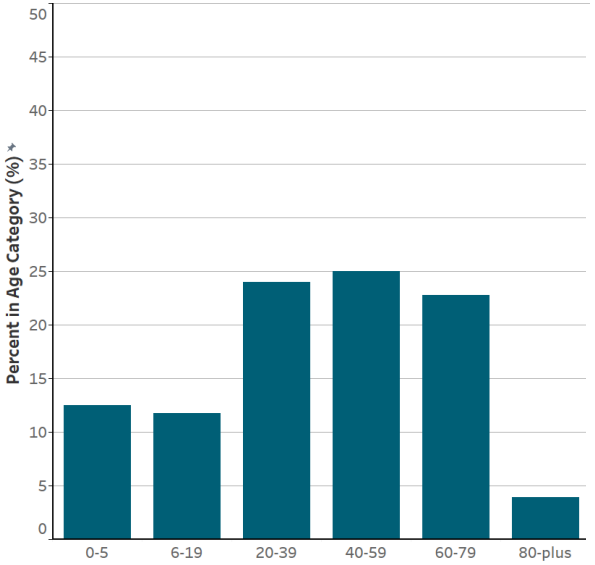
More non-typhoidal *Salmonella* bloodstream and urinary tract infections in people over 60 years of age.

Distribution of age categories and sample types in human non-typhoidal *Salmonella* cases from 2025

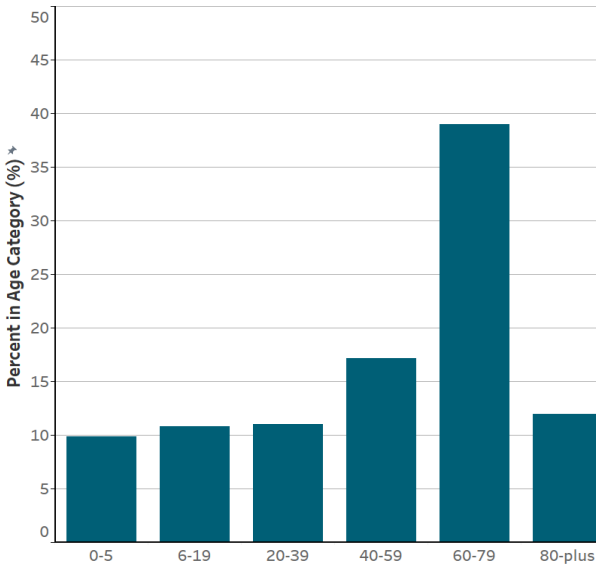
All sample types



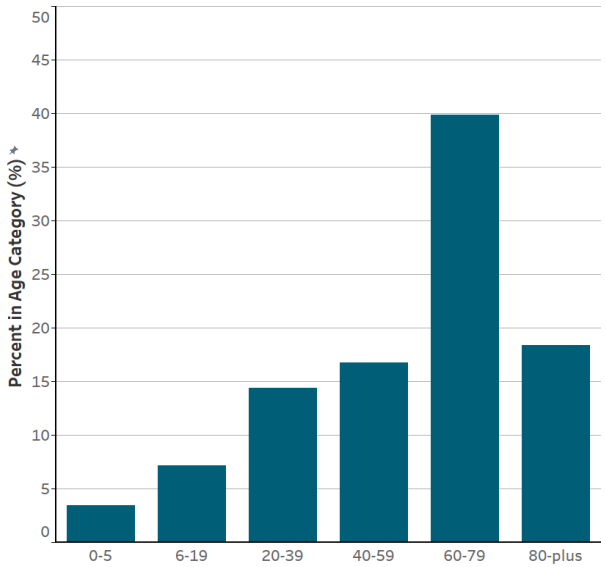
Stool



Blood



Urine

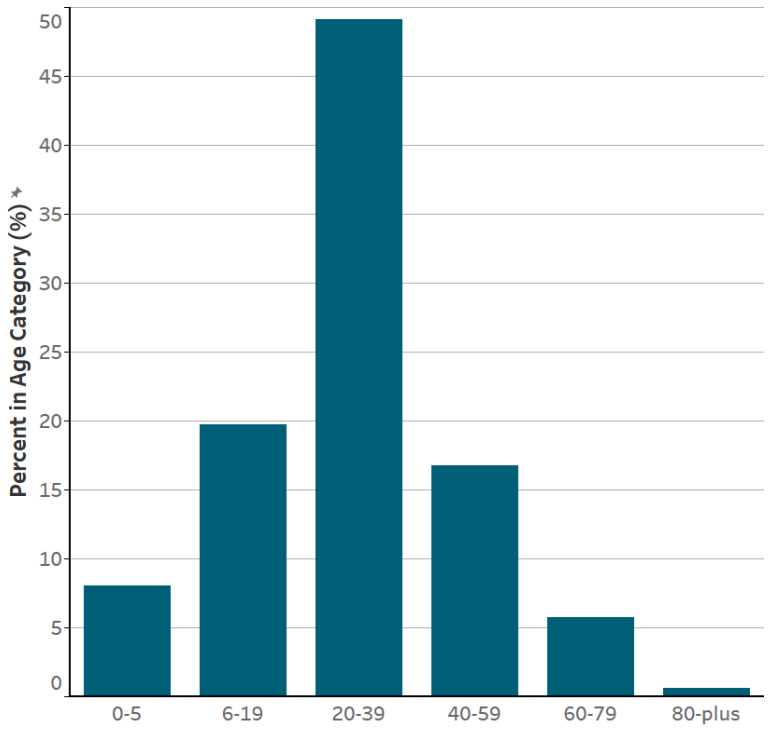


Note – unknown and other sample types, and unknown ages are not shown

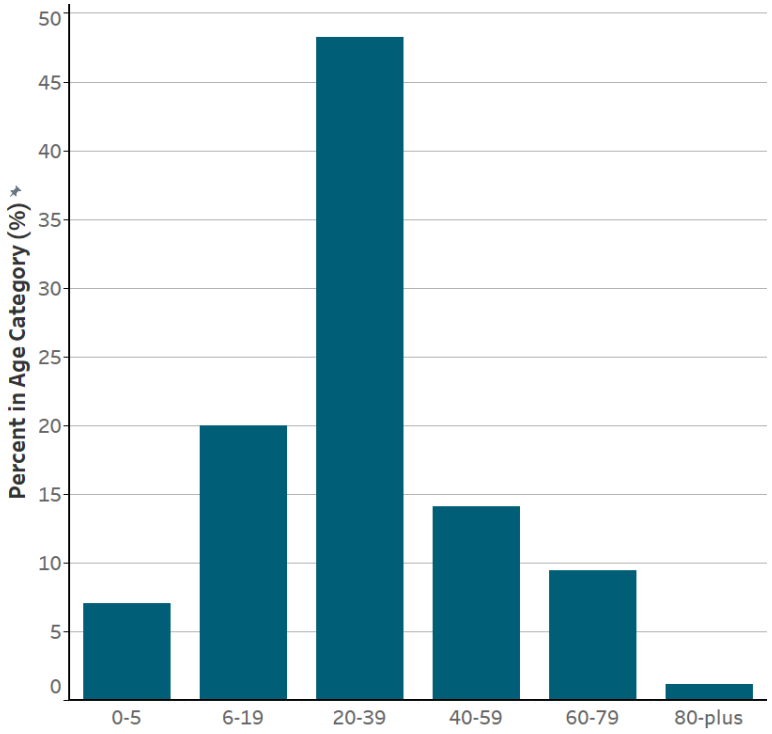
More typhoidal *Salmonella* infections in people 20 to 39 years of age.

Distribution of age categories and sample types in human typhoidal *Salmonella* cases from 2025

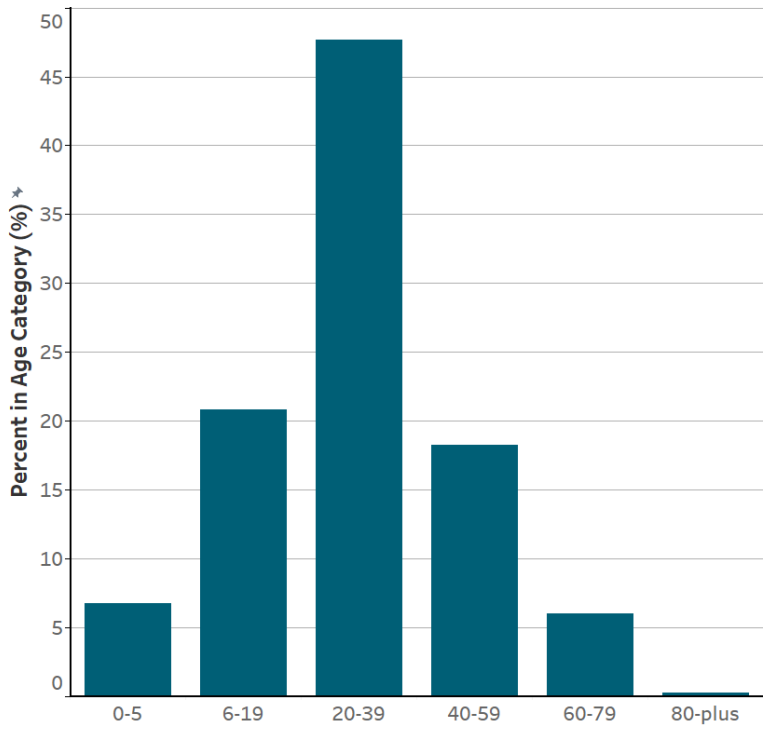
All sample types



Stool



Blood



Note – unknown and other sample types, and unknown ages are not shown

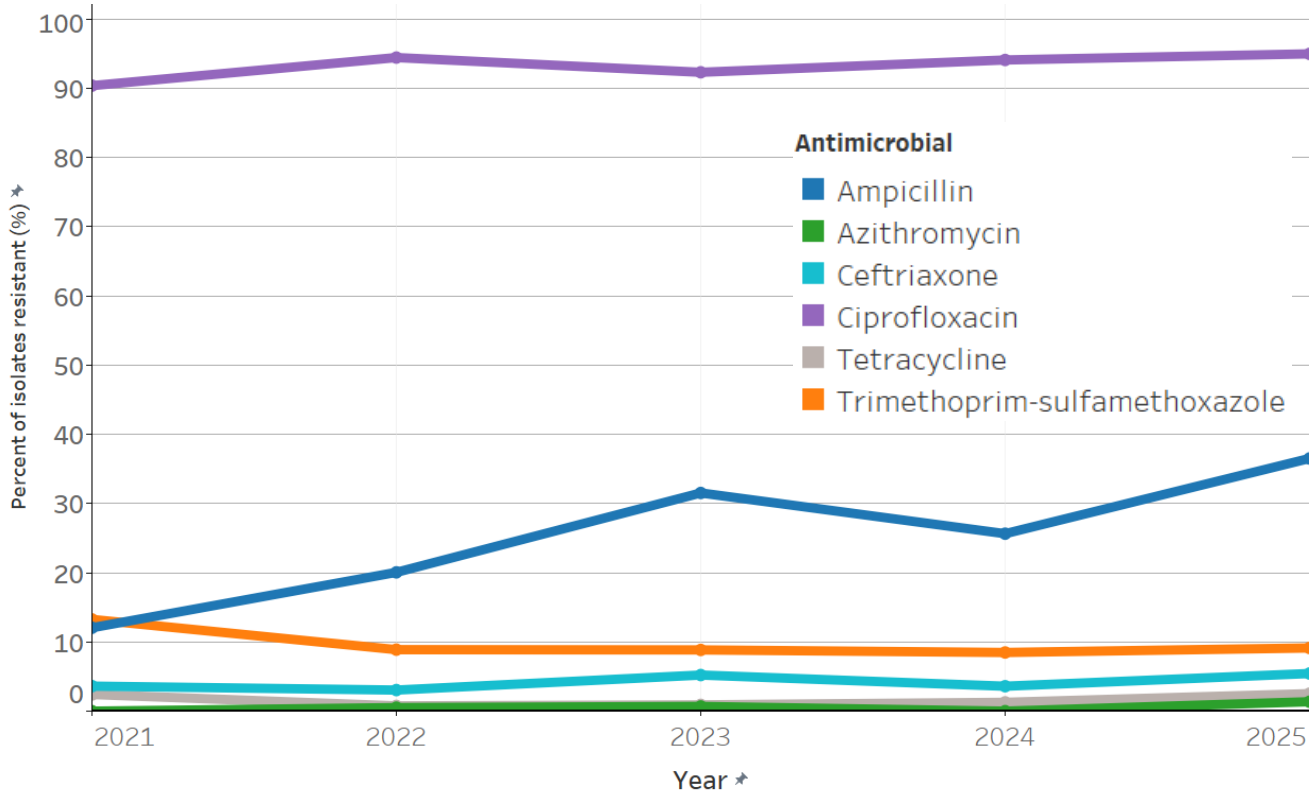
Human Typhoidal *Salmonella*

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Extremely high resistance to ciprofloxacin has implications for treatment selection.

- **Extremely high** resistance to ciprofloxacin (ranging from 90% to 95%)
- **High** resistance to ampicillin; increased from 2021 (12%) to 2025 (37%)
- **Moderate** resistance to trimethoprim-sulfamethoxazole in 2021 **decreased to low** resistance in 2022 and beyond



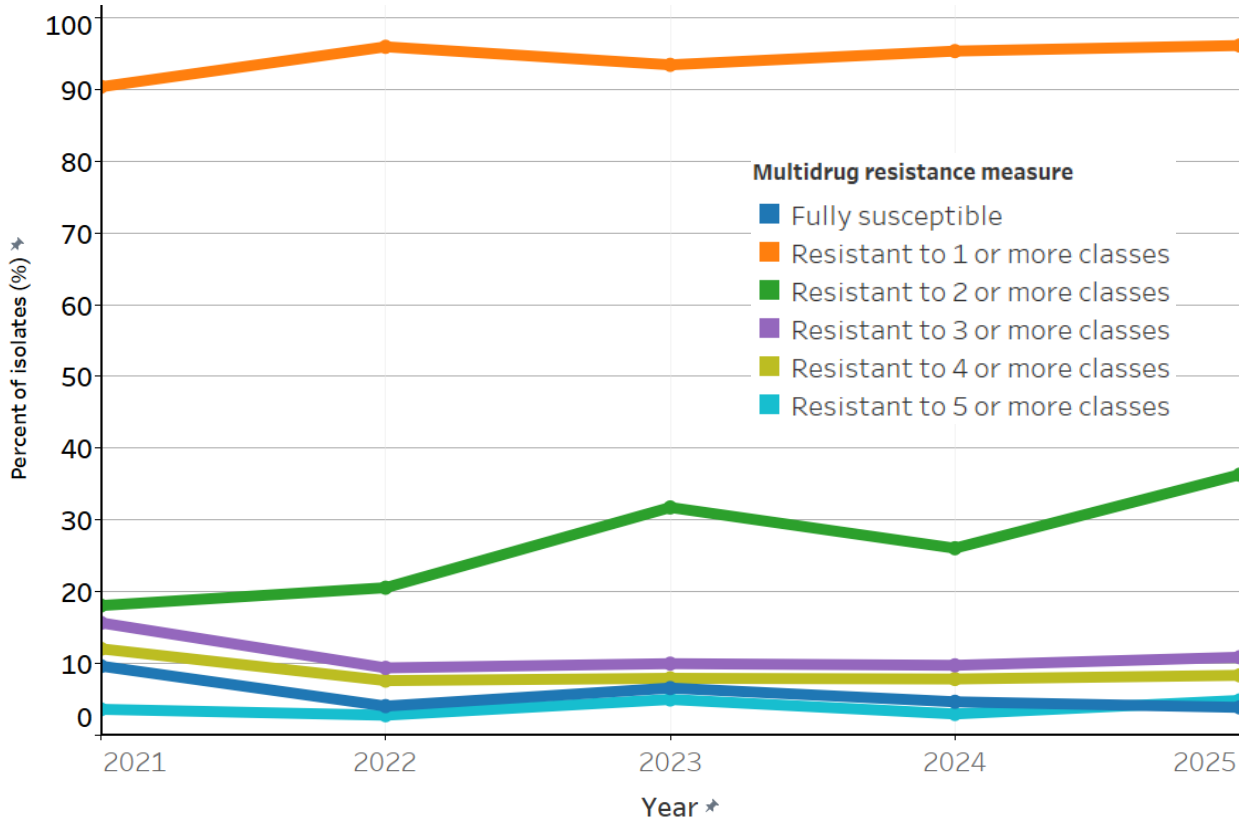
Wide regional variation, sparse data and small numbers of isolates make interpretation of regional difference challenging.

Region	2021		2022		2023		2024		2025	
	% R SXT	Total Isolates	% R SXT	Total Isolates	% R SXT	Total Isolates	% R SXT	Total Isolates	% R SXT	Total Isolates
National	13	83	9	394	9	441	9	472	9	515
Atlantic	0	2	25	8	0	7	8	24	13	15
British Columbia	11	19	3	76	1	99	4	93	5	92
Ontario	11	46	10	204	9	231	11	219	9	280
Prairies	9	11	8	85	15	79	4	110	5	101
Quebec	60	5	14	21	20	25	23	26	41	27

Legend	20 or fewer isolates	Rare 0-0.1%	Very low 0.1% to 1%	Low >1% to 10%	Moderate >10% to 20%	High >20% to 50%	Very high >50% to 70%	Extremely high >70%

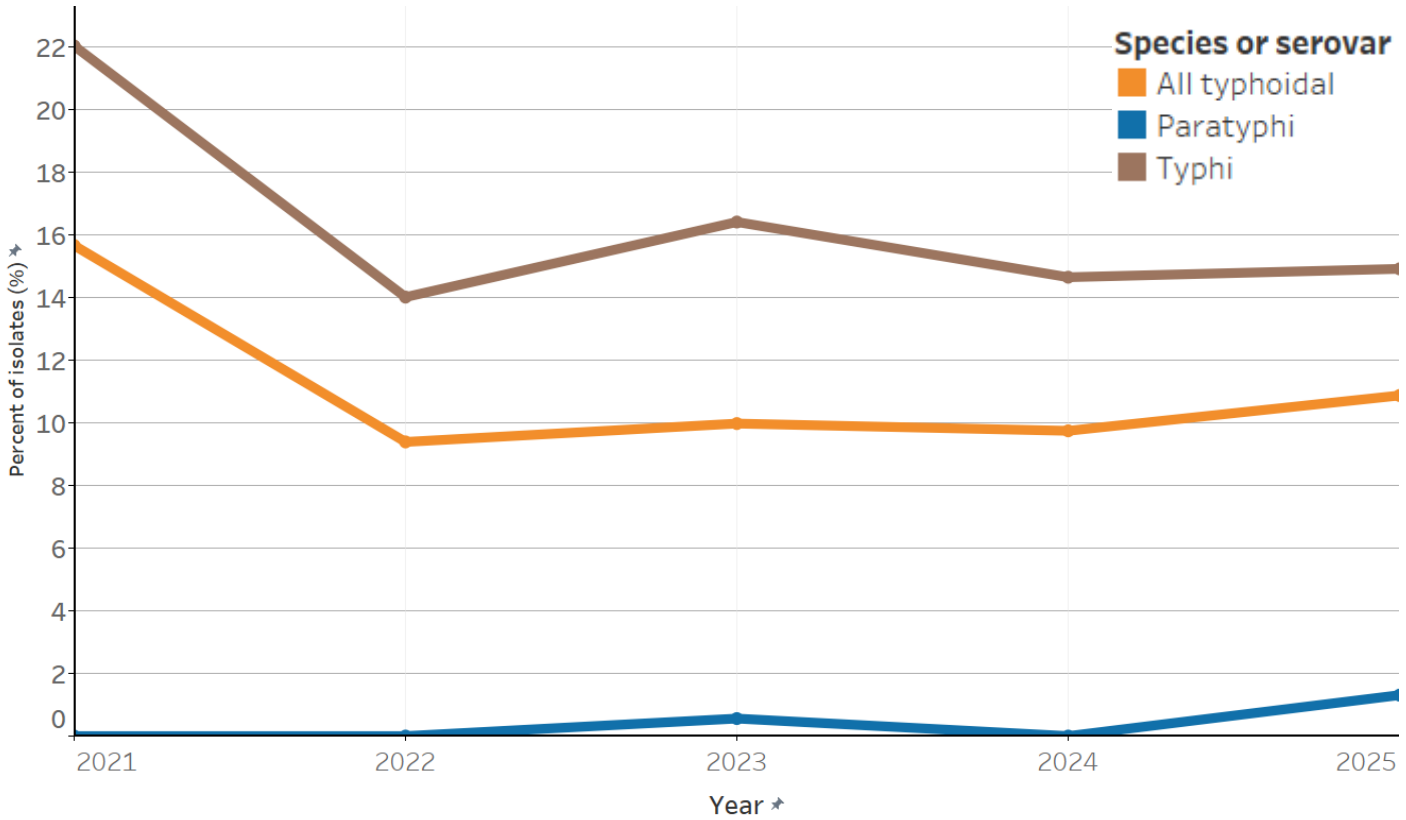
Few isolates fully susceptible and isolates predominantly resistant to 1 antimicrobial class.

- **Variable** full susceptibility (ranging between 4% and 10%)
- **Variable and high** resistance to 2 or more classes (2021; 18% and 2025; 36%)
- **Variable** with **moderate to low** resistance to 3 or more classes (2021; 16% and 2025; 11%)



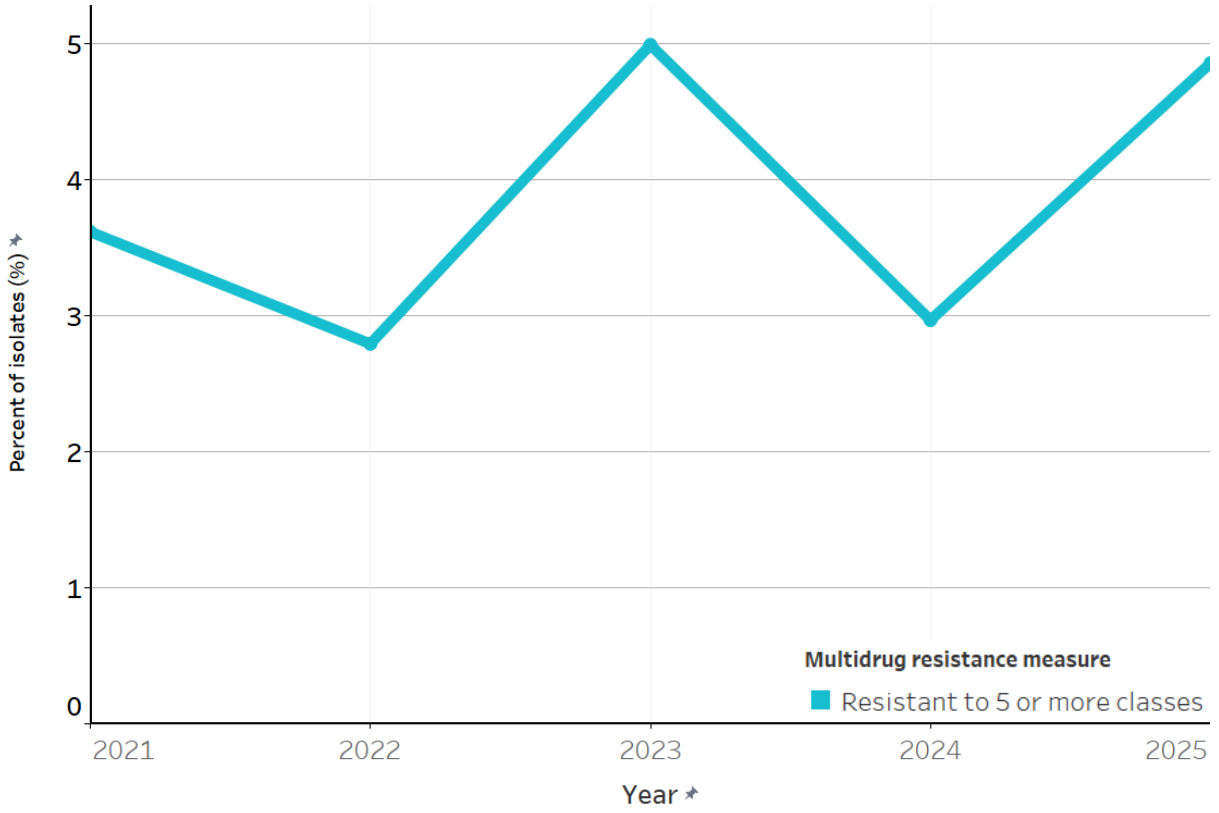
Resistance to 3 or more antimicrobial classes more common among *Salmonella* Typhi isolates

- Multidrug resistance (MDR) was consistently more common in *S.* Typhi than in *S.* Paratyphi.
- Among *S.* Typhi isolates, MDR frequency decreased from 22% in 2021 to 14% in 2022 and remained relatively stable thereafter (15-16%).
- MDR was **very low** to **low** among *S.* Paratyphi isolates, remaining below 2%



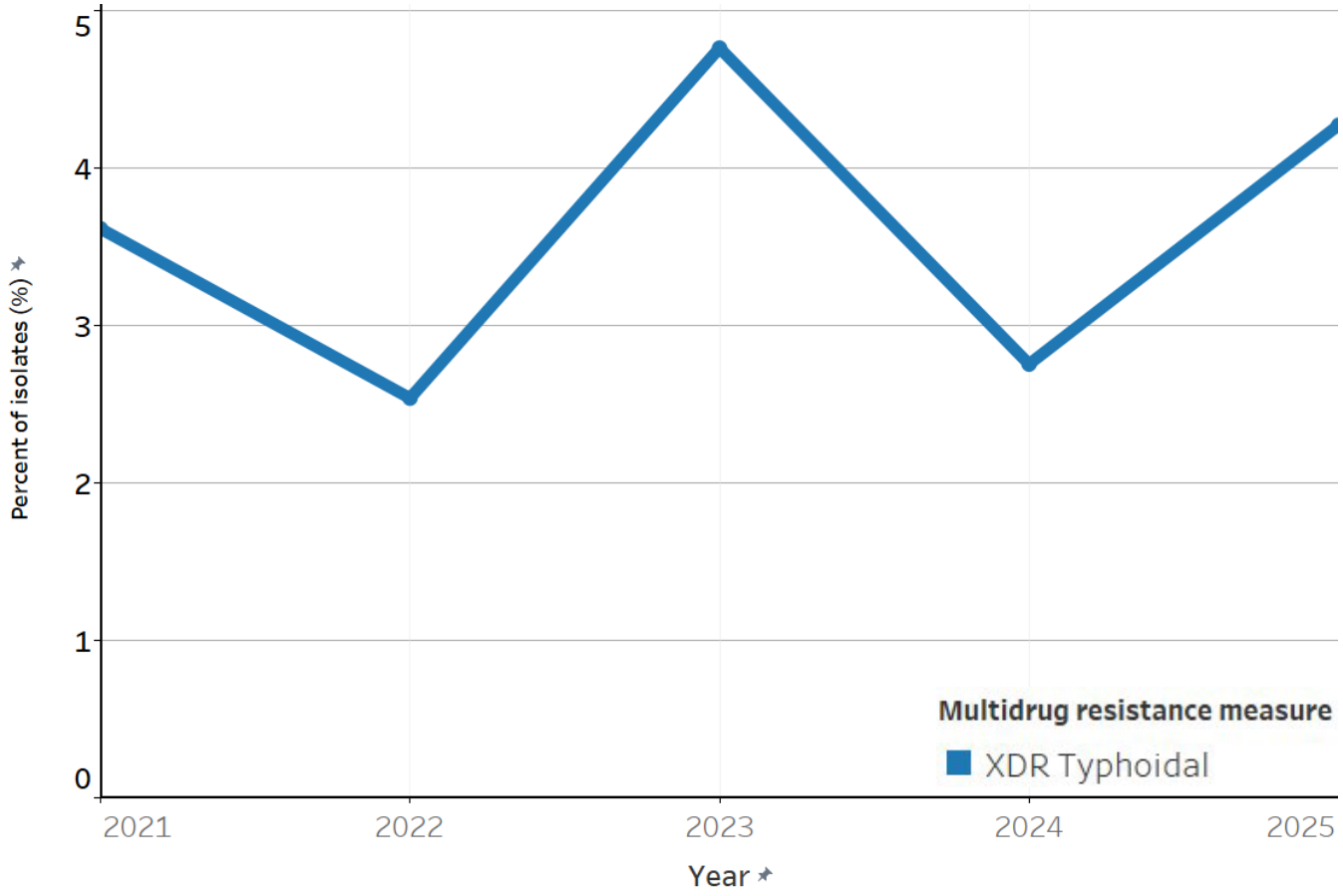
Maximum resistance between 2021 and 2025 was resistance to 5 antimicrobial classes and the frequency was low.

- **Low** resistance to 5 or more classes (2021; 4% and 2025; 5%)
- Patterns of resistance for 2025 isolates resistant to 5 classes – All *S.* Typhi
  - Cephalosporins, Folate pathway inhibitors, Penicillins, Phenicols, Quinolones (n=20)
  - Folate pathway inhibitors, Macrolides, Penicillins, Phenicols, Quinolones (n=2)
  - Cephalosporins, Folate pathway inhibitors, Penicillins, Quinolones, Tetracyclines (n=2)
  - Beta lactam inhibitors, Folate pathway inhibitors, Macrolides, Penicillins, Quinolones (n=1)
- Since 2020, **no** resistance to 6 or more classes



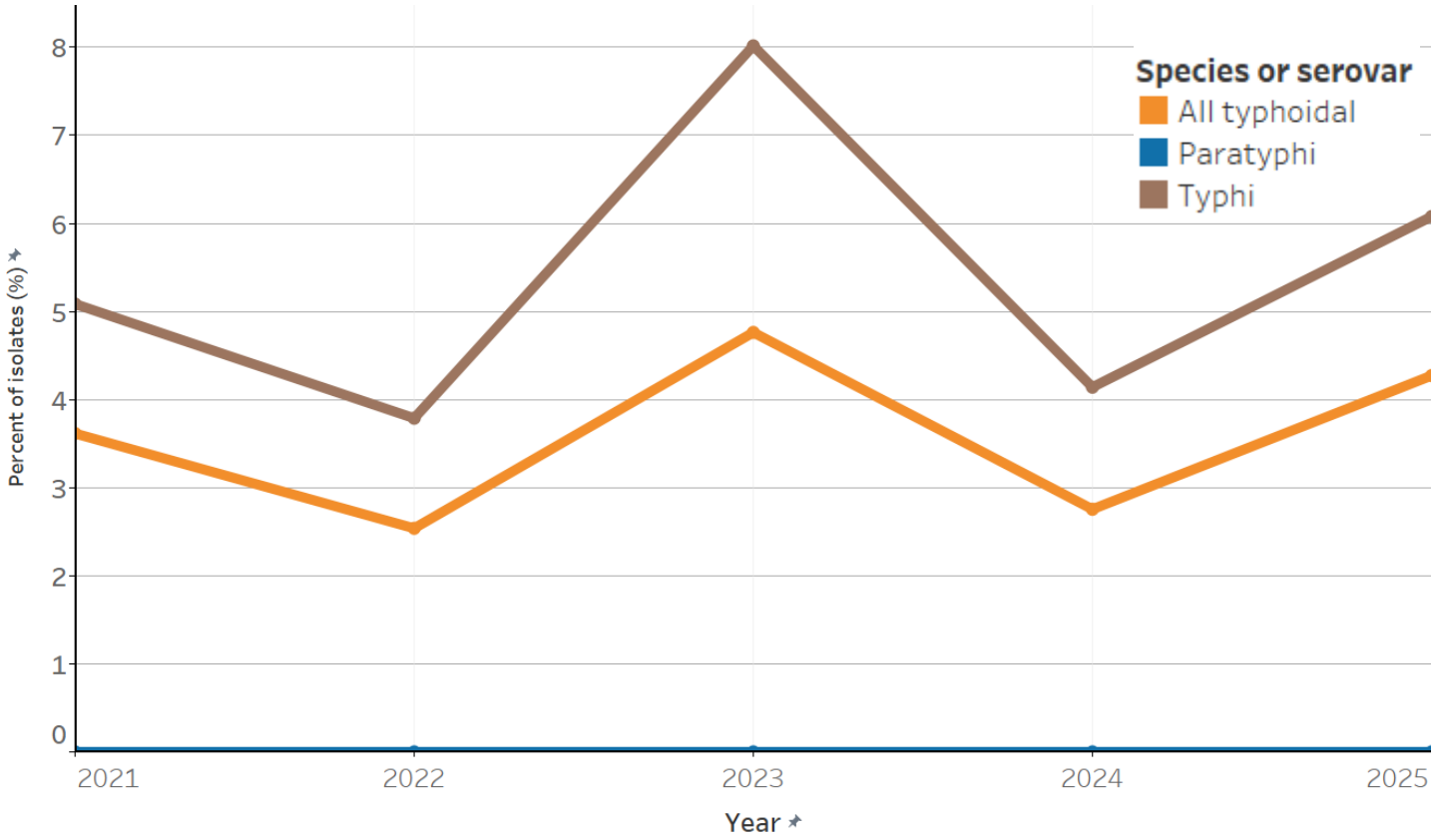
Extensive drug resistance fluctuated between low to moderate

- Extensively drug-resistant (XDR) typhoidal *Salmonella* was identified each year from 2021 to 2025
- XDR frequency fluctuated over time, ranging from 3% to 5% of isolates.



XDR was only observed in *Salmonella* Typhi

- No XDR isolates were identified among *S.* Paratyphi during 2021-2025.
- Among *S.* Typhi isolates, XDR frequency fluctuated between approximately 4% and 8%, peaking in 2023.



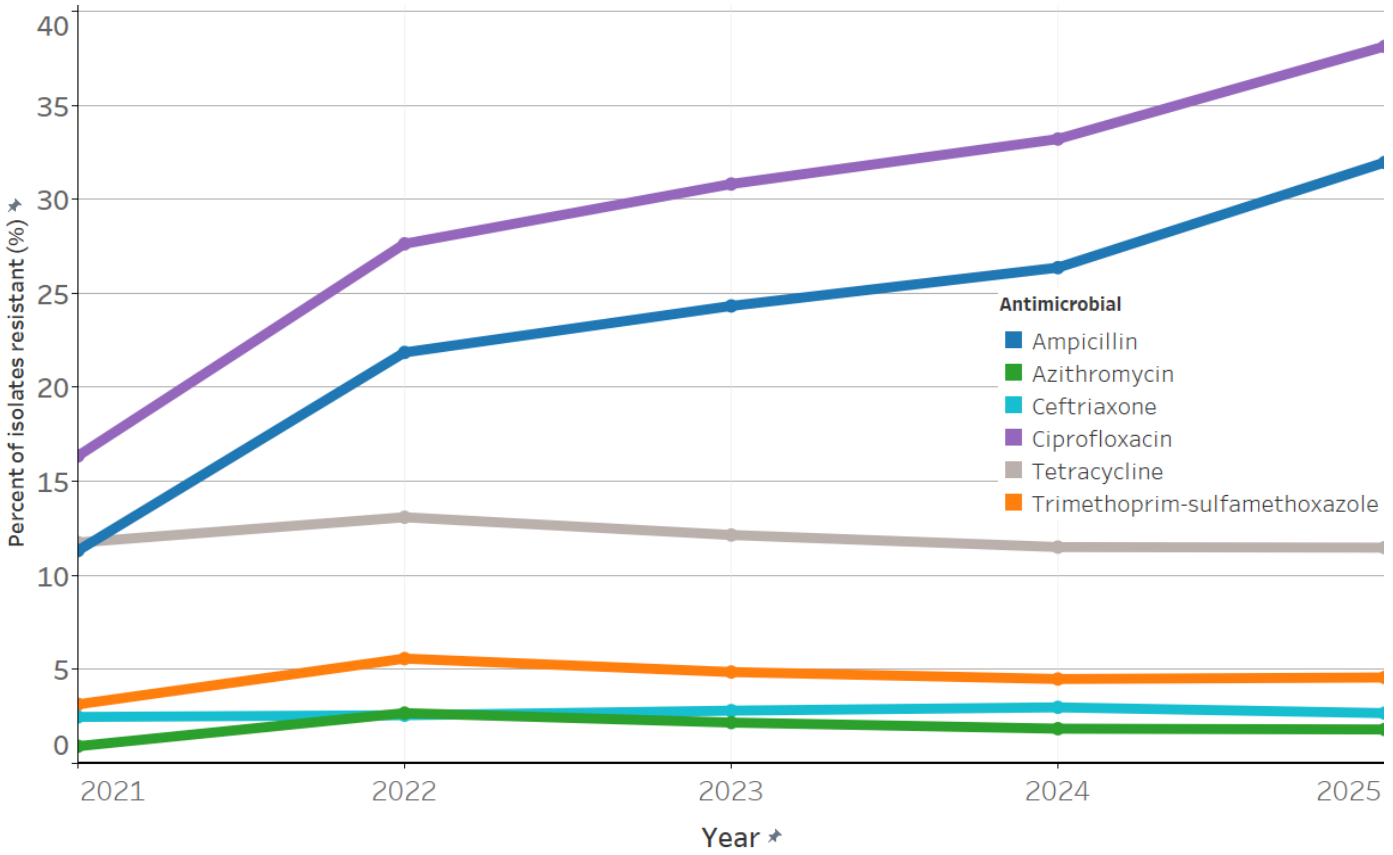
Human Non-Typhoidal *Salmonella*

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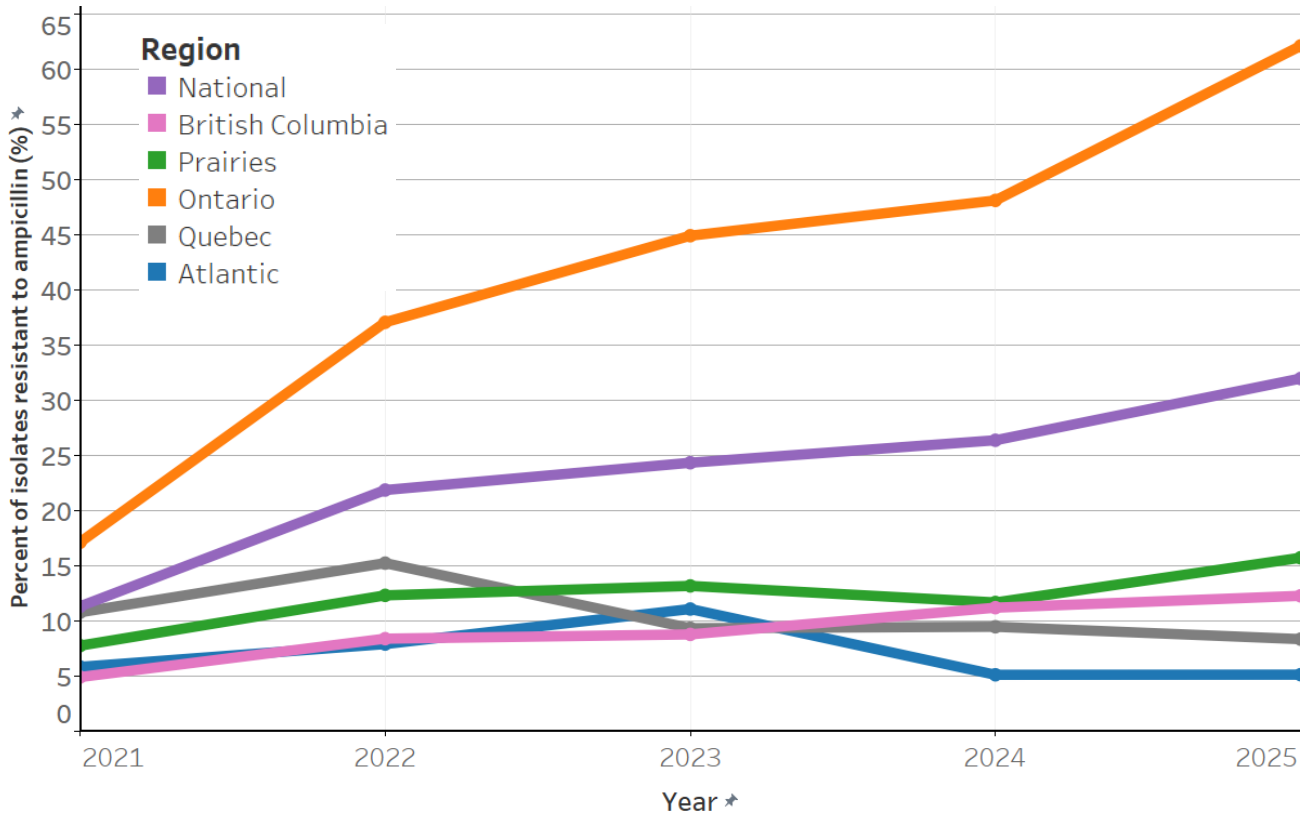
Resistance to ciprofloxacin and ampicillin continuing to increase.

- **Moderate** resistance to ciprofloxacin and ampicillin **increased** to **high**
- **Moderate** and relatively stable resistance to tetracycline
- **Low** and relatively stable resistance to ceftriaxone, trimethoprim-sulfamethoxazole and azithromycin



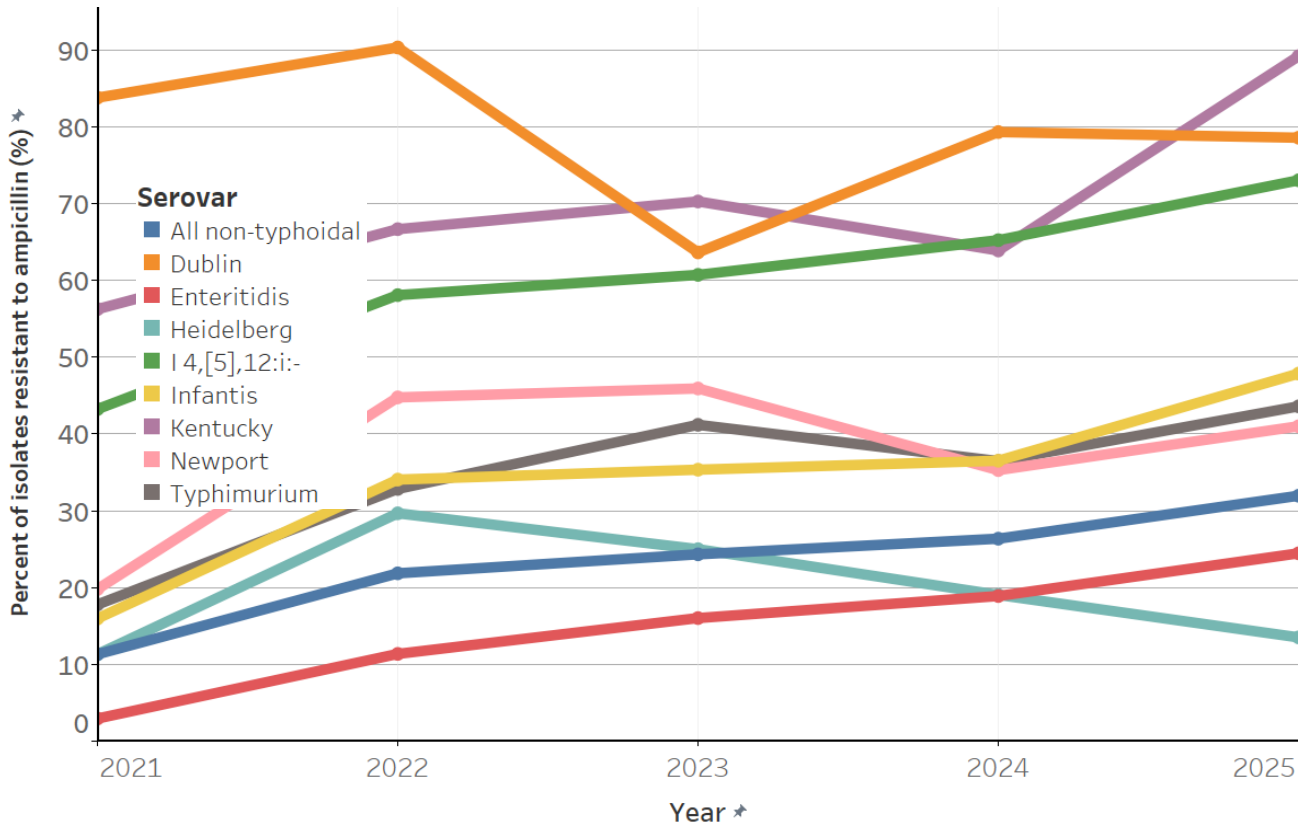
Ampicillin resistance varied substantially across regions from 2021-2025

- Compared to the frequency of ampicillin resistance nationally
  - Ontario consistently reported the highest frequency.
  - Quebec exceeded the national frequency only in 2021, after which resistance remained consistently lower in all provinces, compared to the national average.



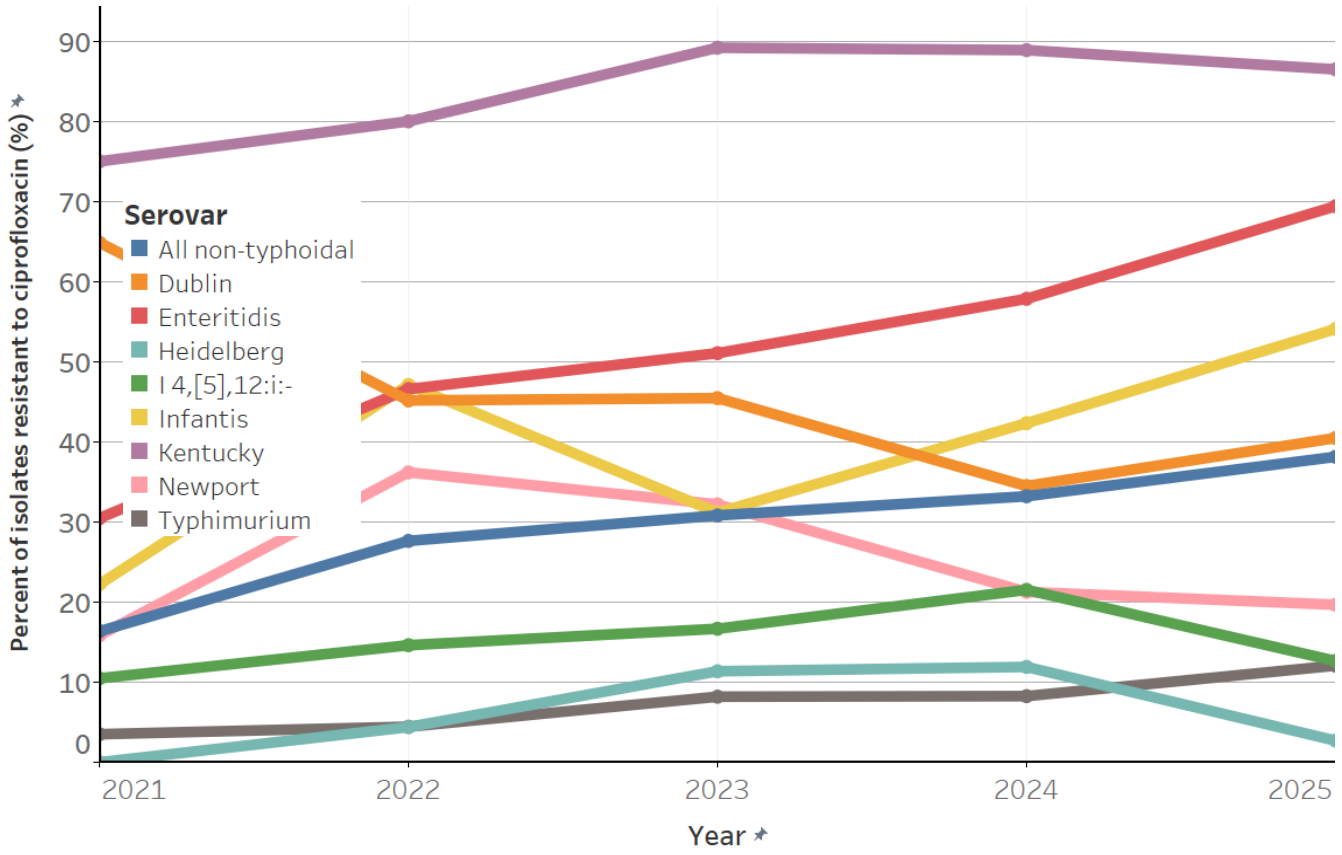
Extremely high ampicillin resistance in *S.* Dublin, *S.* Kentucky and *Salmonella* I 4,[5],12:i:- in 2025

- Compared to the frequency of ampicillin resistance in all non-typhoidal serovars
    - *S.* Dublin, *S.* Kentucky and *Salmonella* I 4,[5],12:i:- were consistently **substantially higher**
    - *S.* Enteritidis was consistently **lower**



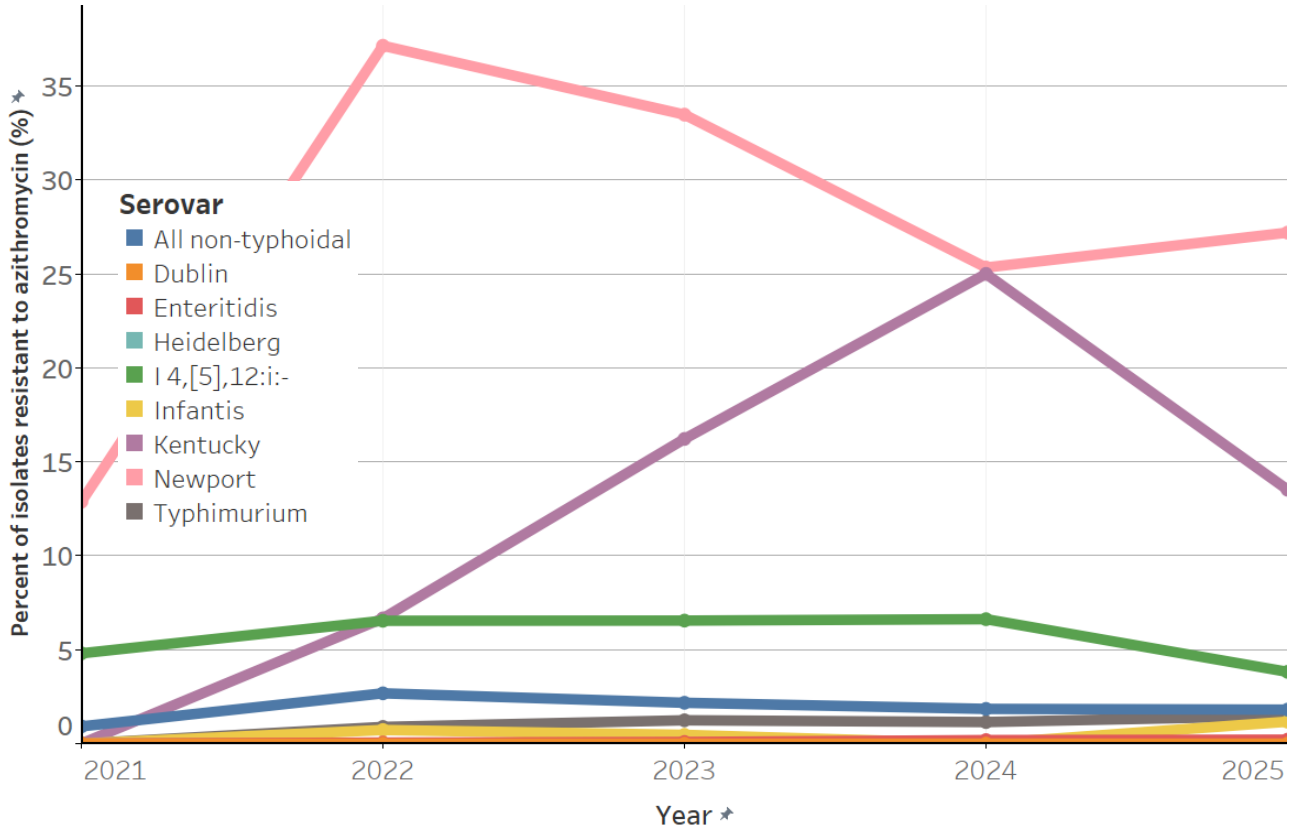
Ciprofloxacin resistance is substantially higher in *S.* Kentucky and *S.* Enteritidis.

- Compared to the frequency of ciprofloxacin resistance in all non-typhoidal serovars
  - *S.* Kentucky and *S.* Enteritidis were **substantially higher**
  - *Salmonella* I 4,[5],12:i:-, *S.* Heidelberg and *S.* Typhimurium were consistently **lower**



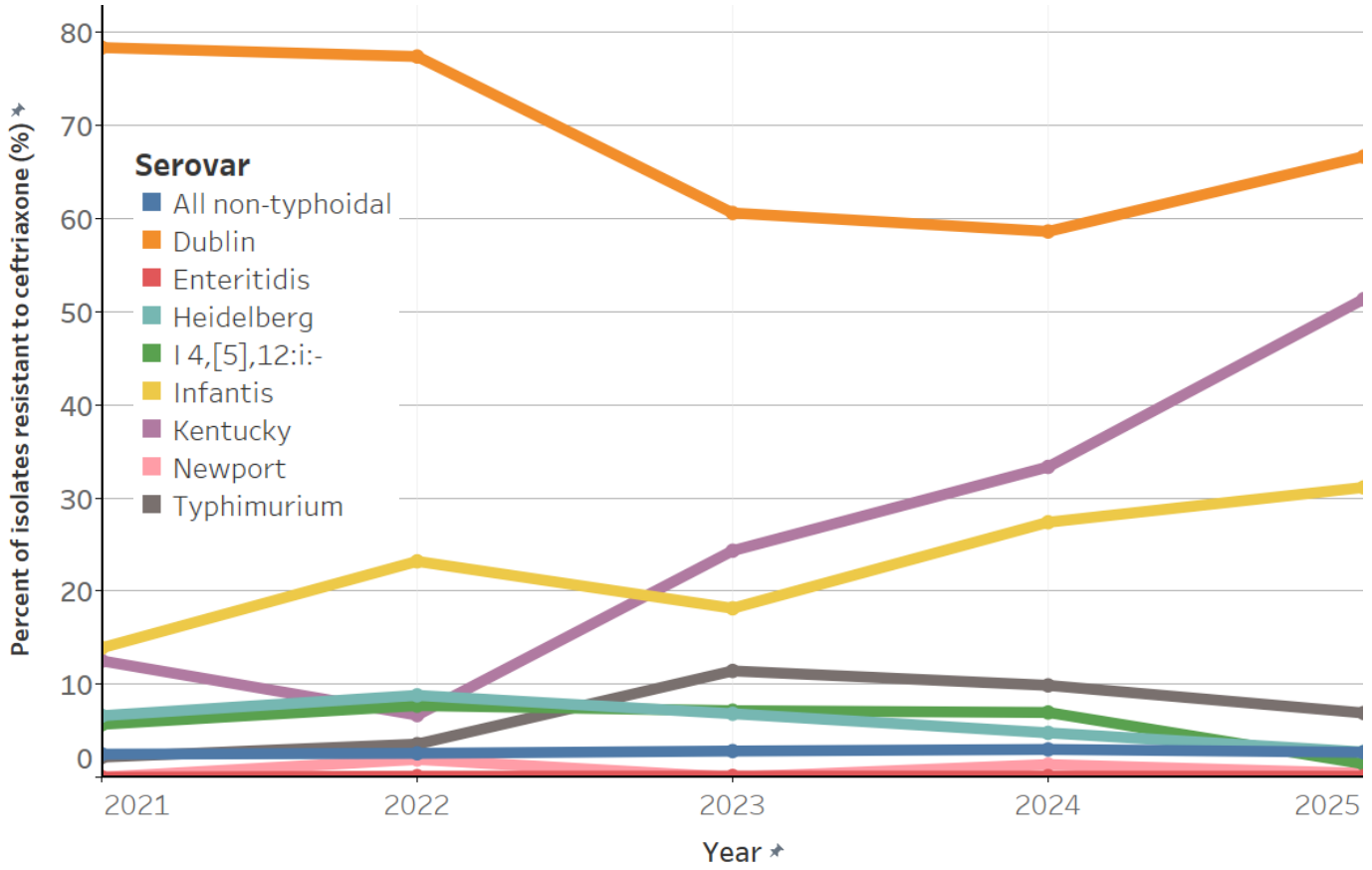
Azithromycin resistance remains highest *S.* Newport in 2025

- Compared to the frequency of azithromycin resistance in all non-typhoidal serovars
  - *S.* Newport resistance remains **high**
  - *S.* Kentucky resistance has dropped to **moderate** in 2025
  - *Salmonella* I 4,[5],12:i:- was **higher** than most other serovars, but still **low resistance**



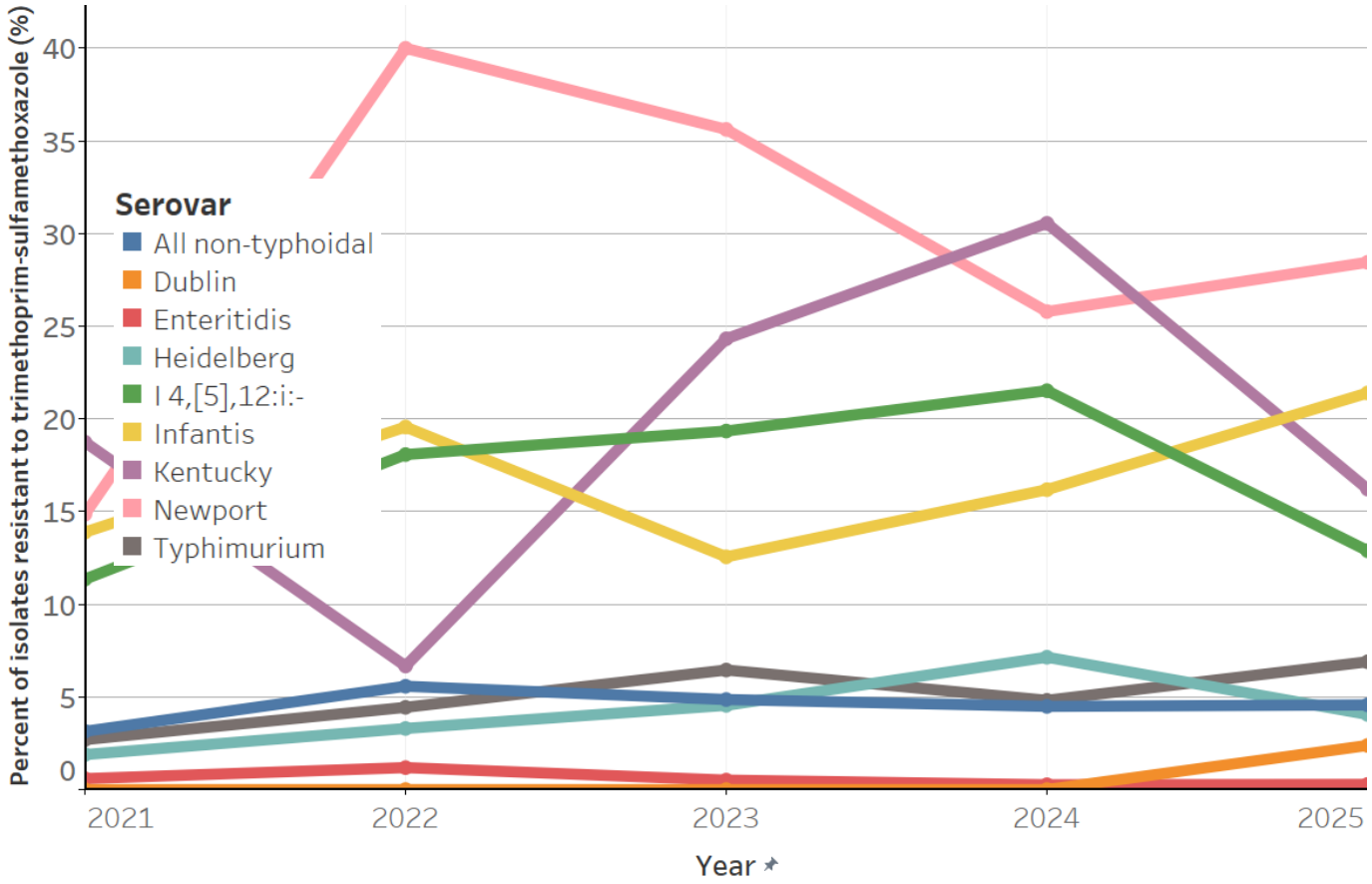
Ceftriaxone resistance increased to high in *S.* Kentucky and *S.* Infantis.

- Compared to the frequency of ceftriaxone resistance in all non-typhoidal serovars
  - Highest in *S.* Dublin
  - *S.* Kentucky increased from **high** to **very high**
  - *S.* Infantis remains **high** and is continuing to increase



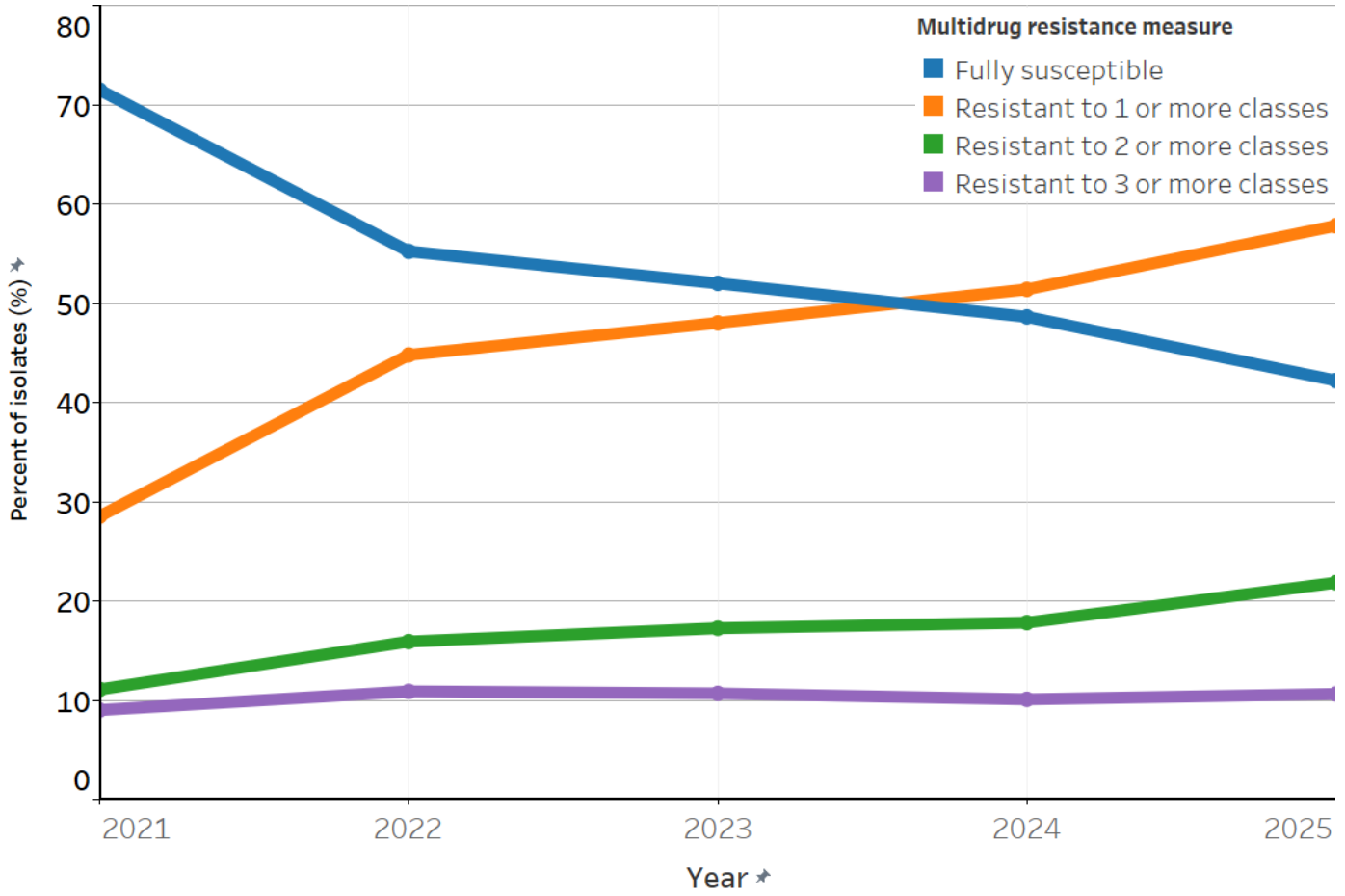
Trimethoprim-sulfamethoxazole resistance was high in *S.* Infantis and *S.* Newport in 2025

- Compared to the frequency of trimethoprim-sulfamethoxazole resistance in all non-typhoidal serovars
  - *S.* Kentucky, *S.* Newport, *Salmonella* I 4,[5],12:i:- and *S.* Infantis were **substantially higher**
  - *S.* Dublin and *S.* Enteritidis were lower since 2021



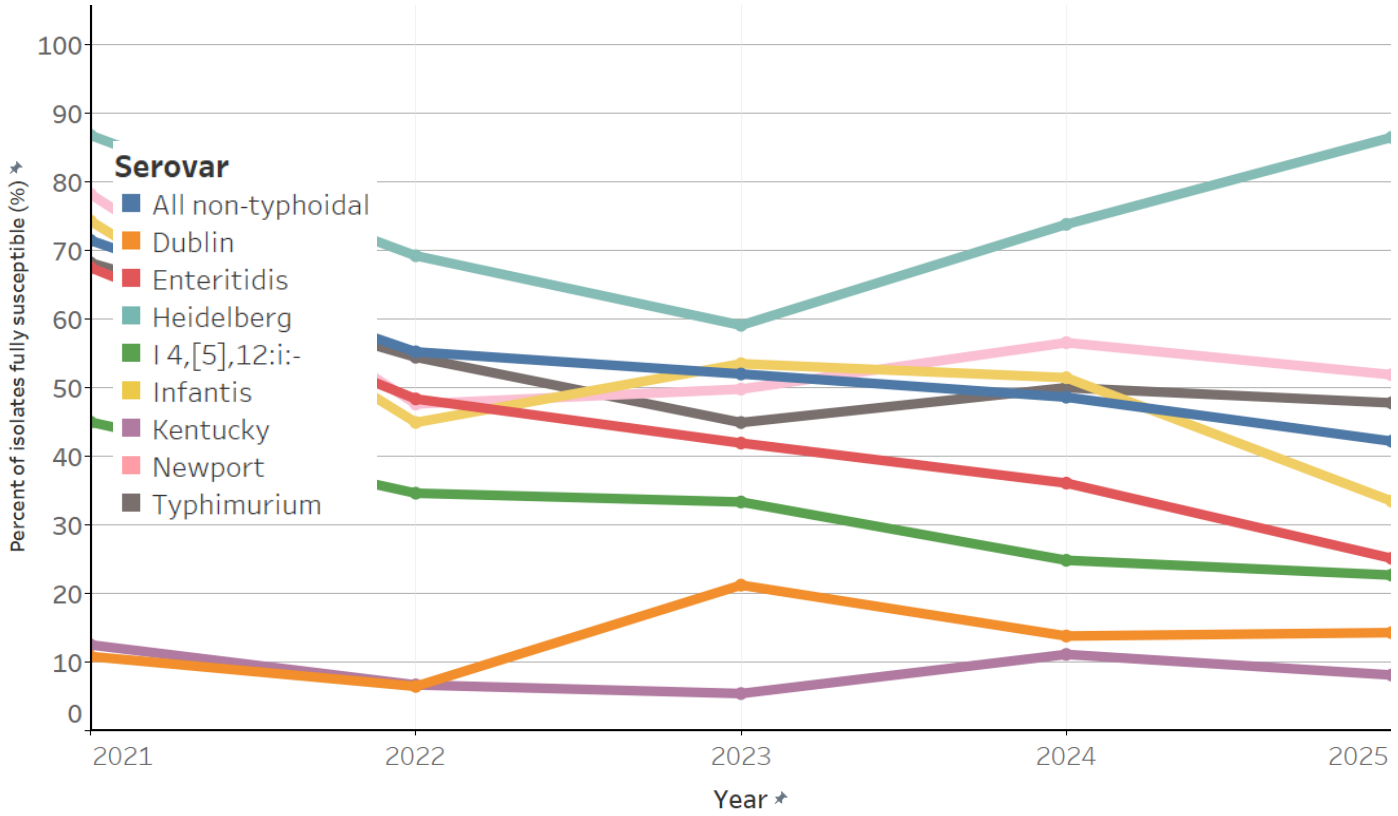
Increasing resistance to 1 and 2 classes and decreasing full susceptibility.

- **Decreased** full susceptibility since 2021 (2021; 71% and 2025; 42%)
- **Moderate** resistance to 2 or more classes, **increased** to **high** in 2025 (2021; 11% and 2025; 22%)
- **Low** to **moderate** resistance to 3 or more classes, relatively **stable** (2021; 9% and 2025; 11%)



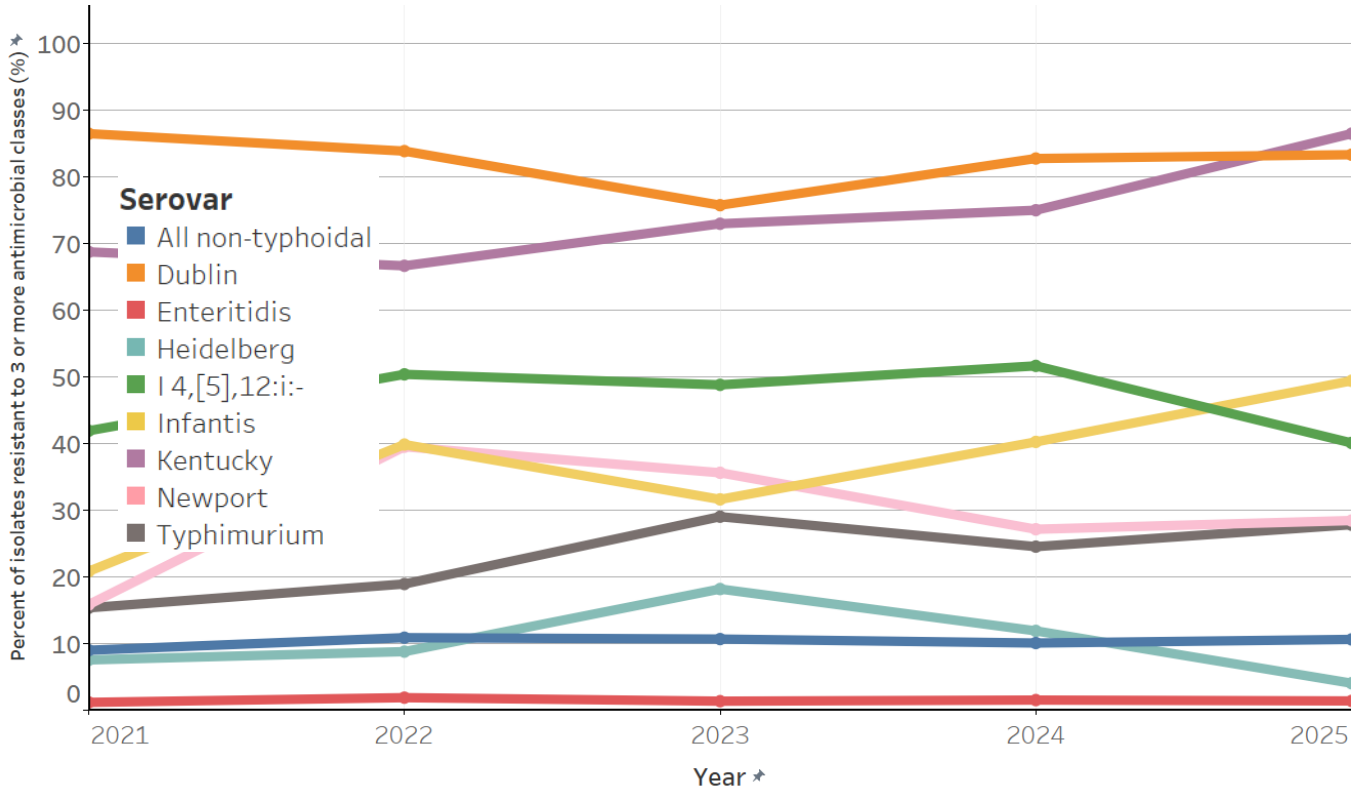
Fully susceptible is substantially lower in *S.* Kentucky, *S.* Dublin and *Salmonella* I 4,[5],12:i:-.

- Compared to the frequency of fully susceptible in all non-typhoidal serovars
  - *S.* Kentucky and *S.* Dublin were **substantially lower**
  - *S.* Enteritidis and *Salmonella* I 4,[5],12:i:- was also **lower**
  - *S.* Heidelberg was **higher**



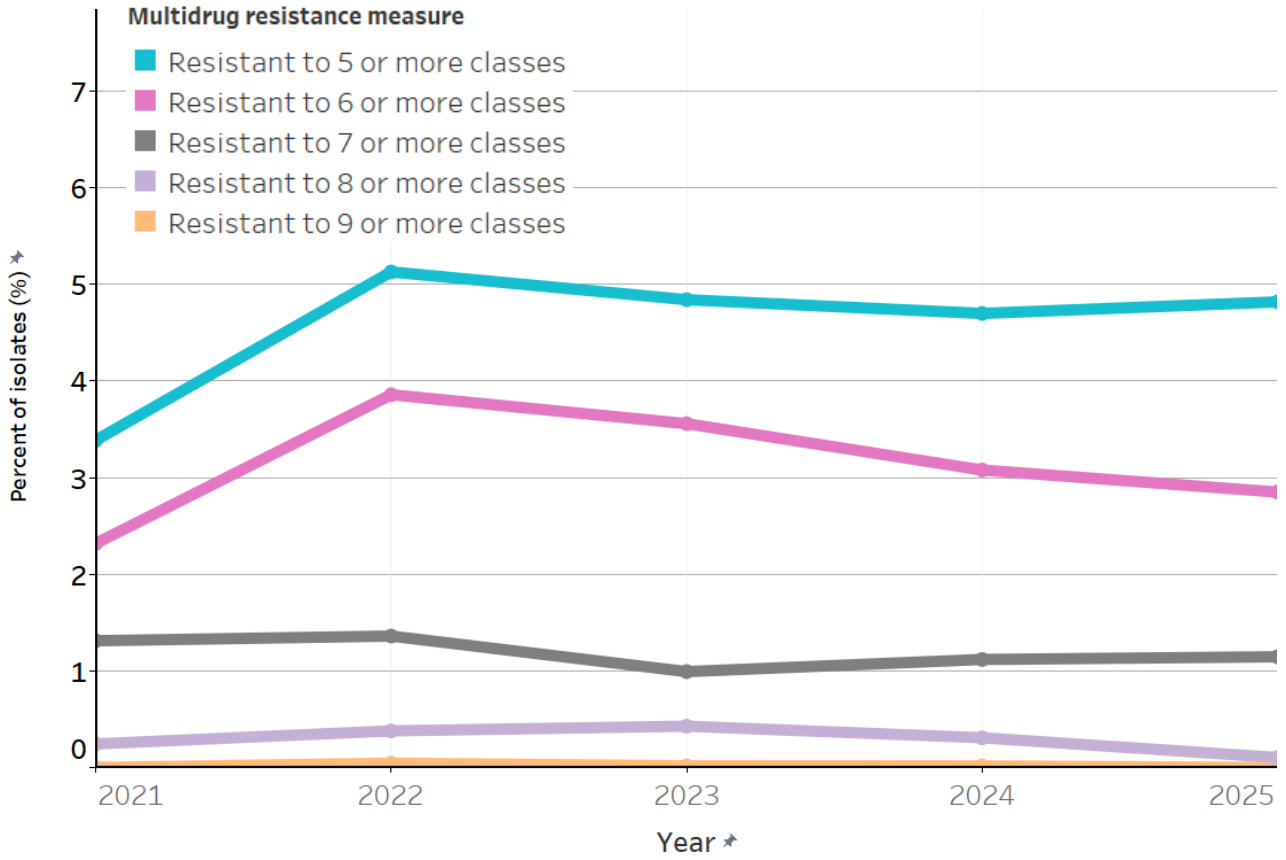
Multidrug resistance varied considerably by serovar

- *S.* Dublin and *S.* Kentucky consistently exhibited **very high** to **extremely high** levels of multidrug resistance
- *Salmonella* I 4,[5],12:i:-, *S.* Infantis, *S.* Newport and *S.* Typhimurium have also demonstrated **high** levels of multidrug resistance in 2025
- Most other serovars maintained low levels of multidrug resistance



Resistance to 8 or more classes was very low however reported.

- **Low** resistance to 5 or more classes remained relatively stable at 5% from 2022-2025
- **Low** resistance to 6 or more classes (ranging from 2% to 4%)
- **Low** and **stable** resistance to 7 or more classes (ranging from 1.0% to 1.4%)
- **Very low** and **stable** resistance to 8 or more classes (ranging from 0.1% to 0.4%)

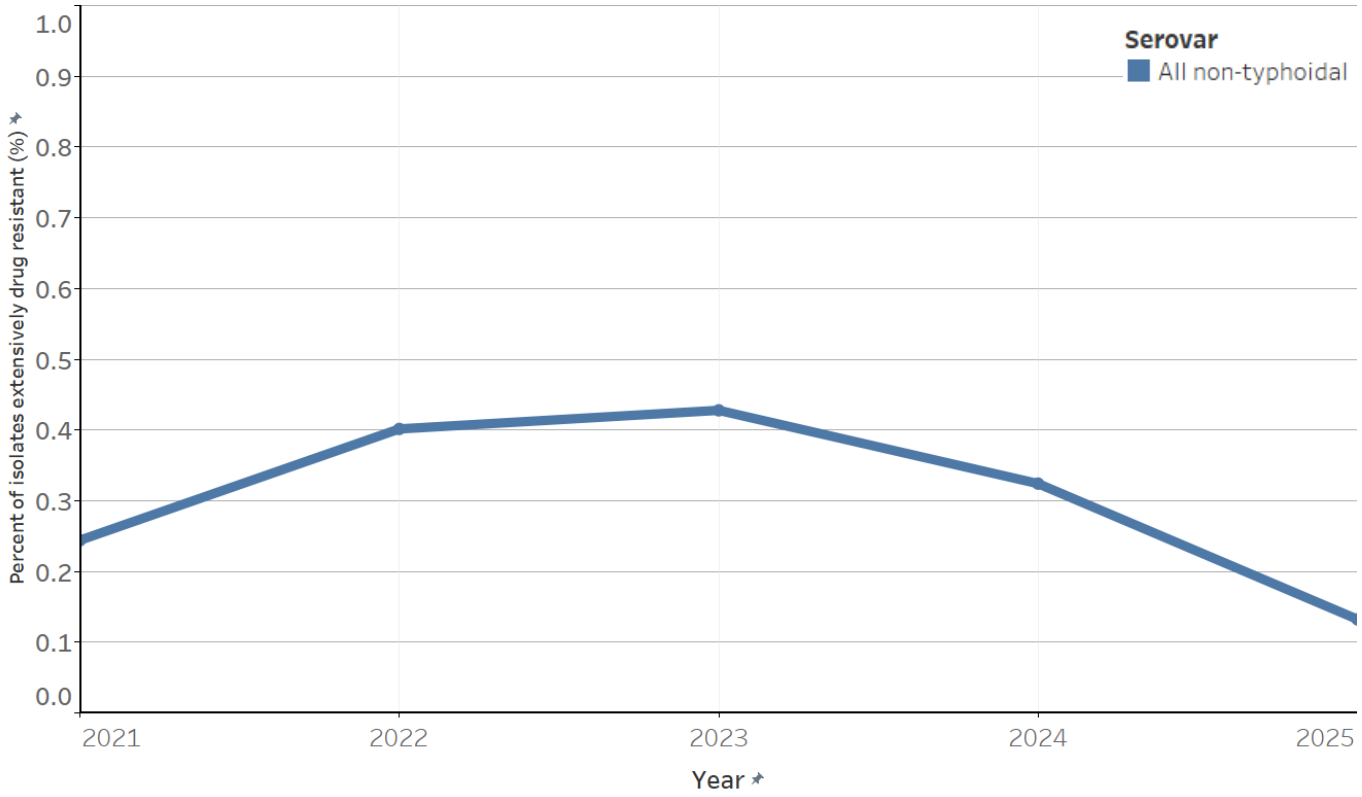


Resistance to 9 classes including Category I antimicrobials was infrequent, only present in 4 isolates.

- Rare resistance to 9 or more classes (2 isolates in 2022, 1 isolate in 2023 and one isolate in 2024).
- Maximum resistance seen in 2025 was **resistance to 8 antimicrobial classes** (n=7)
  - Aminoglycosides, cephalosporins, folate pathway inhibitors, macrolides, penicillins, phenicols, quinolones, tetracyclines (n=6)
  - Aminoglycosides, cephalosporins, folate pathway inhibitors, penicillins, phenicols, polymyxins, quinolones, tetracyclines (n=1)
  - All 7 isolates detected resistance to 9 or 10 antimicrobials including 2-3 Category I antimicrobials
  - *Salmonella* I 4,[5],12:i:- (n=3), *S.* Infantis (n=2), *S.* Kentucky (n=1) and *S.* Corvallis (n=1)

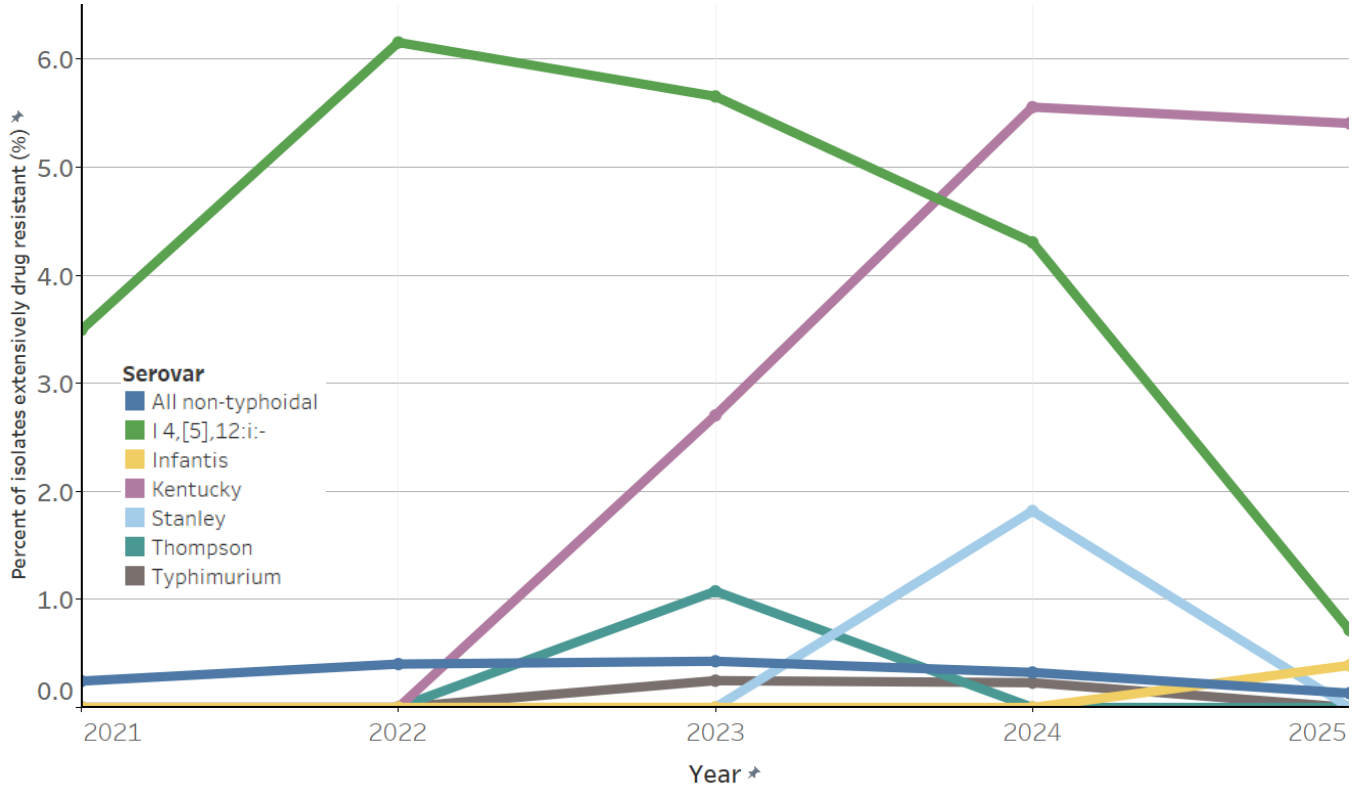
XDR remains very low among non-typhoidal *Salmonella*

- Although uncommon, XDR isolates continue to be detected through surveillance.
- XDR isolates accounted for fewer than 1% of isolates in all years.
    - National XDR frequency ranged from 0.13% in 2025 to 0.43% in 2023.



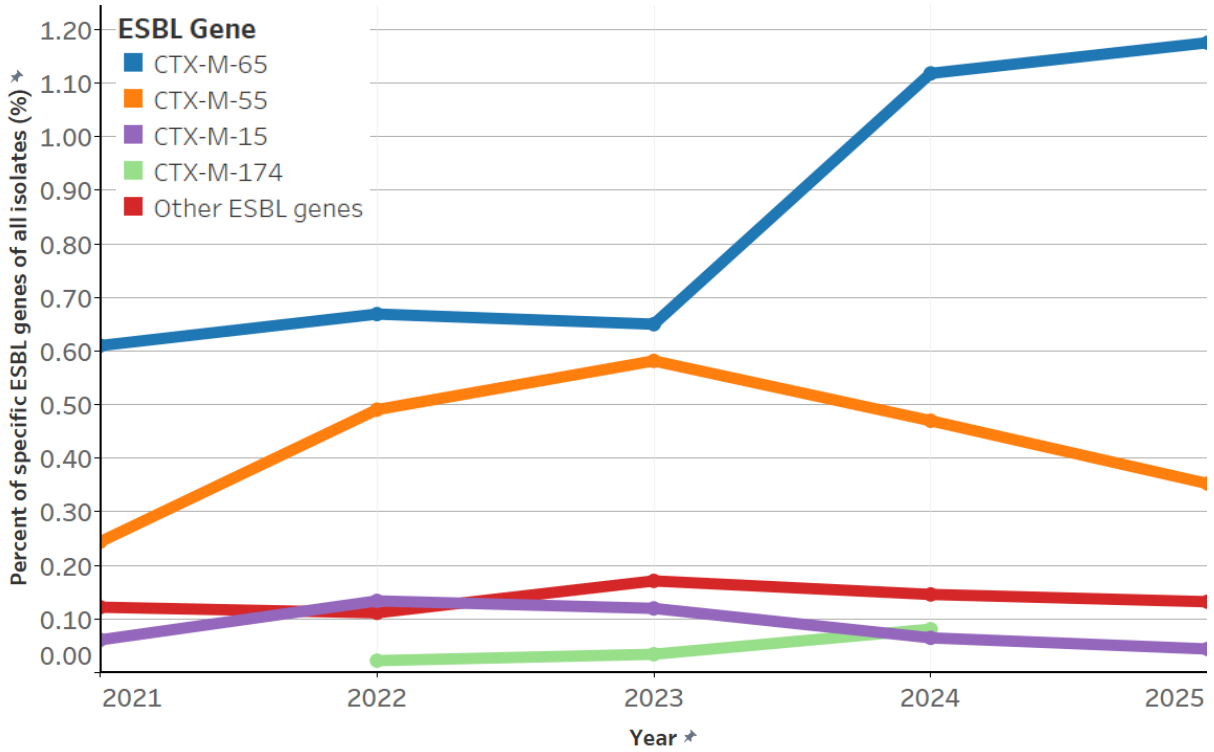
XDR Remains most frequent in *S.* Kentucky

- Compared to the frequency of XDR in all non-typhoidal serovars
  - XDR *Salmonella* I 4,[5],12:i:- were consistently higher
  - XDR *S.* Kentucky was higher in 2023 and beyond, despite small isolate counts



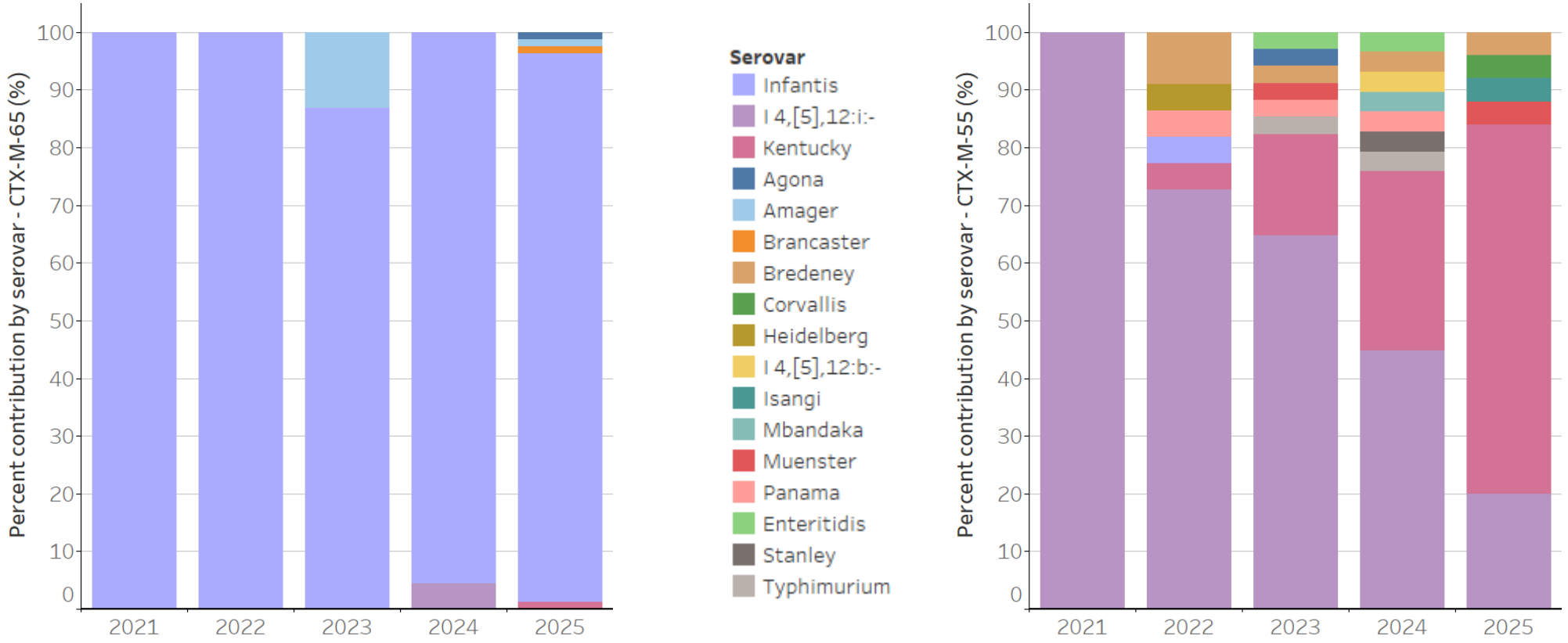
Overall ESBL genes in human non-typhoidal *Salmonella* have increased since 2021, drive by an increase in CTX-M-65

- ESBL genes remained uncommon
- Overall ESBL frequency in non-typhoidal *Salmonella* isolates increased from 1% in 2021 to 1.9% in 2024 and decreased slightly to 1.8% in 2025
  - **CTX-M-65** was the predominant ESBL gene and increased since 2021.
  - **CTX-M-55** was the second most common ESBL gene and had a variable trend.



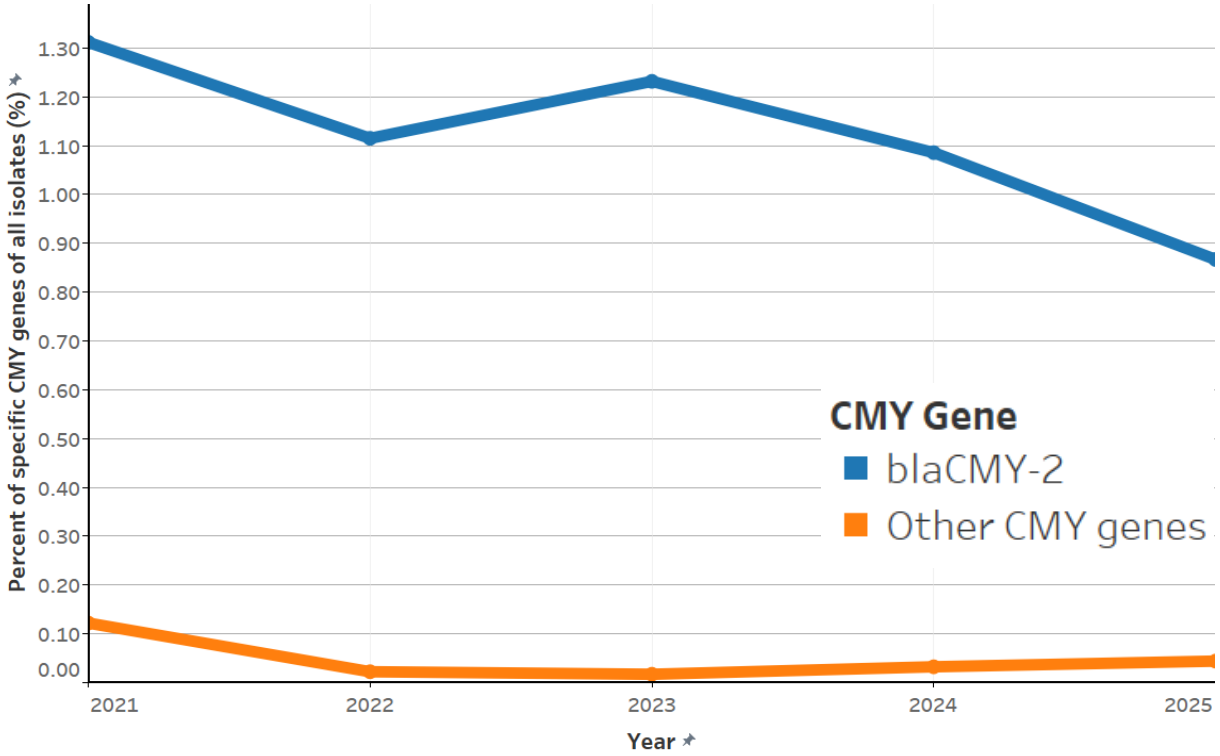
ESBL gene distribution was strongly concentrated within a small number of serovars

- *bla*$_{\text{CTX-M-65}}$ predominately in *S.* Infantis
- *bla*$_{\text{CTX-M-55}}$ predominately in *Salmonella* I 4,[5],12:i:- and *S.* Kentucky



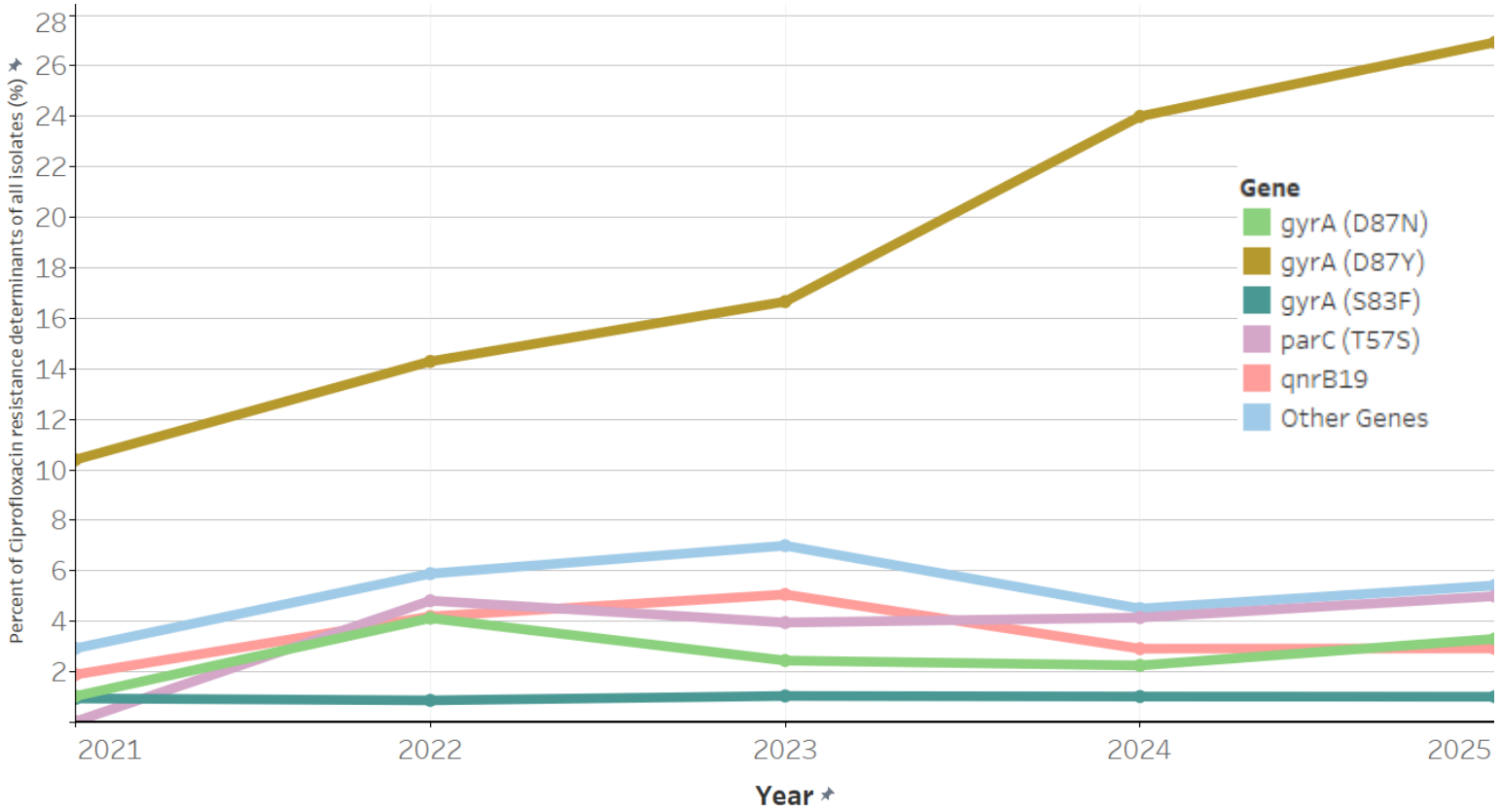
bla$_{CMY-2}$ remained the predominant CMY gene despite a slight decrease from 2021 to 2025

- CMY genes remained uncommon, ranging from approximately 1% to 1.4% of all isolates between 2021 and 2025.
- bla$_{CMY-2}$, the predominant CMY gene, decreased slightly from 1.3% in 2021 to 0.9% in 2025
  - Identified in *S.* Dublin, *S.* Heidelberg, and *S.* Typhimurium.
- Other CMY genes remained rare, ranging from 0.02% to 0.12% of isolates annually.
  bla$_{CMY-4}$ *bla*$_{CMY-44}$ *bla*$_{CMY-54}$ *bla*$_{CMY-61}$



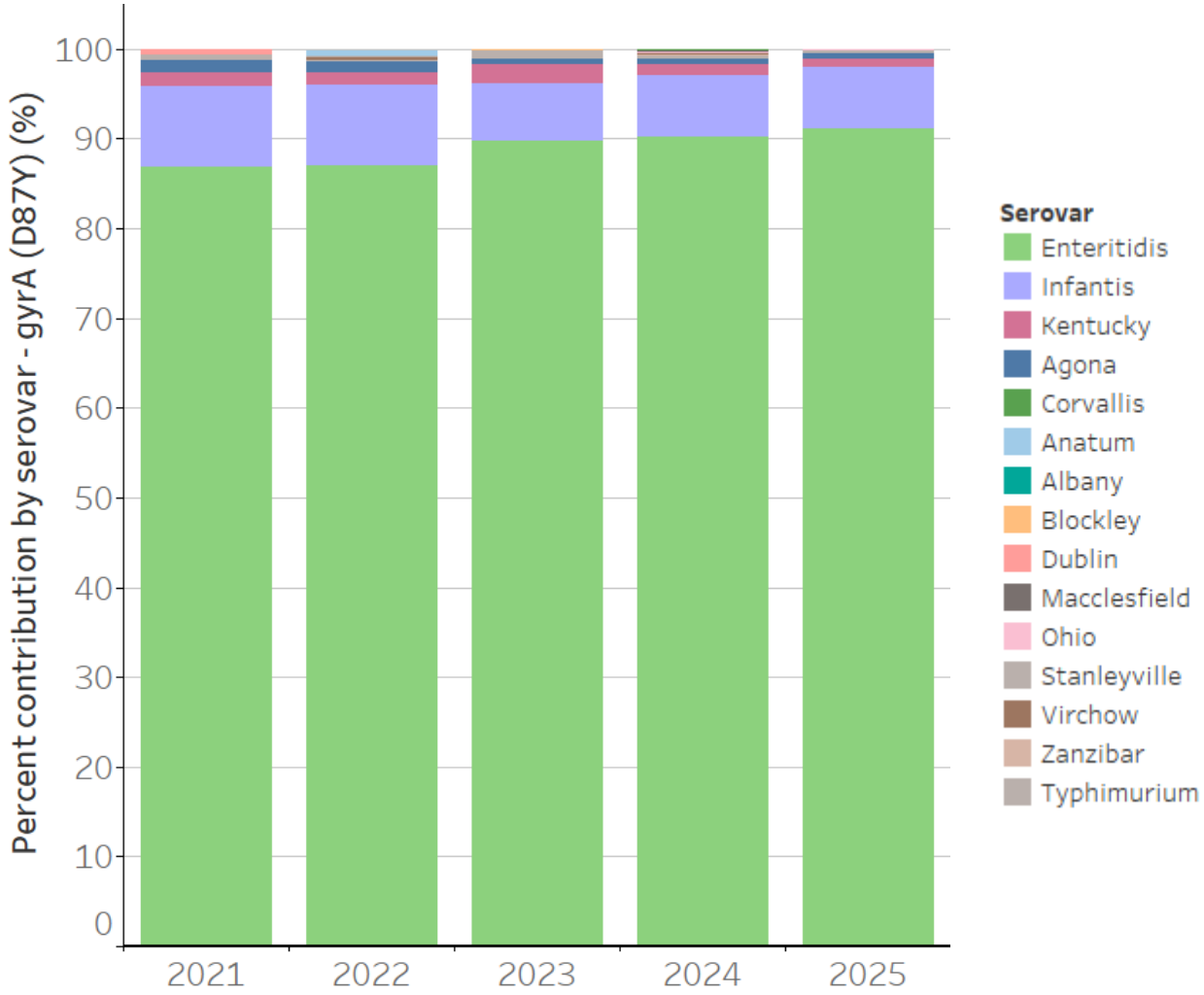
Ciprofloxacin resistance determinants were dominated by *gyrA* (D87Y), which increased since 2021

- *gyrA* (D87Y) was the predominant ciprofloxacin resistance determinant and increased from approximately 10% in 2021 to 27% in 2025.
- Other quinolone resistance determinants, including additional *gyrA* and *parC* mutations and quinolone resistance genes were less common



The increase in the *gyrA* (D87Y) determinant was driven primarily by *Salmonella* Enteritidis

- *Salmonella* Enteritidis had the majority of D87Y mutations, followed by *S.* Infantis and *S.* Kentucky



Take Away Messages – Human *Salmonella*

- High ciprofloxacin resistance persisted in typhoidal *Salmonella*
- Ciprofloxacin and ampicillin resistance increased among non-typhoidal *Salmonella*.
- XDR isolates remained uncommon but continue to be detected in both *S. Tyhpi* and non-typhoidal *Salmonella*.
- Resistance patterns vary substantially by region and serovar.
- A small number of serovars account for a disproportionate burden of antimicrobial resistance:
    - *S*. Dublin, *S*. Kentucky, *Salmonella* I,4,[5],12:i:-, *S*. Newport, *S*. Infantis and S. Enteritidis

Human *Campylobacter*

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

Canada

Most *Campylobacter* infections do NOT require treatment with antimicrobials.

- *Campylobacter* infections most commonly cause self-limiting diarrhea
  - Treatment with antimicrobials is not required or recommended

- Treatment with antimicrobials is considered:
  - When clinical signs are severe or prolonged
    - >6 diarrheal episodes/day, bloody diarrhea, diarrhea lasting >1 week, persistent fever
  - When patient is immunocompromised

  - Culture and susceptibility testing directed treatment options include azithromycin or ciprofloxacin (alternative)

bugsanddrugs.org/CFF1EDAF-526D-4B32-852A-25E3E7F1872E
IDSA 2017 Clinical Practice Guidelines for the Diagnosis and Management of Infectious Diarrhea

Campylobacter has a high incidence rate in Canadians.

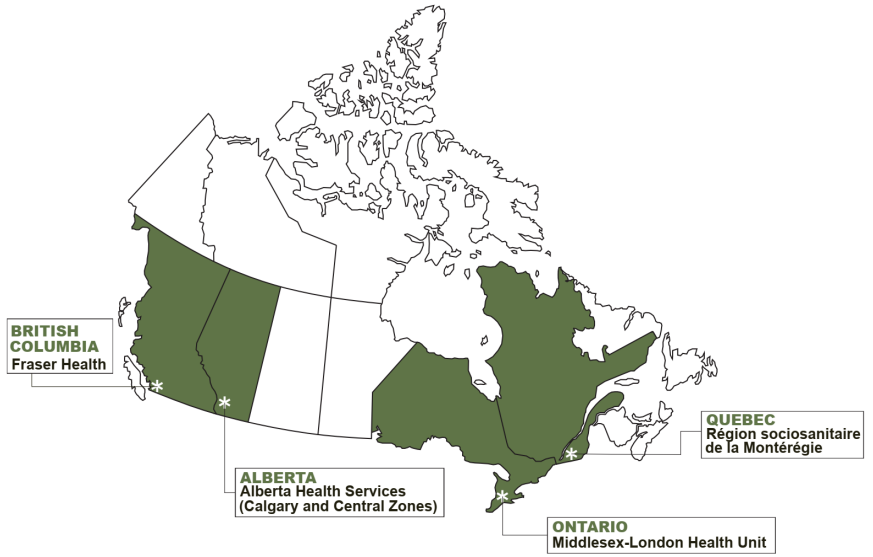
- Incidence rates of Canadians with *Campylobacter* in 2024

	2024 Incidence Rates (Cases/100,000 population)
Campylobacter	17.64

- Source of data – Canadian Notifiable Disease Surveillance System (CNDSS) Notifiable Diseases Online

FoodNet Canada (FNC), the integrated sentinel site surveillance network for enteric disease in Canada.

- *Campylobacter* isolates submitted for Whole Genome Sequencing (WGS) and antimicrobial susceptibility testing (AST) represent a subset of all FNC *Campylobacter* cases
- Some laboratories within various FNC sentinel sites have implemented culture independent diagnostic testing for *Campylobacter.* As a result, the number of culture-confirmed isolates available for WGS and AST may be reduced.
- <1% of cases were excluded due to unresolved data discrepancies
- Data from 2021-2025 are presented with all sentinel sites combined



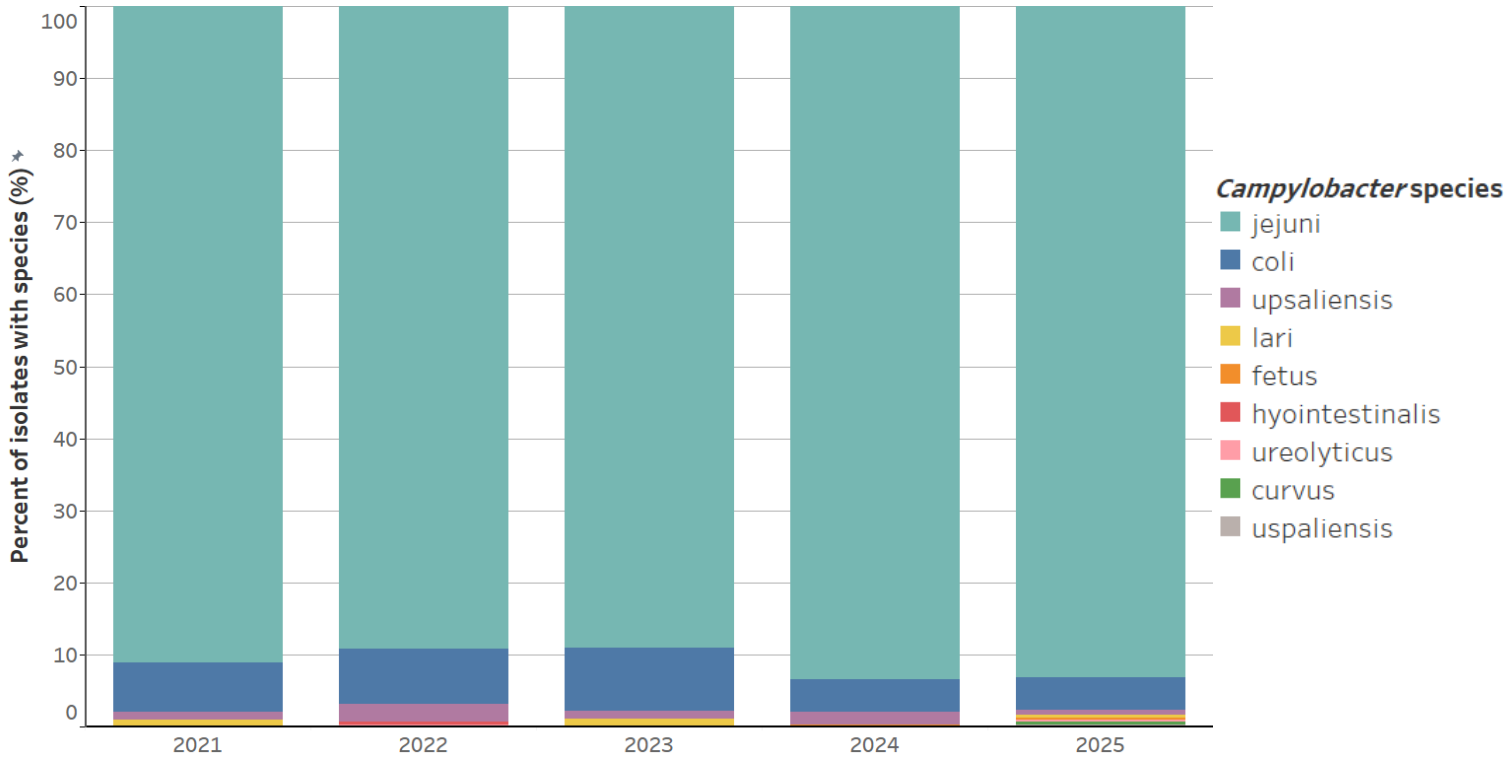
About FoodNet Canada - Canada.ca

IMPORTANT NOTE – Data for 2023, 2024 and 2025 are preliminary and subject to change

C. jejuni is the predominant *Campylobacter* species in humans.

- In 2025, 93% of the cases were *C. jejuni*
- Between 2021 and 2025, *C. jejuni* ranged between 89% and 93% of all cases

- *Campylobacter* predominantly causes gastrointestinal infections*



*2025 case demographic and metadata were unavailable for a subset of cases; however, *Campylobacter* species and antimicrobial resistance data were available for these cases and included in the analysis.

Note: only culture-confirmed *Campylobacter* isolates are included in CIPARS analyses.

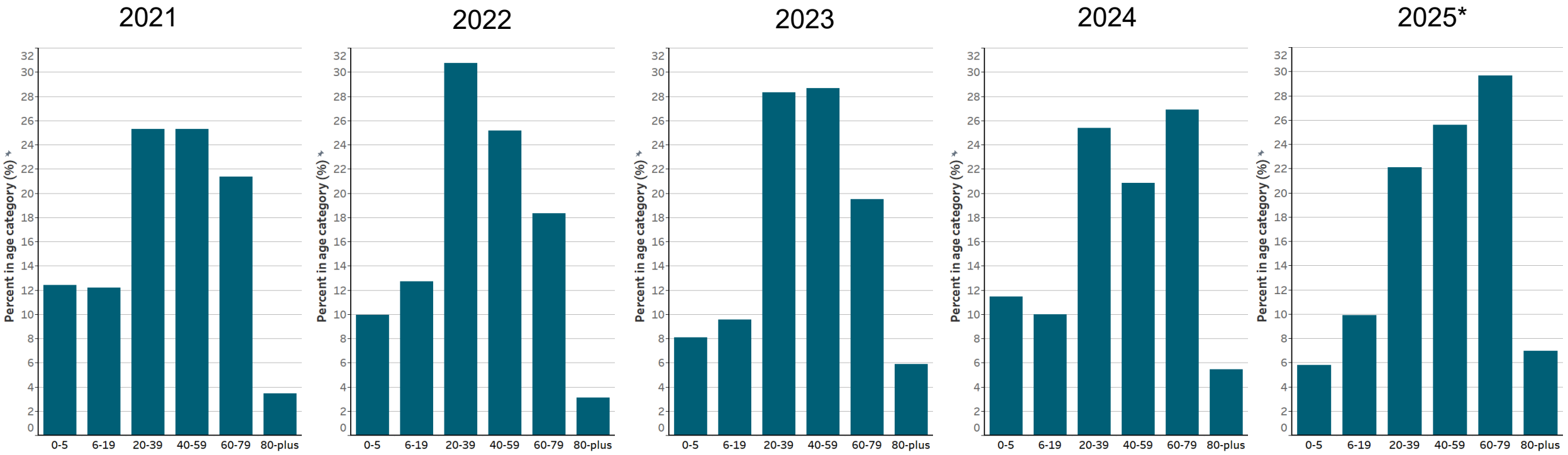
More *Campylobacter* cases in males than females.

- Between 2021 and 2025, males with *Campylobacter* ranged between 54% and 59% of all cases with available metadata*
    - In 2025, 59% of cases with available metadata were male*

*2025 case demographic and metadata were unavailable for a subset of cases; however, *Campylobacter* species and antimicrobial resistance data were available for these cases and included in the analysis.

Variable distribution of age categories in *Campylobacter* cases.

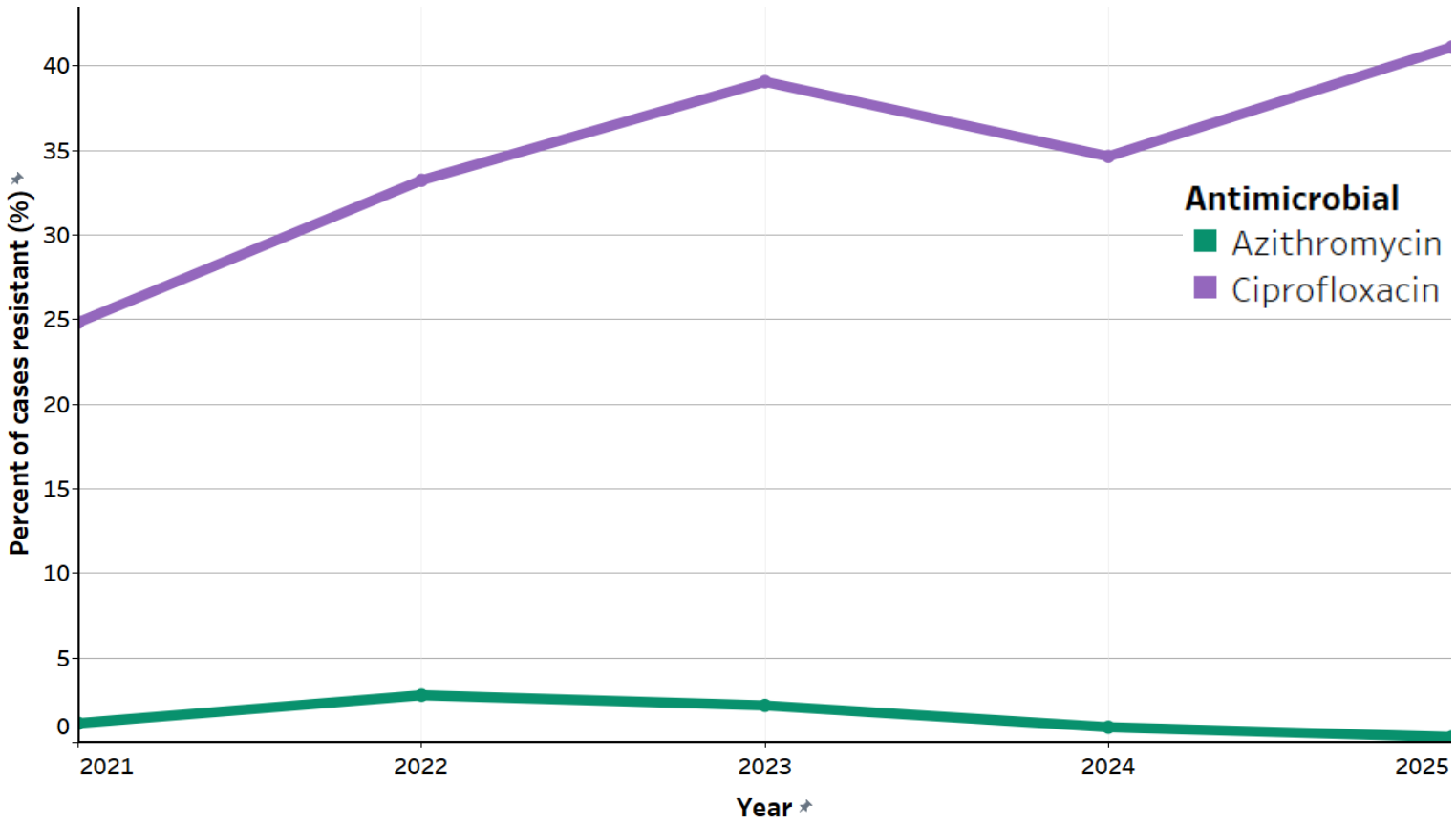
Distribution of age category in human *Campylobacter* cases



*2025 case demographic and metadata were unavailable for a subset of cases; however, *Campylobacter* species and antimicrobial resistance data were available for these cases and included in the analysis.

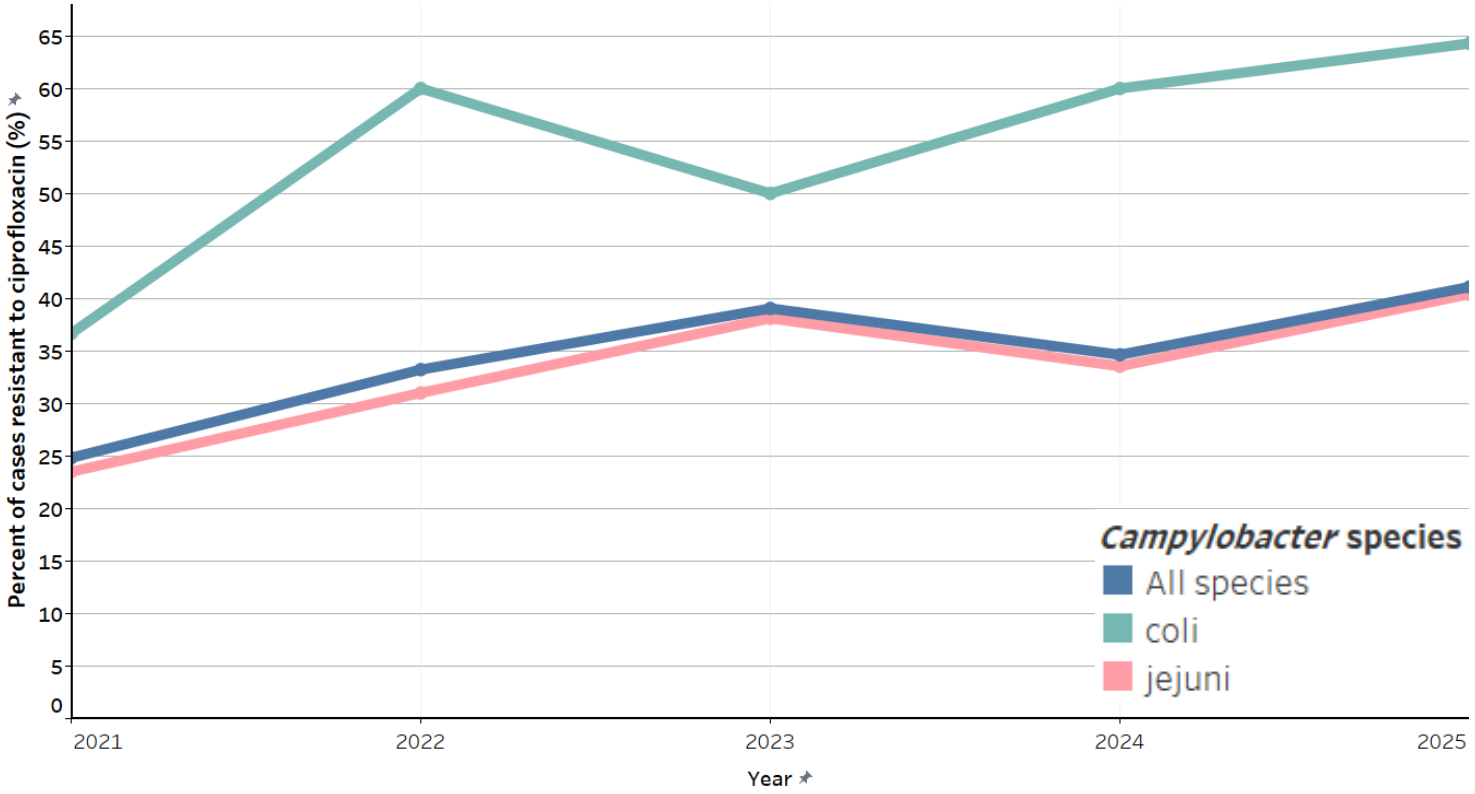
Higher resistance to ciprofloxacin compared to azithromycin.

- **Variable** and **high** resistance to ciprofloxacin, 41% in 2025
- **Low** to **very low** resistance to azithromycin, 0.3% in 2025



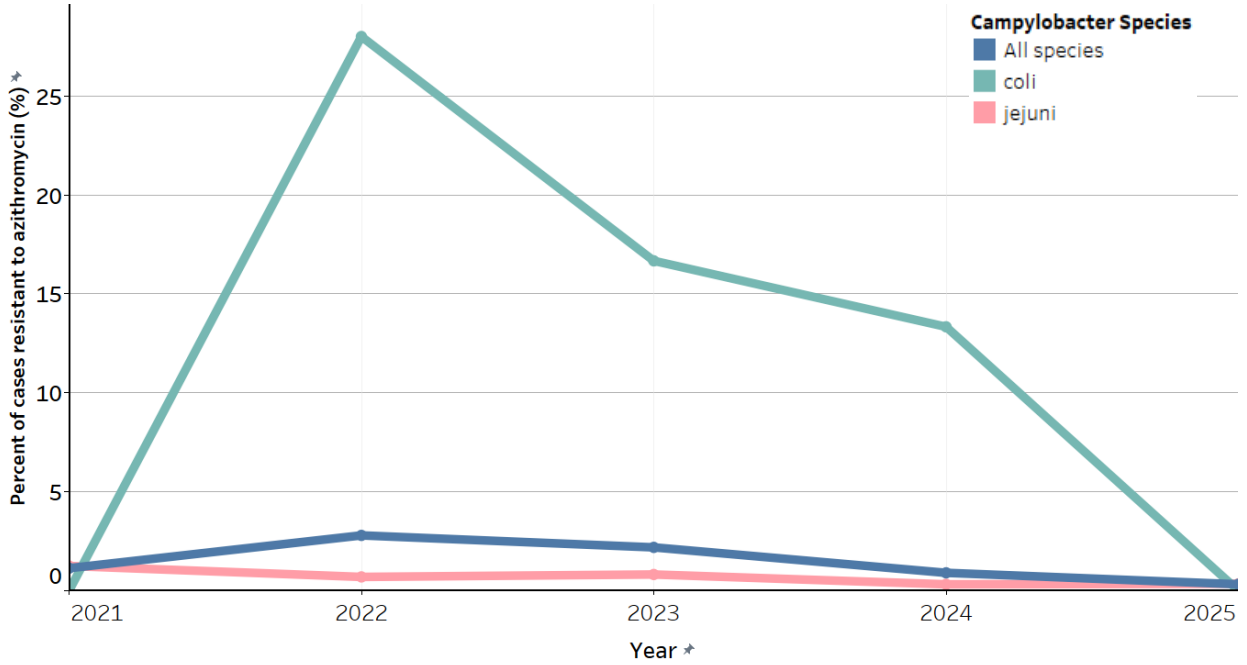
Higher resistance to ciprofloxacin in *C. coli.*

- Compared to the frequency of ciprofloxacin resistance in all *Campylobacter* species
  - *C. coli* was **variable** and **higher**, 64% in 2025 (**Note:** smaller number of cases, some years <20 cases)
  - *C. jejuni* was **similar**, 40% in 2025



Higher resistance to azithromycin in *C. coli.*

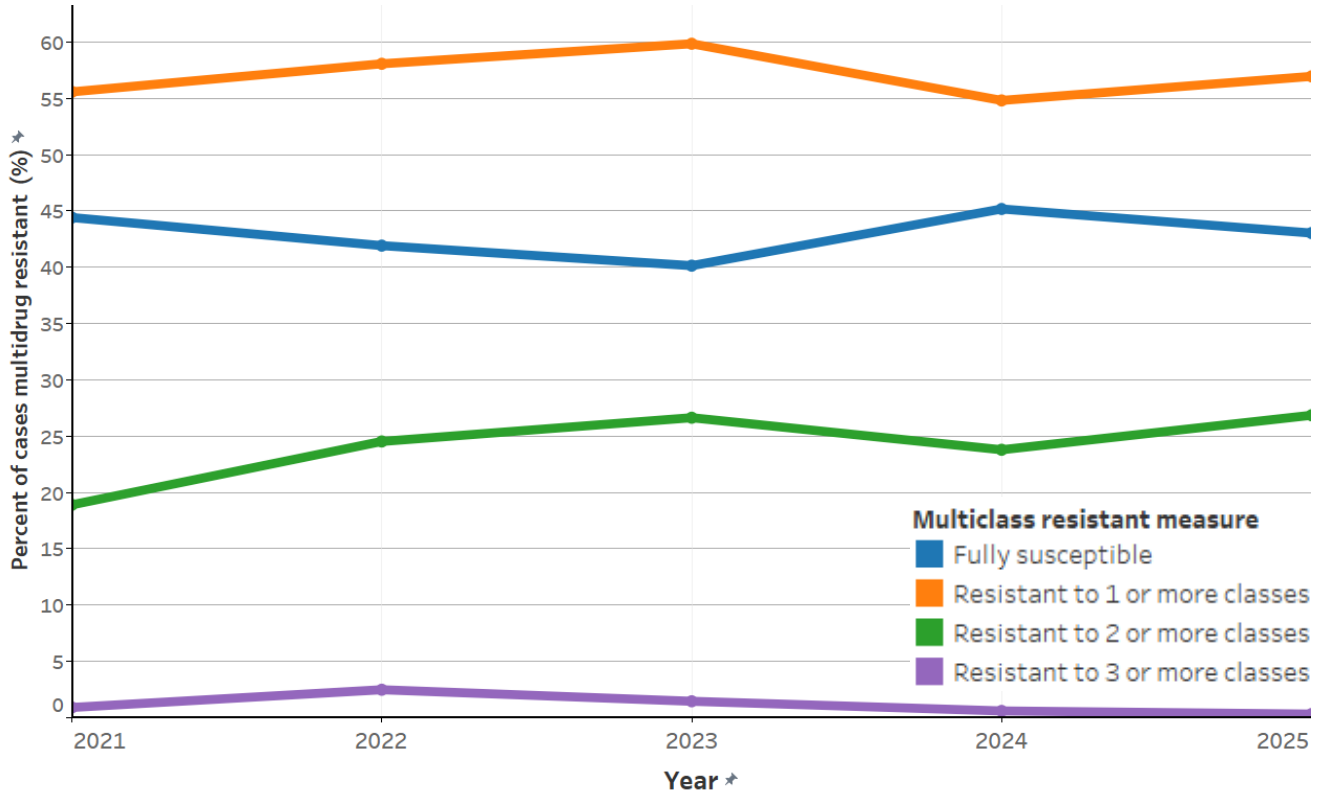
- Compared to the frequency of azithromycin resistance in all *Campylobacter* species
  - *C. coli* was variable and generally **substantially higher** in 2022-2024 (**Note:** smaller number of cases, some years <20 cases).
    - There were no *C.coli* isolates resistant to azithromycin in 2021 or 2025.
  - *C. jejuni* was generally **lower**, 0.35% in 2025



Resistance to 3 or more antimicrobial classes was low to very low.

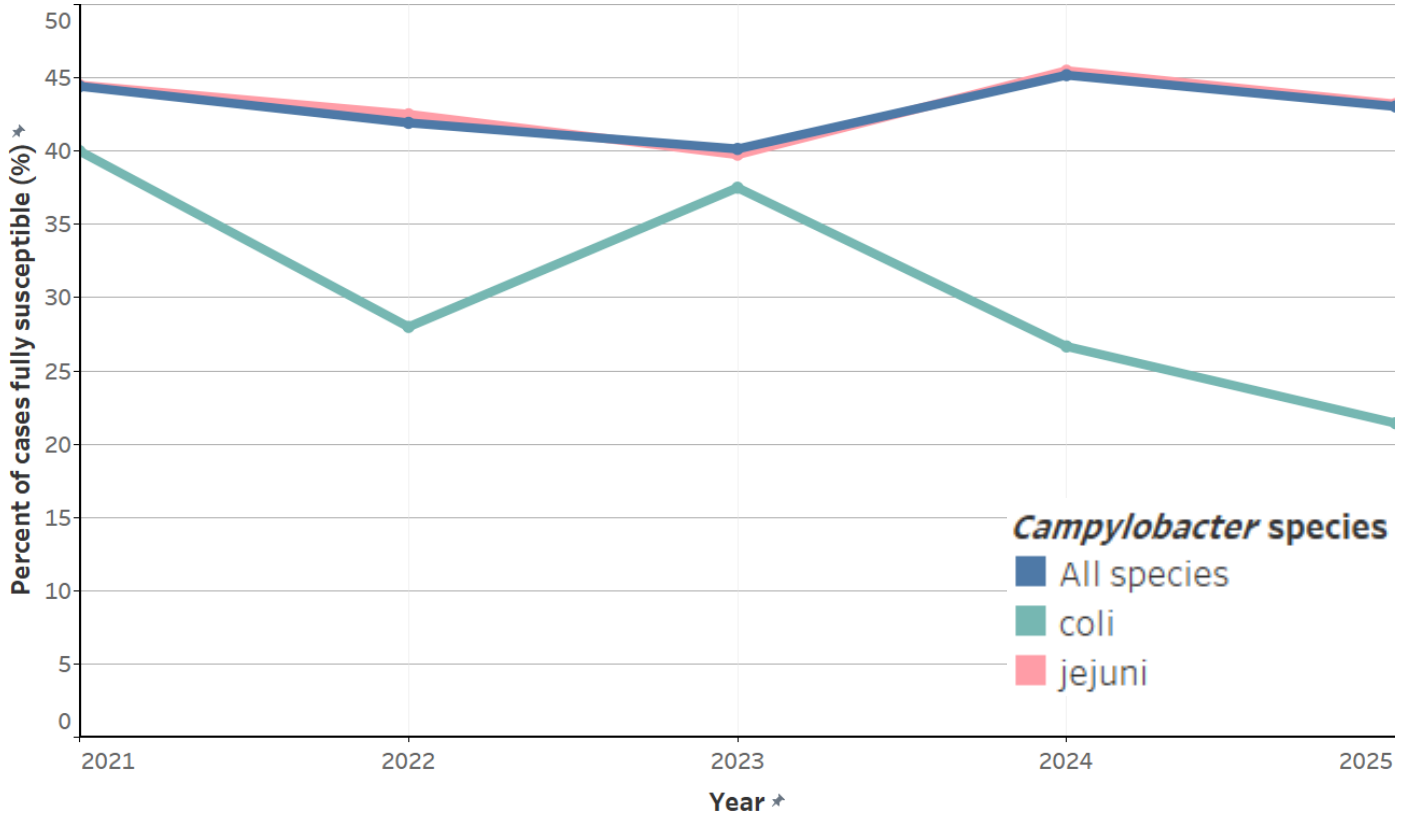
- **Variable** full susceptibility, 43% in 2025

- **Relatively stable** and **low** to **very low** resistance to 3 or more classes, 0.3% in 2025



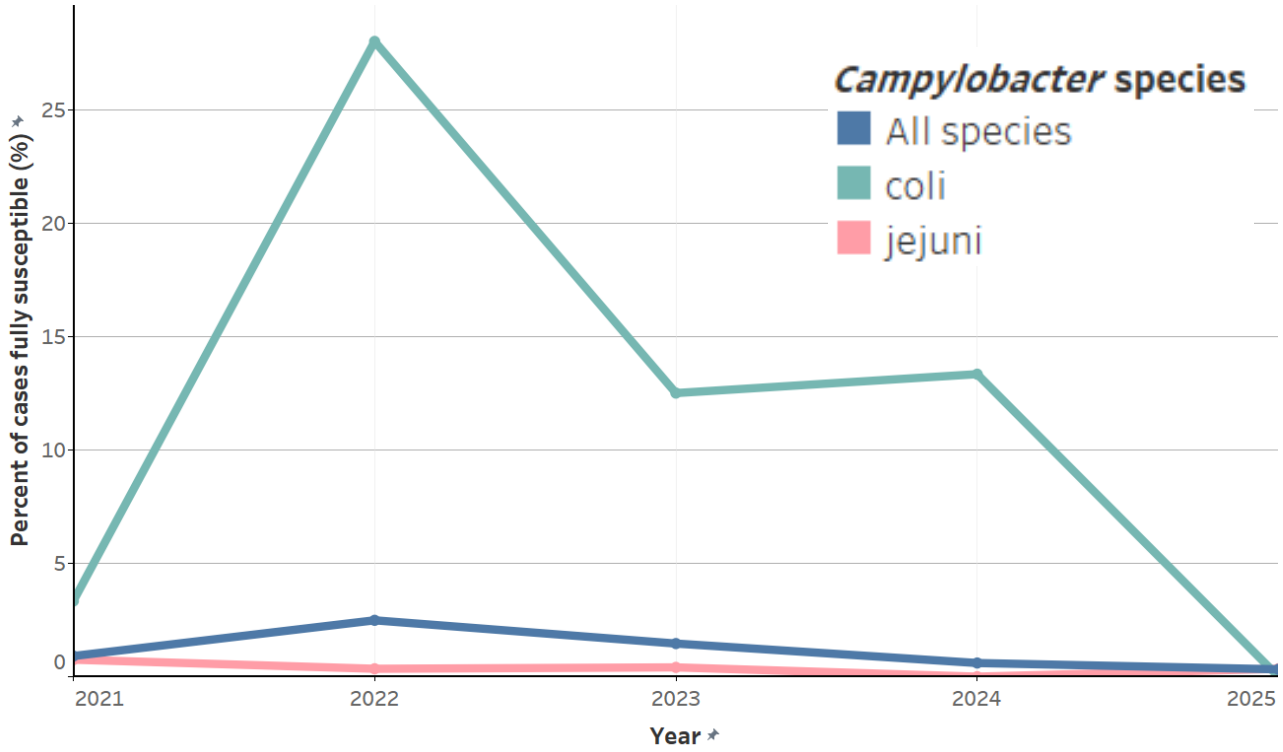
In general, less *C. coli* cases were fully susceptible.

- Compared to the frequency of fully susceptible in all *Campylobacter* species
  - *C. coli* was **variable** and generally **lower** (**Note:** smaller number of cases, some years <20 cases)
  - *C. jejuni* was **similar**, 43% in 2025



Higher resistance to 3 or more classes in *C.* coli cases.

- Compared to the frequency of resistance to 3 or more classes in all *Campylobacter* species
  - *C. coli* was **variable**, however, no *C. coli* isolates were resistant to 3 or more classes in 2025 (Note: smaller number of cases, some years <20 cases).
  - *C. jejuni* was **generally lower**, with only one isolate resistant to 3 or more antimicrobial classes in 2025



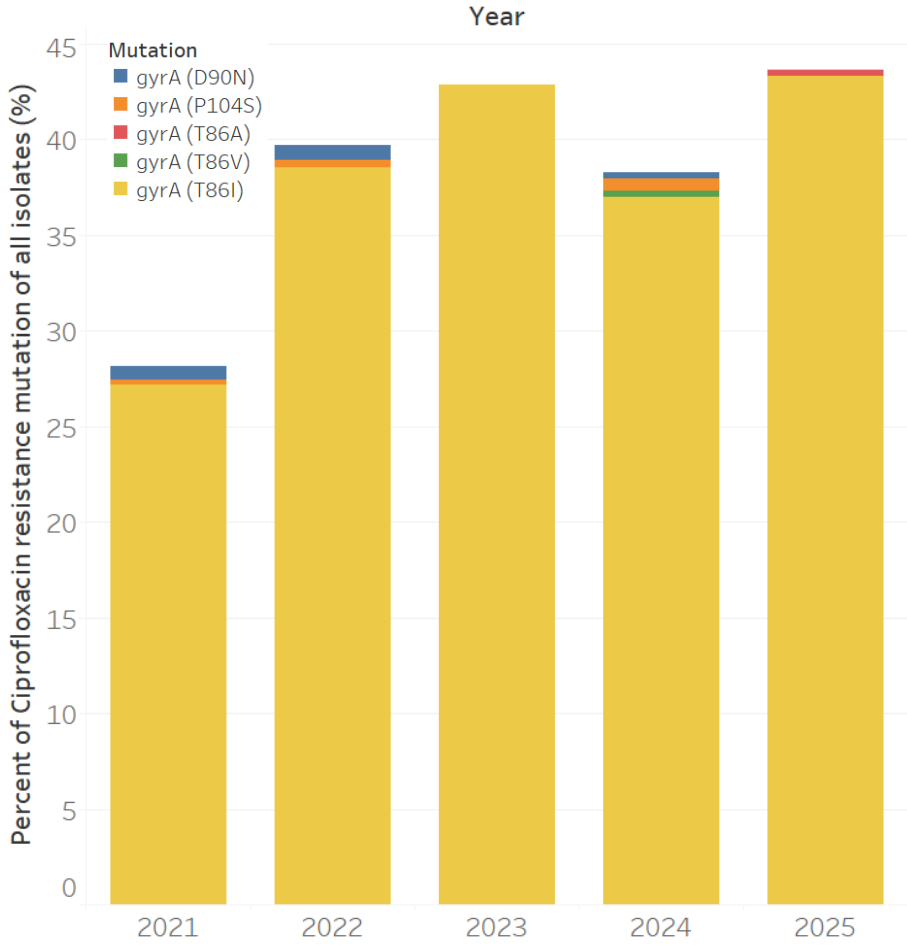
Cases with resistance to 5 or more antimicrobial classes are infrequent; could complicate treatment, if required.

- Maximum resistance seen between 2021 and 2025 was **resistance to 5 antimicrobial classes** (n=3, *C. coli;* n=1, *C. jejuni*)
  - Resistance to aminoglycosides, lincosamides, macrolides, quinolones and tetracyclines including resistance to 6 antimicrobials

- Maximum resistance seen in 2025 was **resistance to 4 antimicrobial classes** (n=1; *C. jejuni*)
  - Resistance to lincosamides, macrolides, quinolones and tetracyclines including resistance to 6 antimicrobials

Ciprofloxacin resistance determinants were dominated by *gyrA* (T86I)

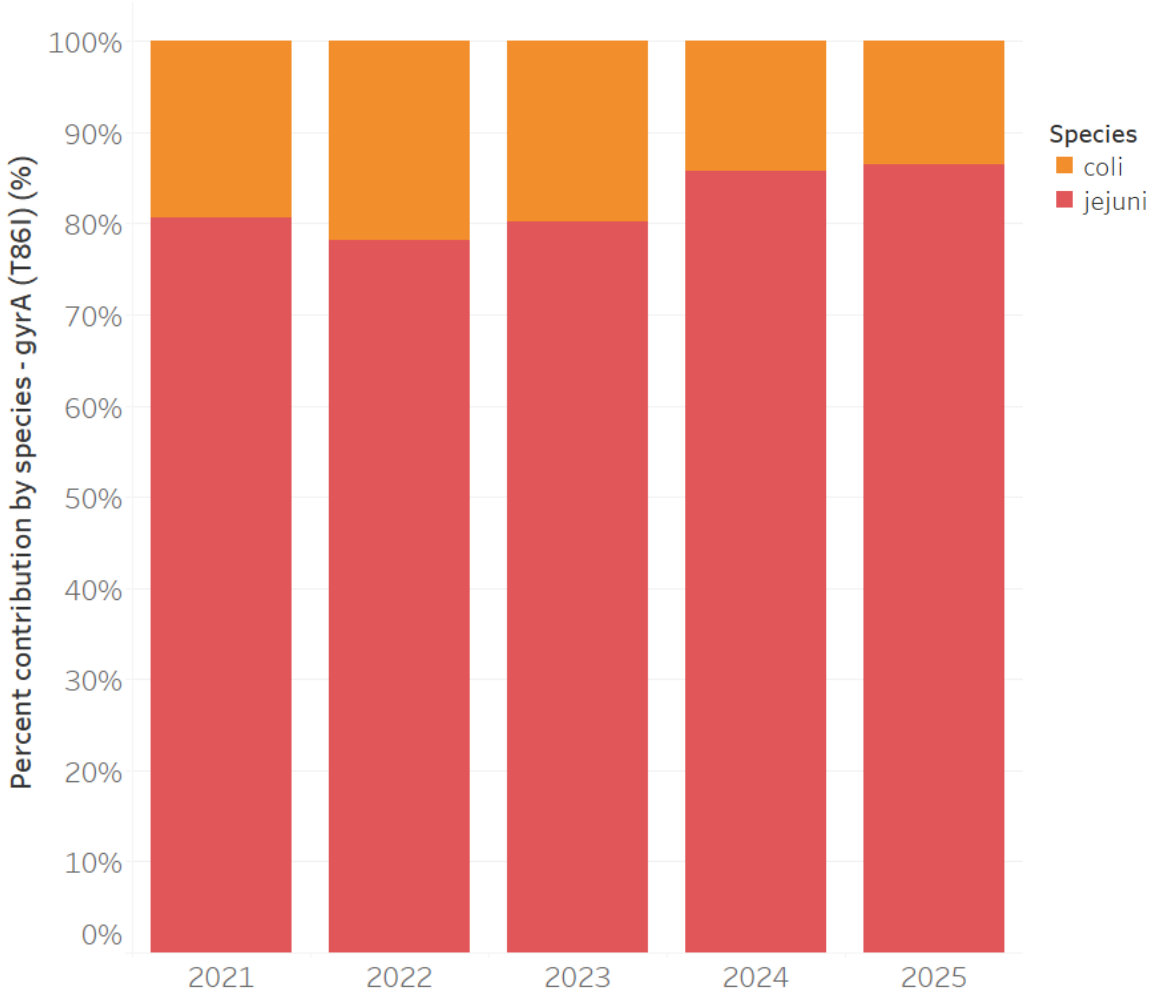
- *gyrA* (T86I) was the predominant ciprofloxacin resistance determinant
- Other *gyrA* mutations, including *gyrA* (D90N), *gyrA* (P104S), *gyrA* (T86A) and *gyrA* (T86V) were detected infrequently



- NOTE: 39% of Ciprofloxacin resistant isolates contained more than one *gyrA* mutation. Each gene mutation is counted separately.

gyrA (T86I) was primarily detected in *C. jejuni*

- *C. jejuni* accounted for the majority (78%-87%) of *gyrA (*T86I*)*-positive isolates
- *C. coli* contributed a smaller proportion of detections each year (13%-22%)



Take Away Messages – Human *Campylobacter*

- *C. jejuni* remained the predominant *Campylobacter* species (>90% of human infections).
- Ciprofloxacin resistance remained **high** and increased over time, while azithromycin resistance remained **very low**.
- *C. coli* consistently exhibited higher resistance levels than *C. jejuni*.
- More than half of *Campylobacter* cases were resistant to at least one antimicrobial class.
- Resistance to ≥3 classes was **very low** to **low** and primarily observed in *C. coli*.

Where can I find more information?

CIPARS interactive data visualizations

https://health-infobase.canada.ca/cipars/

CARSS interactive data visualizations

Human *Salmonella*: https://health-infobase.canada.ca/carss/

CIPARS website

https://www.canada.ca/en/public-health/services/surveillance/canadian-integrated-program-antimicrobial-resistance-surveillance-cipars.html

FNC website

https://www.canada.ca/en/public-health/services/surveillance/foodnet-canada.html

FNC interactive data visualizations

https://health-infobase.canada.ca/foodnet-canada/

Acknowledgements

- NML Division of Bacteriology and Enteric Diseases and PulseNet Canada
- Provincial Public Health Laboratories
- FoodNet Canada Sentinel Sites (*Campylobacter*)
- National Enteric Surveillance Program (NESP)

Questions

Contact Information for CIPARS Human Component

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