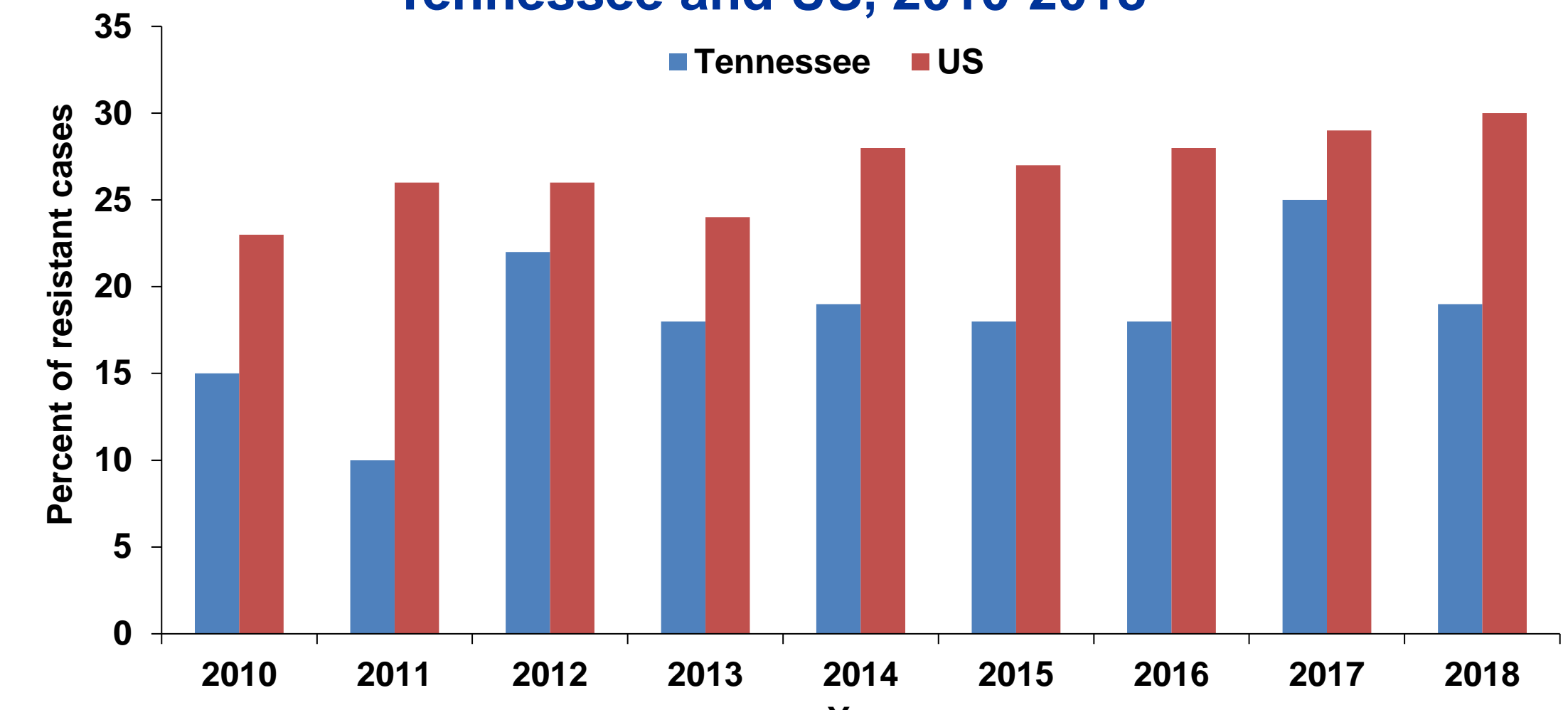


BACKGROUND

- Campylobacter* causes an estimated 1.5 million infections each year in the US with approximately 448,400 (29%) infections caused by antimicrobial resistant strains
- Resistance to quinolones (e.g., nalidixic acid and ciprofloxacin) has not changed in Tennessee in recent years (Figure 1). However, rates are still lower than the national trends
- Campylobacter* infection is commonly attributed to consuming poultry products. However, past studies were limited for attribution
- Tennessee collected a standardized set of exposures on sporadic *Campylobacter* cases from 2016-2018
- We analyzed these data to test attribution hypotheses

Figure 1. Fluoroquinolone-resistant *Campylobacter* cases, Tennessee and US, 2010-2018*



* Only *C. jejuni* and *C. coli* cases are shown.

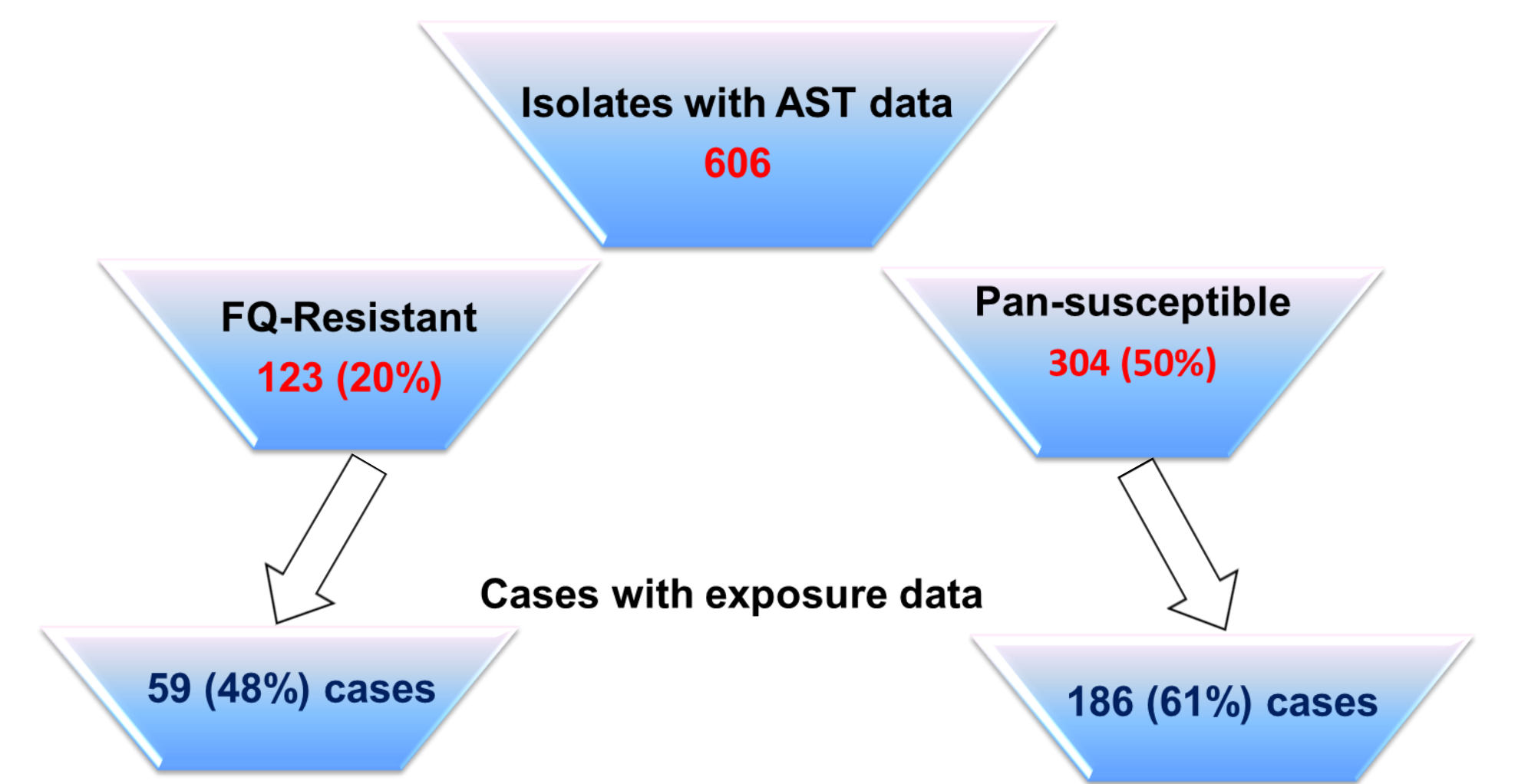
METHODS

- Tennessee submitted all human *Campylobacter* isolates to CDC's National Antimicrobial Resistance Monitoring System (NARMS)
- Antimicrobial susceptibility testing (AST) and whole genome sequencing (WGS) were performed on the *Campylobacter* isolates
- Isolates with MIC ≥ 1 for ciprofloxacin and/or ≥ 32 for nalidixic acid or isolates with *gyrA* (86) gene, the common predictor of fluoroquinolone (FQ) resistance, were categorized as FQ-resistant cases
- Food/non-food exposures in the 7 days prior to the illness onset were compared between FQ-resistant cases and pan-susceptible cases. Outbreak-associated cases were excluded.
- Univariate analysis and cross-tabulation were performed to estimate the odds ratio (OR) and *p*-value using Epi Info 7

RESULTS

- A total of 606 *Campylobacter* cases had susceptibility profiles (Figure 2):
 - 20% were resistant to FQ
 - 50% had no resistance to antibiotics (pan-susceptible)
- Exposure history was available for about half of the cases in each group:
 - 48 % of FQ-resistant cases
 - 61% of pan-susceptible cases

Figure 2. Fluoroquinolone-resistant and pan-susceptible *Campylobacter* cases with exposure data, Tennessee, 2016-2018*



* The remaining isolates, 179 (30%) of 606, were resistant to traditional antibiotics and were not included in this analysis

- All 59 FQ-resistant cases with exposure data were resistant to both ciprofloxacin and nalidixic acid by AST and included in the analysis (Table 1):
 - 28 were also resistant to tetracycline
 - 9 were also resistant to other traditional drugs.
- Genetic resistance patterns were available for 54 (92%) of 59 FQ-resistant isolates:
 - 85% of them expressed *gyrA* (86) gene mutation

Table 1. Phenotypic and genotypic profiles of Fluoroquinolone-resistant cases with exposure data, Tennessee, 2016-2018

Resistance pattern*	Number of cases identified by AST	Number of cases identified by WGS	<i>gyrA</i> (86) gene
CipNal	22	19	16
CipNalT	28	26	25
CipNal + ≥ 2 more drugs	9	9	5
Total	59	54 (92%)	46 (85%)

* Cip (ciprofloxacin), Nal (nalidixic acid), T (tetracycline)

Table 2. Most commonly reported exposures among FQ-resistant and pan-susceptible cases*

Exposure	FQ-resistant cases (N=59) n (%)	Pan-susceptible cases (N = 186) n (%)	OR	<i>p</i> -value
Food				
Handled raw fish/seafood	8 (14)	9 (5)	3.1	0.03
Ate chicken/food containing chicken	48 (81)	126 (67)	2.1	0.03
Ate any seafood	10 (17)	15 (8)	2.3	0.05
Ate any fish or fish products	9 (15)	18 (10)	1.7	0.16
Ate pork/food containing pork	25 (42)	63 (34)	1.4	0.15
Drank pasteurized cow's/goat's milk	22 (37)	51 (27)	1.3	0.21
Handled raw poultry	22 (37)	58 (31)	1.3	0.23
Ate soft cheese as queso fresco/brie	12 (20)	30 (16)	1.3	0.28
Handled raw meat	26 (44)	74 (40)	1.2	0.33
Ate or drank any dairy products	48 (81)	145 (78)	1.2	0.36
Non-food				
Reported international travel	9 (15)	7 (4)	4.6	0.00
Visited/worked/lived on animal setting	13 (22)	31 (17)	1.4	0.22
Used water from a private well	11 (19)	27 (15)	1.3	0.28
Had household with diarrhea	8 (14)	22 (12)	1.2	0.43
Had contact with any live poultry	12 (20)	37 (20)	1.0	0.53

* Exposures are sorted in order by magnitude of the OR from the biggest to the smallest

- Consumption of chicken (OR 2.1, *p*-value 0.03) and handling raw fish/seafood (OR 3.1, *p*-value 0.03) were significantly associated with FQ-resistant cases



- No significant differences among other food exposures noted
- Non-food exposures were reported by fewer cases.
- International travel was more likely associated with FQ-resistant cases (OR 4.6, *p*-value 0.004)

CONCLUSIONS

- Pairing susceptibility data with exposure data was useful for testing hypotheses about *Campylobacter* source attribution
- Consumption of chicken and handling of raw fish/seafood were significantly associated with fluoroquinolone-resistant cases
- Fluoroquinolone-resistant *Campylobacter* infections can be acquired domestically or internationally

LIMITATIONS

- Small sample size of isolates submitted to SPHL
- NARMS susceptibility data for some isolates were not available for analysis
- Limited exposure data collected from cases

RECOMMENDATIONS

- Improve submission of *Campylobacter* clinical isolates to the SPHL for confirmation, molecular subtyping and susceptibility testing
- Whole Genome Sequencing (WGS) of *Campylobacter* isolates will provide additional predicted resistance data but must be coupled with rigorously collected exposure data to better understand the source attribution of different strains
- More control efforts are needed to understand and reduce fluoroquinolone resistance

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