

CDFA AUS Multi-Year Report on the California-Specific NARMS Data—2014-2023
Campylobacter

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Scope of Report and California Significance: As part of the core mission of the California Department of Food and Agriculture (CDFA) Antimicrobial Use and Stewardship (AUS) program to inform efforts to mitigate antibiotic resistance and identify emerging areas of concern and potential public health threats, as data is available, AUS will generate regular reports to monitor antibiotic resistance and reduced susceptibility trends of four common bacteria, some of which cause foodborne illness in humans and others that are monitored as indicators, by utilizing NARMS data from samples collected from food-producing animals slaughtered in California at the time of processing.

Disclaimer: Antibiotic resistance, which includes measures of reduced susceptibility, is a highly complex problem influenced by many factors. The data CDFA AUS have presented here can be used to monitor several years of bacterial susceptibility to drugs important in human medicine. These bacteria can be common causes of foodborne illness or may be monitored as indicator bacteria; both are found in samples from livestock slaughtered in California. These data are best used to monitor trends over multiple years; yet, drawing conclusions to prompt specific interventions should be avoided. Additionally, caution should be applied when making broad generalizations or host species comparisons, understanding these data's limitations in reflecting differences in production practices for these animal species. Finally, caution must be applied when interpreting these data, as they are not representative of on-farm resistance profiles due to cross-contamination during transport, animal holding, and processing.¹⁻³ They, therefore, should **not** be used as a surrogate to reflect the impact of on-farm antibiotic use on public health.



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Introduction

Antibiotics are life-saving drugs vital to protect people and animals from bacterial infections. Antibiotic resistance occurs when bacteria evolve in a way that renders antibiotics ineffective. Resistance can be intrinsic due to specific structural or functional properties of the bacteria, but it can also occur naturally secondary to environmental pressures and can be acquired from other bacteria. Resistance to antibiotics makes common infections in people and animals a challenge, or even impossible, to treat. While the number of human deaths in the U.S. from antibiotic resistance has decreased since 2013, there remain approximately 2.8 million antibiotic-resistant infections diagnosed per year, causing 35,000 fatalities.⁴ The impact of antibiotic resistance is observed in a high percentage of human foodborne illnesses associated with antibiotic-resistant bacteria, resulting in increased morbidity and mortality.⁵ In California, the most recent CDC data, from 2017, reported 107 foodborne illness outbreaks, a 9% increase from 2016, highlighting the ongoing need to monitor foodborne illness and resistance trends.^{6,7}

Antibiotic resistance in foodborne bacteria is a significant public health threat. In response to this global concern, the National Antimicrobial Resistance and Monitoring System (NARMS) program was developed in the United States. NARMS is a collaboration between the Centers for Disease Control and Prevention (CDC), the Food and Drug Administration (FDA), and the US Department of Agriculture (USDA) Food Safety and Inspection Services (FSIS). The purpose of NARMS is to provide national surveillance in the U.S. of drug-resistant bacteria that cause foodborne illness by collecting samples from clinically ill humans (CDC), retail meats (FDA), and food animals at the time of slaughter (USDA-FSIS). NARMS' data are regularly published on their online dashboard.⁸

In a concurrent effort to monitor antibiotic resistance trends, the California Department of Food and Agriculture (CDFA) established the Antimicrobial Use and Stewardship (AUS) program. This first-in-the-nation program implements the directives of Food and Agricultural Code (FAC) 14400-14408 to provide educational tools for veterinarians and producers on disease prevention and optimal antibiotic use in food animals and to conduct and disseminate evidence-based research on antibiotic resistance trends.

CDFA AUS generates California-specific reports summarizing NARMS information from USDA-FSIS sampling, as provided to CDFA AUS via Freedom of Information Act (FOIA) requests. These reports aim to evaluate antibiotic susceptibility trends in the most-reported bacterial causes of foodborne illness in samples collected from food animals slaughtered in California and in fulfillment of the mandates of FAC 14405 (a) and (b). This CDFA AUS Multi-Year *Campylobacter* Report provides summary data for USDA-FSIS NARMS *Campylobacter* isolates collected from 2014 through 2023 from animals slaughtered in California.



NARMS Methodology

The complete sampling and laboratory methodologies used by FSIS processing facilities for sample collection and processing can be found online or by contacting USDA FSIS.^{9,10}

Sample Collection

Samples are collected for the NARMS program at FSIS-regulated slaughter facilities across the United States. Only data from FSIS-regulated slaughter facilities in California are included in the California-specific results presented in this report. Notably, these data represent cattle, poultry, and swine that are both raised and slaughtered in California, as well as animals raised in other states but slaughtered in California.

Bacteria identified from testing conducted on NARMS samples by the USDA's Agricultural Research Service are *Salmonella*, *Escherichia coli* (*E. coli*), *Enterococcus*, and *Campylobacter*. *Salmonella* and *Campylobacter* are important causes of foodborne illness in people, whereas *Enterococcus* and *E. coli* are used as indicator bacteria to monitor resistance patterns to antibiotics utilized in the treatment of Gram-negative and Gram-positive bacterial infections. USDA FSIS collects samples at slaughter for the NARMS Cecal Sample Program, which are taken from the intestinal contents of cattle (including dairy and beef cows, steers, heifers, and veal), swine (market swine and sows), chickens, and turkeys. These samples, collected early in the slaughter process, are referred to as "cecal samples" throughout the report. The approach used by NARMS for sample collection, along with their data reporting methods and differing management, husbandry, and antibiotic use practices for various food animal species, complicates both the separation of NARMS data by commodity type for some species (e.g. beef vs. dairy cattle) and the grouping of other species, such as chickens and turkeys, into a single poultry category. Therefore, in this report, AUS presents the NARMS data categorized solely by animal species: cattle, chicken, turkey, and swine. This categorization aims to reduce inaccuracies in data reporting.

FSIS also collects samples as part of its routine verification testing program for Pathogen Reduction/Hazard Analysis Critical Control Point (PR/HACCP). These HACCP samples are taken after the point in the slaughter process where specific practices designed to prevent or eliminate contamination from disease-causing bacteria have already been implemented. Please note that these data are not included in this report.

Antibiotic Susceptibility Testing

The cecal samples collected for NARMS are tested for four target bacteria: *Salmonella*, *Campylobacter*, generic *E. coli*, and *Enterococcus*. The purified bacteria isolated from these samples are referred to as bacterial isolates. These isolates undergo further testing, known as antibiotic susceptibility testing (AST). Details on the corresponding AST methodology for each antibiotic type used for *Campylobacter* isolate testing are available in **Appendix A**. AST testing identifies whether the bacterial isolate is considered susceptible to a panel of antibiotics. This is



accomplished by determining the tested concentration of an antibiotic that inhibits bacterial growth, known as the minimum inhibitory concentration (MIC). The MIC value can be used to categorize the bacteria based on their relation to established cutoff values. NARMS utilizes standardized cutoff values, called breakpoints, established by the Clinical and Laboratory Standards Institute (CLSI) for *Enterococcus*, *Salmonella*, and *E. Coli* or, in the case of *Campylobacter*, epidemiological cut-off values (ECOFFs),¹¹ to interpret MIC values. CLSI breakpoints categorize bacterial isolates as susceptible, intermediate, or resistant to a tested antibiotic based on clinical, pharmacological, and microbiological data. In contrast, ECOFFs, which are also specific to the bacterial species-antibiotic combination, do not factor in clinical parameters or host species into the interpretation of results and distinguish bacterial populations as wild-type and non-wild-type strains. Despite using ECOFFs in their data reporting, NARMS classifies *Campylobacter* isolates as either "susceptible" or "resistant" as described in **Appendix B**. However, for the purposes of this report, because the *Campylobacter* data utilizes ECOFFs as interpretive criteria, we will use the terms 'wild-type' and 'non-wild-type' for the resulting MIC interpretations.¹² According to EUCAST,¹³ isolates designated as wild-type are those that do not exhibit phenotypically detectable acquired mechanisms of resistance to the antibiotic being evaluated. Conversely, non-wild-type isolates possess acquired mechanisms of resistance to the antibiotic being tested, which is reflected as reduced susceptibility.

The specific NARMS antibiotic panel used for testing depends on the bacteria being analyzed. The NARMS panel used to test *Campylobacter* isolates can be found in **Appendix C** of this report. Some of the antibiotics included in this panel are used therapeutically in food animals, while others are not. For those antibiotics that are not used in food animals, alternative drug formulations within the same antibiotic class may still be approved for such use. Additional details regarding this information are provided in **Appendix C**.

Whole Genome Sequencing

Whole genome sequencing (WGS) is a methodology used to enhance antibiotic resistance surveillance by identifying known antibiotic resistance genes that bacteria may possess. While, for some bacteria, WGS may correlate highly with the resistance observed in the environment, not all antibiotic resistance is caused by genetic alterations; and, bacteria carrying resistance genes do not necessarily display resistance in laboratory testing or a clinical setting.

Campylobacter

General Overview

Campylobacter is the leading cause of human diarrheal illness in the United States and is classified by the CDC as a "Serious Threat."¹⁴ In 2019, drug-resistant *Campylobacter* was responsible for 70 human deaths, marking a 150% increase since 2013.⁴ The most common symptoms of infection include diarrhea (often bloody), stomach cramps, nausea, and vomiting.¹⁵⁻¹⁷ In rare cases,



infection can lead to a neurological condition called Guillain-Barré Syndrome.¹⁶⁻¹⁸ Infection during pregnancy can result in miscarriage, stillbirths, and neonatal deaths.¹⁹ While most infections are mild and resolve without treatment or antibiotics, in some cases, the infection can cause more severe illness. As the third leading cause of hospitalization for gastroenteritis, 10% or more of foodborne illness cases caused by *Campylobacter* require hospitalization.¹⁶ Individuals who experience severe illness or belong to higher-risk groups—such as infants, young children, adults over the age of 65, pregnant women, and individuals with weakened immune systems—may require treatment with antibiotics.¹⁶⁻¹⁸

Outbreaks caused by *Campylobacter* are rare, but they are becoming increasingly common. Recent multi-drug-resistant outbreaks have been linked to contact with puppies from pet store settings.²⁰ Notably, most cases do not occur as part of an outbreak, and many minor infections go undiagnosed or unreported.¹⁷ One way individual people can become sick from *Campylobacter* is by consuming undercooked meat or raw milk.

Unlike in people, *Campylobacter* typically does not cause disease in most food animal species. It is considered a normal component of the bacterial population in their gastrointestinal tracts, and can be intermittently shed in their feces.^{21,22} *Campylobacter* can contaminate food products if proper precautions are not taken during the slaughter and processing of animals, or their edible products, for consumption. Additionally, fecal contamination during milking increases the risk of human illness when raw milk is consumed.

In people who develop moderate to severe infections, or for those who are at high risk for complications, the selection of antibiotics to treat illnesses caused by *Campylobacter* is typically guided by the patient's AST results.²³ Since *Campylobacter* exhibits inherent resistance to most beta-lactam antibiotics, including amoxicillin, amoxicillin-clavulanate, and cephalosporins, as well as trimethoprim-sulfamethoxazole,²³ first-line antibiotics used to treat human *Campylobacter* infections typically include those from the quinolone class, such as ciprofloxacin, and the macrolide class, including azithromycin and erythromycin.¹⁷

Notably, ciprofloxacin, nalidixic acid, and azithromycin are not used in food animals. Furthermore, no antibiotics from the quinolone class are authorized for use in animal feed in the U.S. While erythromycin, given in medicated feed and water, is approved for use in chickens and turkeys, data indicate that its use in poultry raised in California is rare.²⁴ Similarly, although other macrolide drug formulations are approved for use in animal feed, their usage in California-raised food animals appears to be minimal.²⁴ Some injectable antibiotics from the quinolone and macrolide classes are approved for use in food animals, including erythromycin in cattle. However, these drugs are generally administered to individual animals suffering from diseases that pose significant risks to their health and welfare if left untreated. For a comprehensive list of approved drugs and details regarding the use of antibiotics in food animal production, please refer to **Appendix C**.



Number of Samples Screened and Isolates That Underwent AST

The number of samples screened as part of the NARMS Cecal Sample Program is facility-dependent and based on the production volume and the target number of bacterial isolates needed for AST as determined by NARMS, while aiming to make the data representative of the industry.¹⁰ Cecal samples are obtained from individual cattle and swine, but are combined from five birds for chicken and turkey sampling procedures.¹⁰

The number of samples screened and *Campylobacter* isolates obtained for the NARMS Cecal Sample Program from food animals slaughtered in California are presented in **Table 1**. The number of these bacterial isolates that underwent AST by animal species is shown in **Table 2**. A total of 1,205 *Campylobacter* isolates were obtained from 2,916 screened NARMS cecal samples collected from food animals slaughtered in California between 2014 and 2023. Of those isolates, 978 from cattle, 87 from chickens, 66 from turkeys, and 74 from swine underwent AST testing during this time period.

The yearly number of *Campylobacter* isolates from each animal species used for AST from California-slaughtered food animals, except cattle, is typically below 30. Thirty is the threshold AUS uses for statistical validity and improved predictive value when evaluating cumulative susceptibility data, as recommended by the CLSI M39 guidelines.²⁵ This means that, due to low numbers, the *Campylobacter* AST data for isolates from California-slaughtered food animals tested through NARMS each year may not be representative of the larger population of *Campylobacter* in animals slaughtered in California. Indeed, variations in resistance rates may result from analyzing a limited number of isolates rather than reflecting true changes in susceptibility.²⁶ While the data showing the percent of non-wild-type isolates, which are isolates with phenotypically acquired resistance mechanisms reflecting reduced susceptibility, are presented for each animal species below, interpretations of population trends in *Campylobacter* susceptibility for isolates obtained from chickens, turkeys, and swine cannot be made due to the limited number of isolates tested for these host species.

Table 1. Number of NARMS Cecal Samples from California-Slaughtered Food Animals Screened for Campylobacter and Screening Results, 2014-2023, by Animal Species

Year		Cattle*	Chickens	Turkeys	Swine
2014	Negative	141	7	10	38
	Positive	125	6	3	11
2015	Negative	131	14	12	24
	Positive	90	4	3	10
2016	Negative	140	11	12	56
	Positive	115	2	3	7
2017	Negative	169	5	6	50
	Positive	134	11	7	15
2018	Negative	196	8	7	55
	Positive	165	20	11	13
2019	Negative	191	7	1	27
	Positive	145	19	13	12
2020	Negative	61	4	2	15
	Positive	24	1	2	4
2021	Negative	105	3	2	9
	Positive	27	1	1	0
2022	Negative	75	3	5	35
	Positive	59	44	6	4
2023	Negative	66	0	4	18
	Positive	53	11	9	2

*The cattle category does not include bob veal due to the lack of CA-specific isolates for this cattle group.

Table 2. Number of NARMS Campylobacter Isolates from California-Slaughtered Food Animals that Underwent AST, 2014-2023, by Animal Species

Year	Cattle*	Chickens	Turkeys	Swine
2014	118	6	3	9
2015	87	4	2	9
2016	112	2	3	7
2017	128	11	7	14
2018	158	19	11	13
2019	141	19	13	12
2020	62	5	7	4
2021	60	6	5	0
2022	59	4	6	4
2023	53	11	9	2
Total	978	87	66	74

*The cattle category does not include bob veal due to the lack of CA-specific isolates for this cattle group.

Note: NARMS does not conduct AST on all positive samples. The complete sampling and laboratory methodologies used by USDA FSIS processing facilities for sample collection and processing can be found online or by contacting USDA FSIS.

Number of *Campylobacter* Isolates by Species

There are over 20 species of *Campylobacter*.¹⁷ The two most common species that cause foodborne illness in people are *Campylobacter jejuni* (*C. jejuni*) and *Campylobacter coli* (*C. coli*).¹⁸

Table 3 below shows the distribution of the three *Campylobacter* species found in the NARMS dataset for food-producing animals slaughtered in California: *C. coli*, *C. jejuni*, and *C. lari*. *C. coli* was identified in approximately 35% of the isolates, *C. jejuni* was found in 64%, and *C. lari* represented less than 1% of the isolates. In the California data, the susceptibility patterns of *C. jejuni* and *C. coli* were subjectively similar. Due to the low number of isolates and comparable susceptibility patterns of *C. coli* and *C. jejuni*, all animal-specific data herein represent the results for all three species of *Campylobacter* combined.

Table 3. Total *Campylobacter* Species Identified by NARMS Across All Animal Classes in California-Slaughtered Food Animals, 2014-2023.

<u>Year</u>	<u><i>C. coli</i></u>	<u><i>C. jejuni</i></u>	<u><i>C. lari</i></u>
2014	34	102	0
2015	36	65	1
2016	43	79	2
2017	55	105	0
2018	69	132	0
2019	66	116	3
2020	33	49	1
2021	26	47	1
2022	26	51	1
2023	38	35	2
Total	426	781	11

Trends in Reduced Susceptibility to Antibiotics Using AST
Cattle

Figure 1 displays the percentage of *Campylobacter* isolates from screened NARMS cecal samples collected from cattle slaughtered in California that underwent AST and were categorized as non-wild-type to the antibiotics included in the NARMS AST panel by year. Since 2017, the percentage of non-wild-type isolates with reduced susceptibility to tetracycline has gradually decreased. Despite peaking in 2021, the percentage of non-wild-type isolates with reduced susceptibility to nalidixic acid and ciprofloxacin also appears to be declining in more recent years. Deviations from the wild-type have been minimal for most of the remaining antibiotics, with the percentage of non-wild-type isolates below 5% for most antibiotics or all years reported.

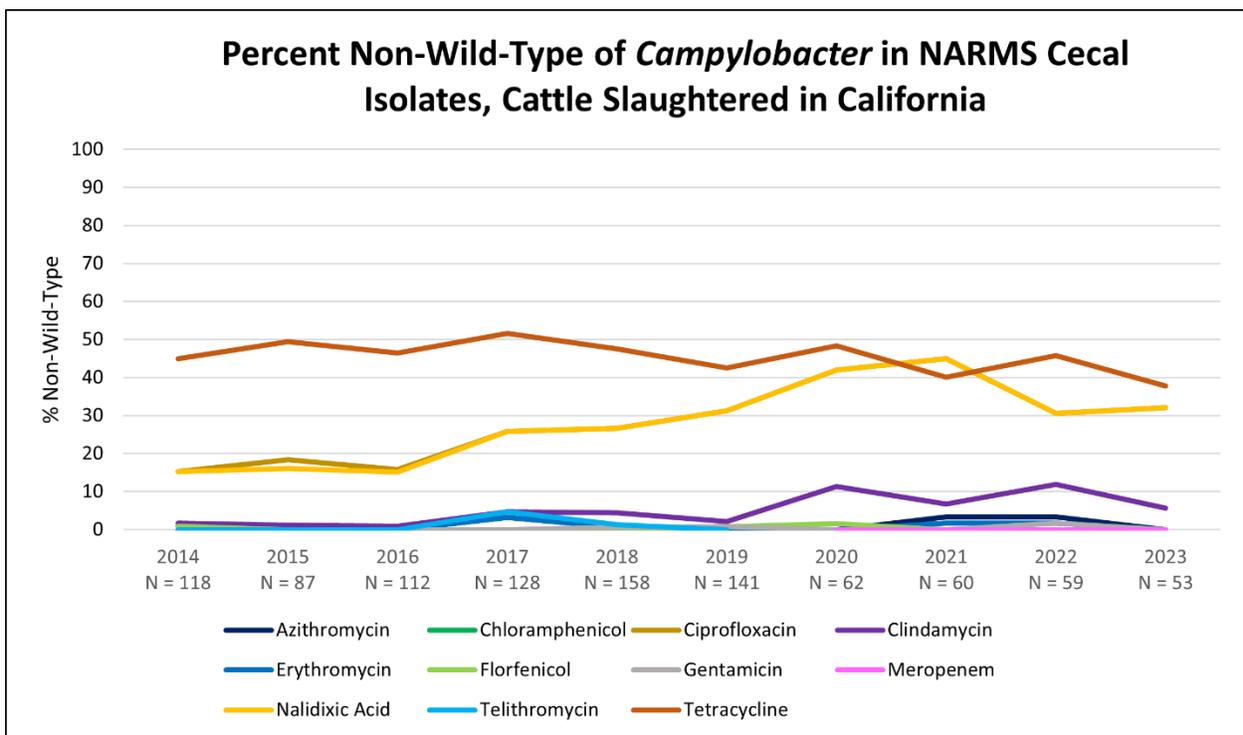


Figure 1. Data Trends in Non-Wild-Type *Campylobacter* Isolates from Cattle Slaughtered in California, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2014-2023
N indicates the number of isolates tested in a given year.

Figure 2 displays a heat map of the same data displayed in **Figure 1**. Antibiotics are listed on the y-axis, and the years of sample collection are on the x-axis. The color of each cell represents the percentage of isolates classified as non-wild-type: blue shades represent a lower percentage of non-wild-type isolates, while red shades represent a higher percentage of non-wild-type isolates, with darker red shades showing the highest percentage of non-wild-type isolates. The number inside each cell represents the exact percentage of non-wild-type isolates, making it easier to identify trends in susceptibility over time and compare deviations from wild-type across different drugs.

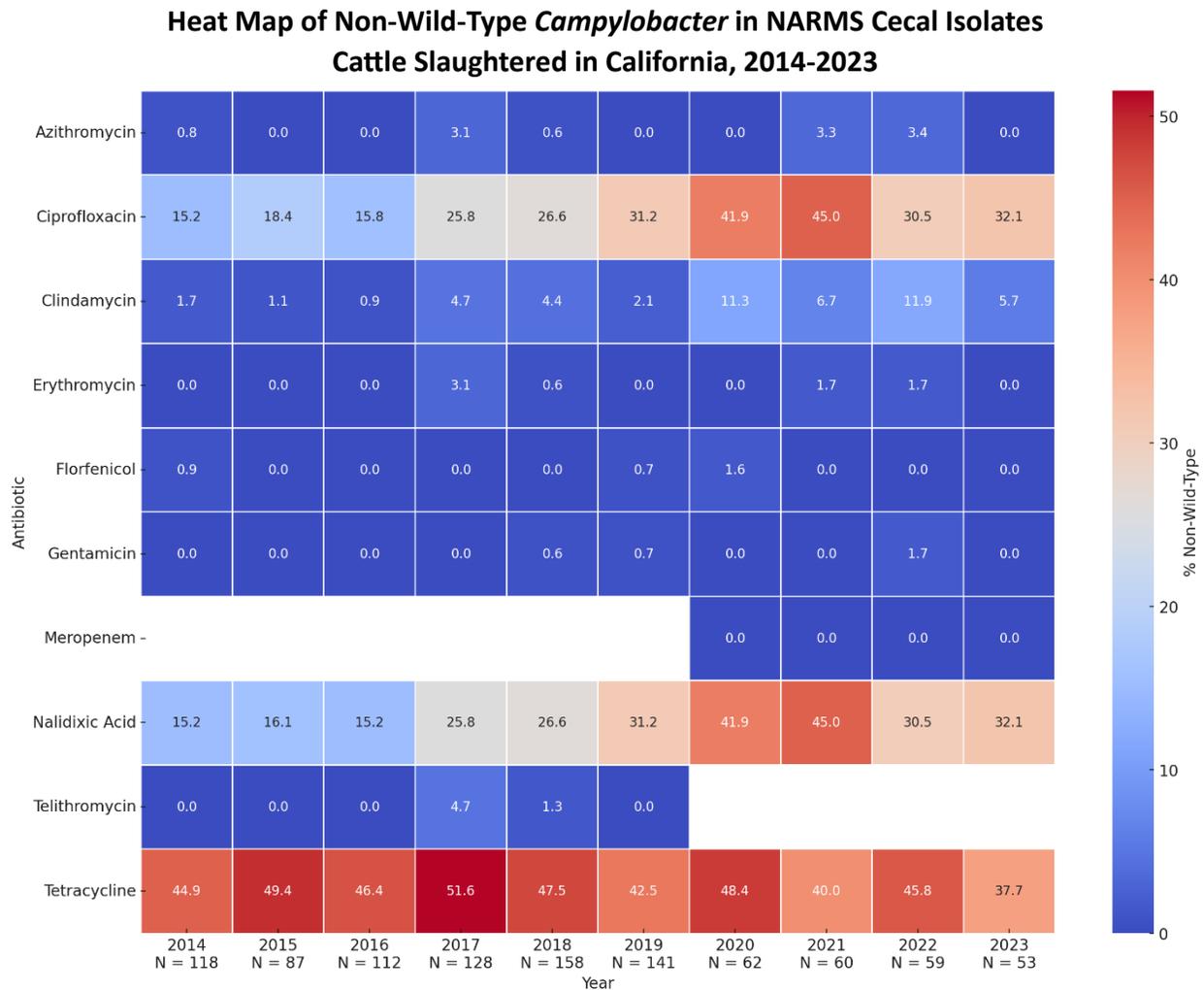


Figure 2. Heat Map Displaying Trends in Non-Wild-Type *Campylobacter* Isolates from Cattle Slaughtered in California, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2014-2023
N indicates the number of isolates tested in a given year.

Chicken

The percentage of *Campylobacter* isolates from screened NARMS cecal samples collected from chickens slaughtered in California that were classified as non-wild-type in relation to the antibiotics included in the NARMS AST panel by year is displayed in **Figures 3 and 4**. Since the number (N) of bacterial isolates that underwent AST each year is below the CLSI-recommended threshold of 30 isolates, meaningful trends in susceptibility for all years in this dataset cannot be determined. As such, an interpretation of the broader chicken cecal data across California cannot be provided.

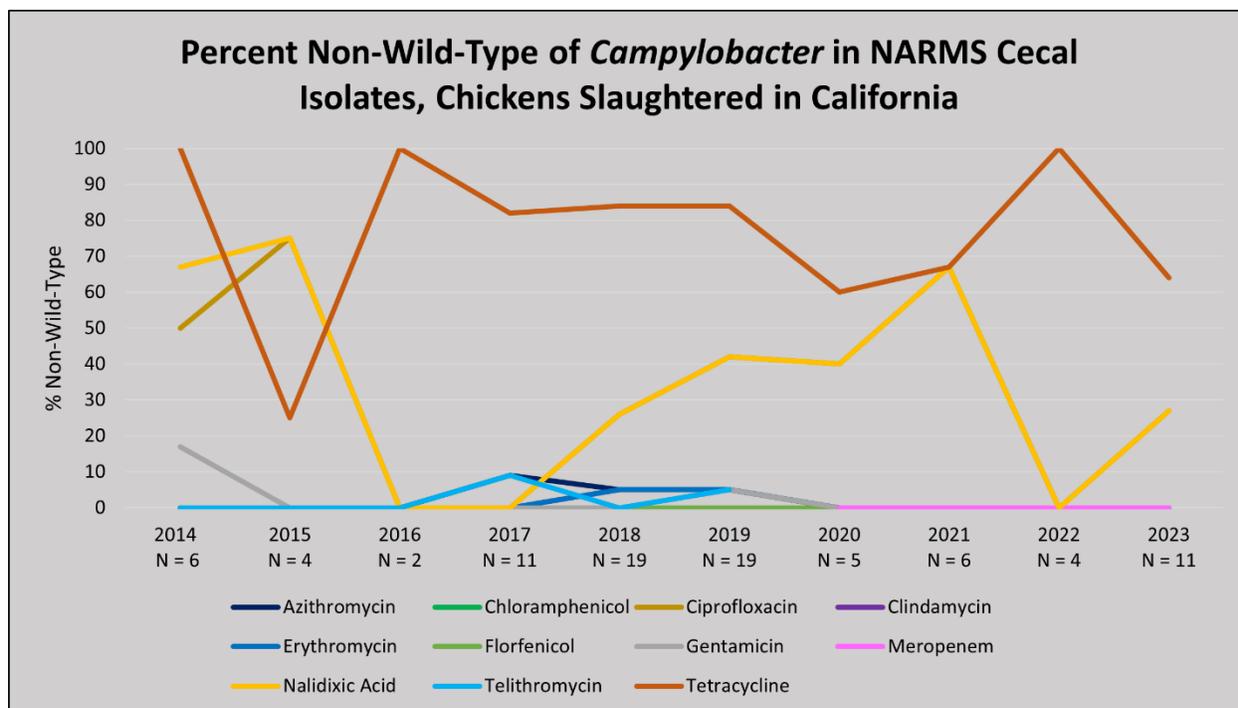


Figure 3. Trends in Non-Wild-Type *Campylobacter* Isolates from Chickens Slaughtered in California, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2014-2023.

N indicates the number of isolates tested in a given year. Years and sample numbers shaded in gray indicate less than 30 isolates; therefore, these numbers should be interpreted with caution and are not considered representative of the broader population of chickens raised or slaughtered in California.

Heat Map of Non-Wild-Type *Campylobacter* in NARMS Cecal Isolates Chickens Slaughtered in California, 2014-2023

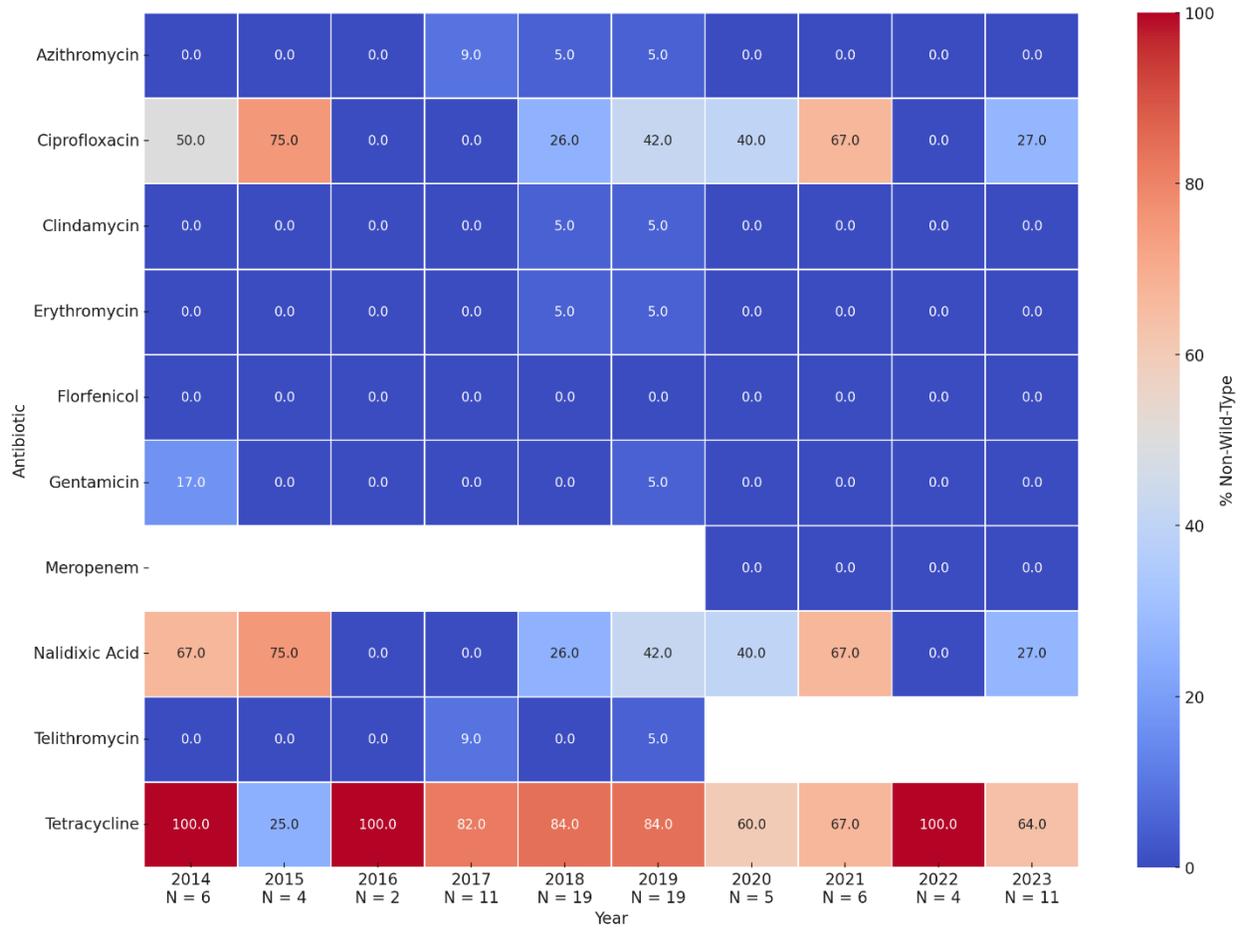


Figure 4. Heat Map Displaying Trends in Non-Wild-Type *Campylobacter* Isolates in Chickens Slaughtered in California, NARMS Cecal Isolates tested with the NARMS Antibiotic Panel, 2014-2023. N indicates the number of isolates tested in a given year. Since less than 30 isolates were tested yearly, these numbers should be interpreted with caution and are not considered representative of the broader population of chickens raised or slaughtered in California.

Turkey

The percentage of all species of *Campylobacter* isolates from screened NARMS turkey cecal samples that underwent AST and were classified as non-wild-type in relation to the antibiotics included in the NARMS AST panel is shown in **Figures 5 and 6**. Since the number (N) of bacterial isolates that underwent AST per year is below the CLSI-recommended threshold of 30 isolates, meaningful trends in susceptibility for all years in this dataset cannot be determined. As such, an interpretation of the broader turkey cecal data across California cannot be provided.

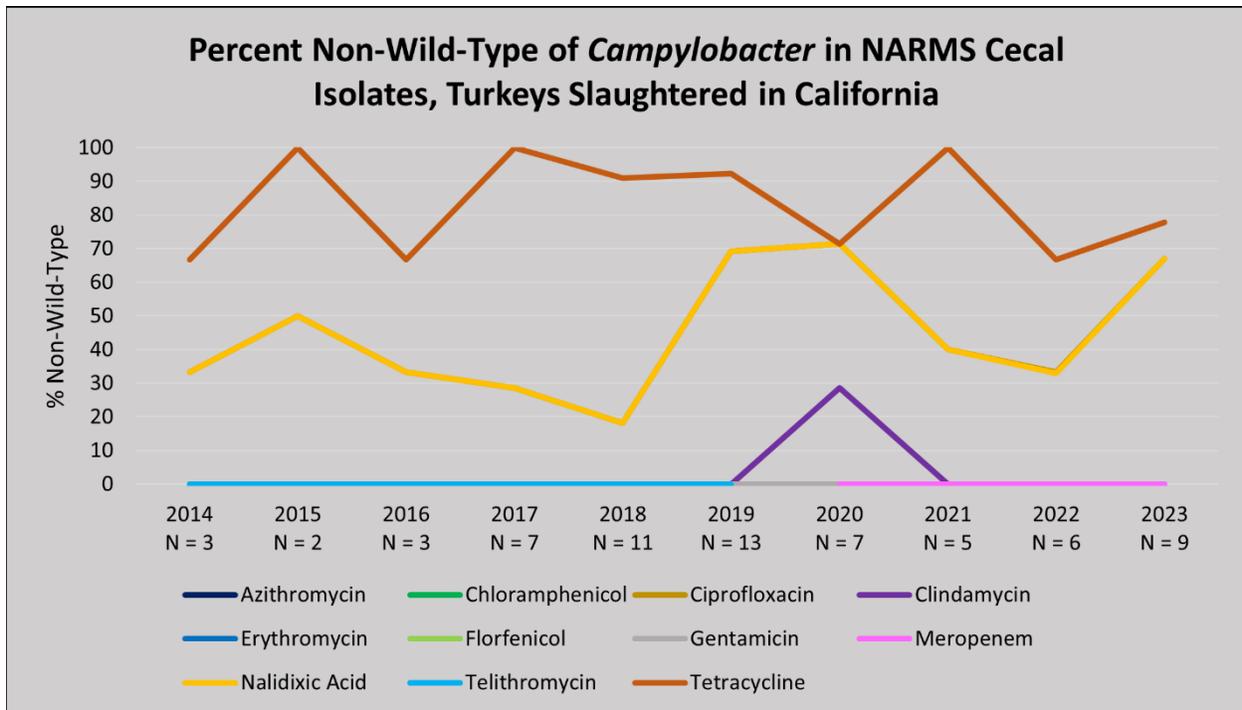


Figure 5. Trends in Non-Wild-Type *Campylobacter* Isolates from Turkeys Slaughtered in California, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2014-2023.

N indicates the number of isolates tested in a given year. Years and sample numbers shaded in gray indicate less than 30 isolates; therefore, these numbers should be interpreted with caution and are not considered representative of the broader population of turkeys raised or slaughtered in California.

Heat Map of Non-Wild-Type *Campylobacter* in NARMS Cecal Isolates, Turkeys Slaughtered in California, 2014-2023

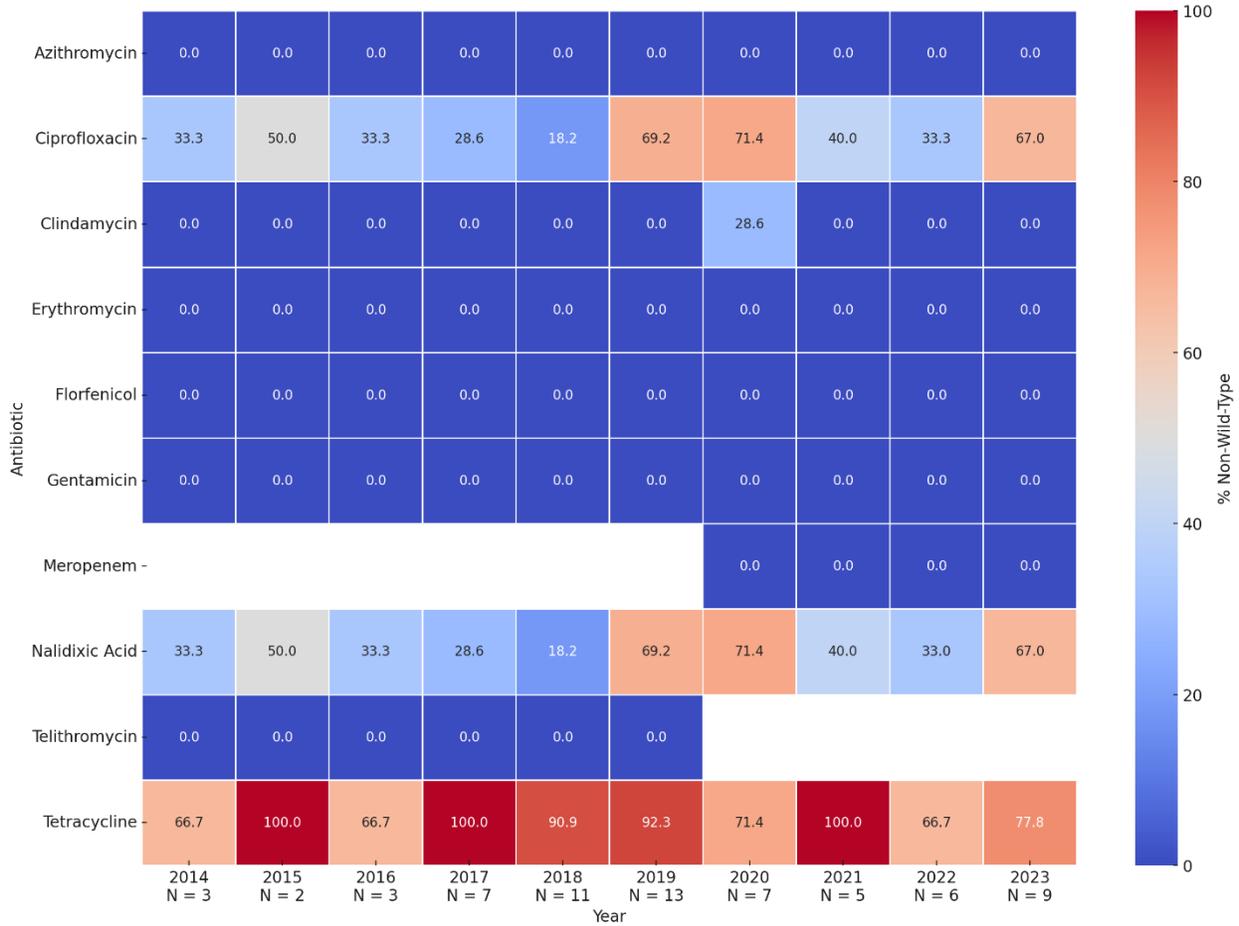


Figure 6. Heat Map Displaying Trends in Non-Wild-Type *Campylobacter* Isolates in Turkeys Slaughtered in California, NARMS Cecal Isolates tested with the NARMS Antibiotic Panel, 2014-2023.

N indicates the number of isolates tested in a given year. Since less than 30 isolates were tested yearly, these numbers should be interpreted with caution and are not considered representative of the broader population of turkeys raised or slaughtered in California.

Swine

The percentage of all species of *Campylobacter* isolates from screened NARMS cecal samples collected from swine slaughtered in California that underwent AST and were classified as non-wild-type in relation to the antibiotics included in the NARMS AST panel by year is displayed in **Figures 7 and 8**. Since the number (N) of bacterial isolates that underwent AST per year is below the CLSI-recommended threshold of 30 isolates, meaningful trends in susceptibility for all years in this dataset cannot be determined. As such, an interpretation of the swine cecal data cannot be provided.

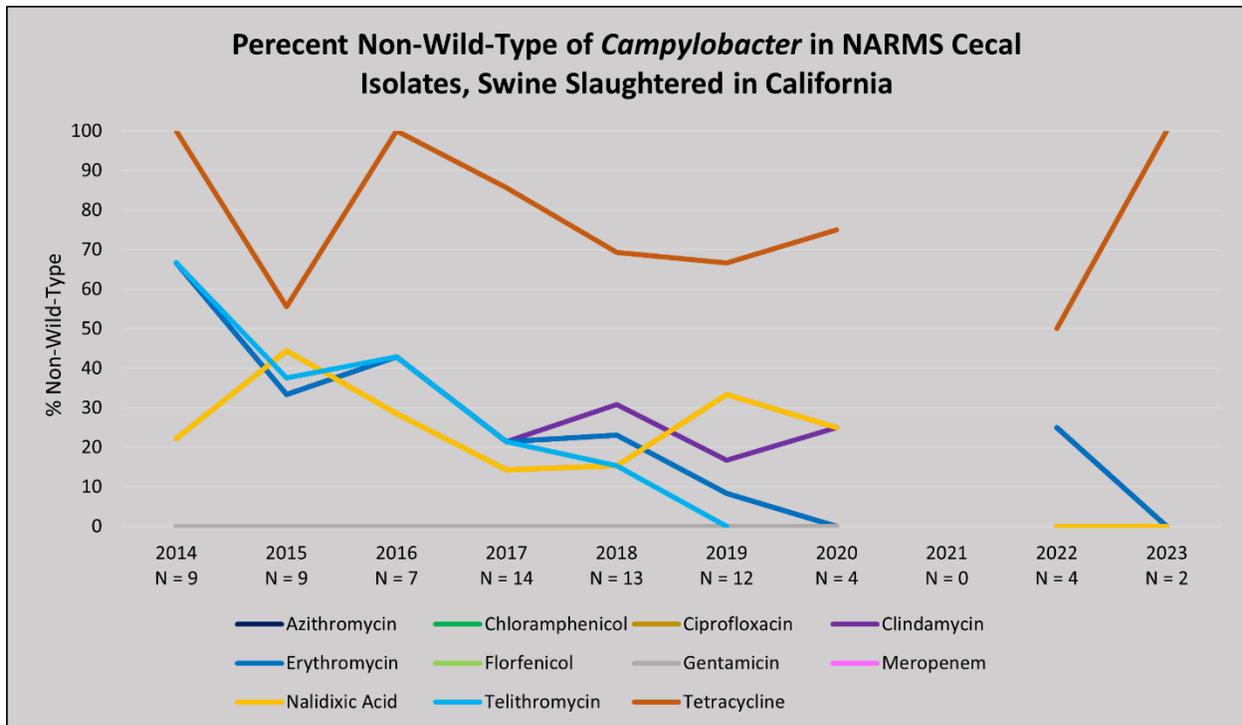


Figure 7. Trends in Non-Wild-Type *Campylobacter* Isolates from Swine Slaughtered in California, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2014-2023.

N indicates the number of isolates tested in a given year. Years and sample numbers shaded in gray indicate less than 30 isolates; therefore, these numbers should be interpreted with caution and are not considered representative of the broader population of swine raised or slaughtered in California.

Heat Map of Non-Wild-Type *Campylobacter* in NARMS Cecal Isolates, Swine Slaughtered in California, 2014-2023

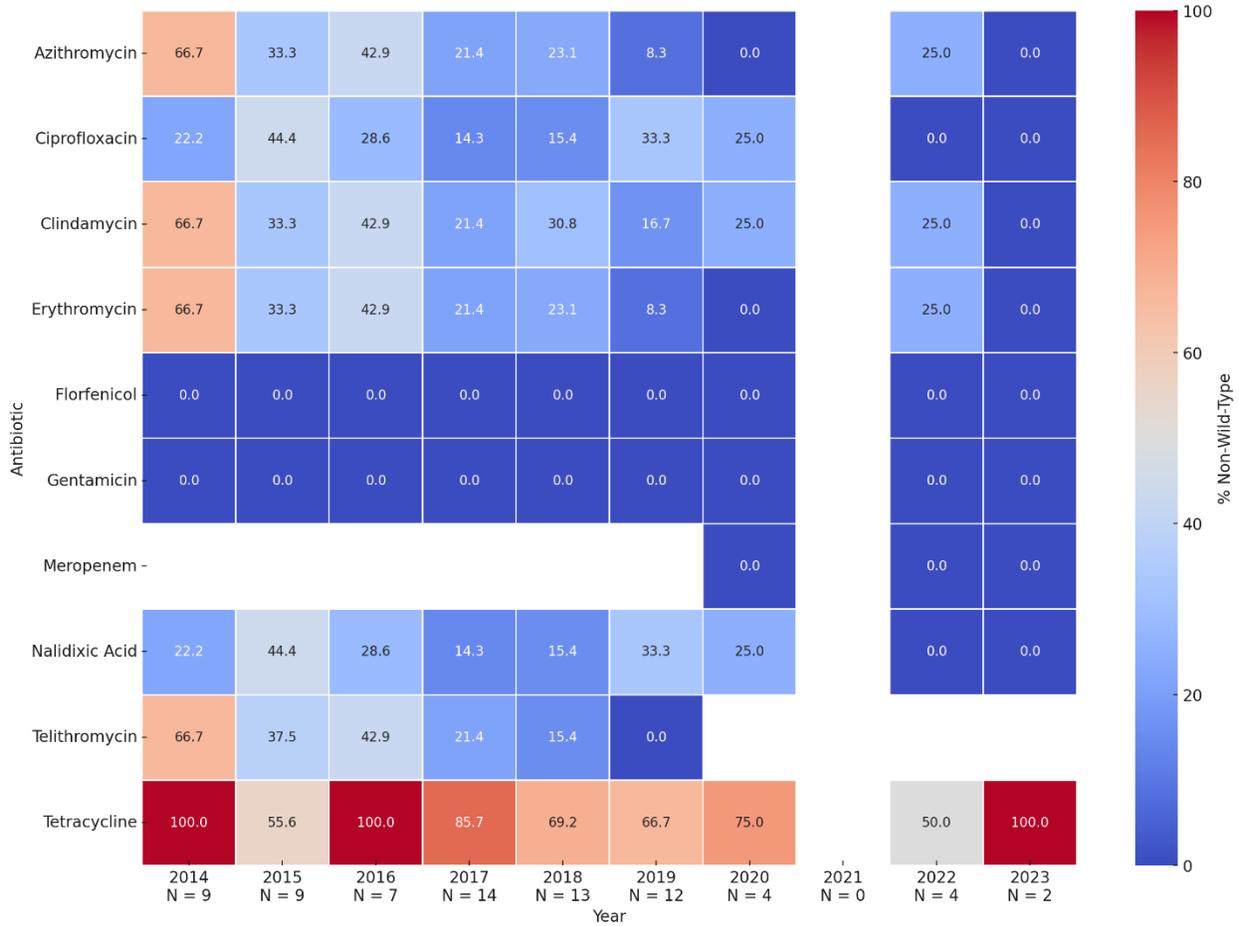


Figure 8. Heat Map Displaying Trends in Non-Wild-Type *Campylobacter* Isolates in Swine Slaughtered in California, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2014-2023.

N indicates the number of isolates tested in a given year. Since less than 30 isolates were tested yearly, these numbers should be interpreted with caution and are not considered representative of the broader population of swine raised or slaughtered in California.



Comparison of California-Specific Antibiotic AST Susceptibility Trends to Other NARMS-Participating States

Data across all NARMS-participating states was obtained from the NARMS Now Integrated Data portal.⁸ Below, trends in reduced susceptibility among all NARMS *Campylobacter* species isolates from food animals slaughtered in California are compared side by side with those from other states contributing to the NARMS Cecal Sampling Program (excluding California data) for antibiotics available in the NARMS Now Integrated Data portal. To further illustrate California's alignment or divergence from susceptibility trends observed in other states participating in the NARMS Cecal Sampling Program, we present a heat map specifically for NARMS cecal isolates from cattle. Heat map comparisons for chickens, turkeys, or swine were not provided due to the low number of isolates from California, which limits meaningful interpretations.

In cattle (**Figure 9**), the percentage of non-wild-type isolates with reduced susceptibility to tetracycline is approximately 20% lower in California-slaughtered cattle compared to the average across other states, with non-wild-type isolates with reduced susceptibility to tetracycline consistently lower in California-slaughtered cattle than in the other states across all years evaluated in this report. For nalidixic acid and ciprofloxacin, which exhibit similar resistance patterns, the percentage of isolates with reduced susceptibility (non-wild-type) appears to be mildly increasing in the data for all other states combined, while, over the past two years, the rate of non-wild-type isolates for these antibiotics has decreased in California-slaughtered cattle. The trends in susceptibility to azithromycin, telithromycin, erythromycin, and gentamicin in cattle isolates show similar patterns when comparing California-specific data to other states.

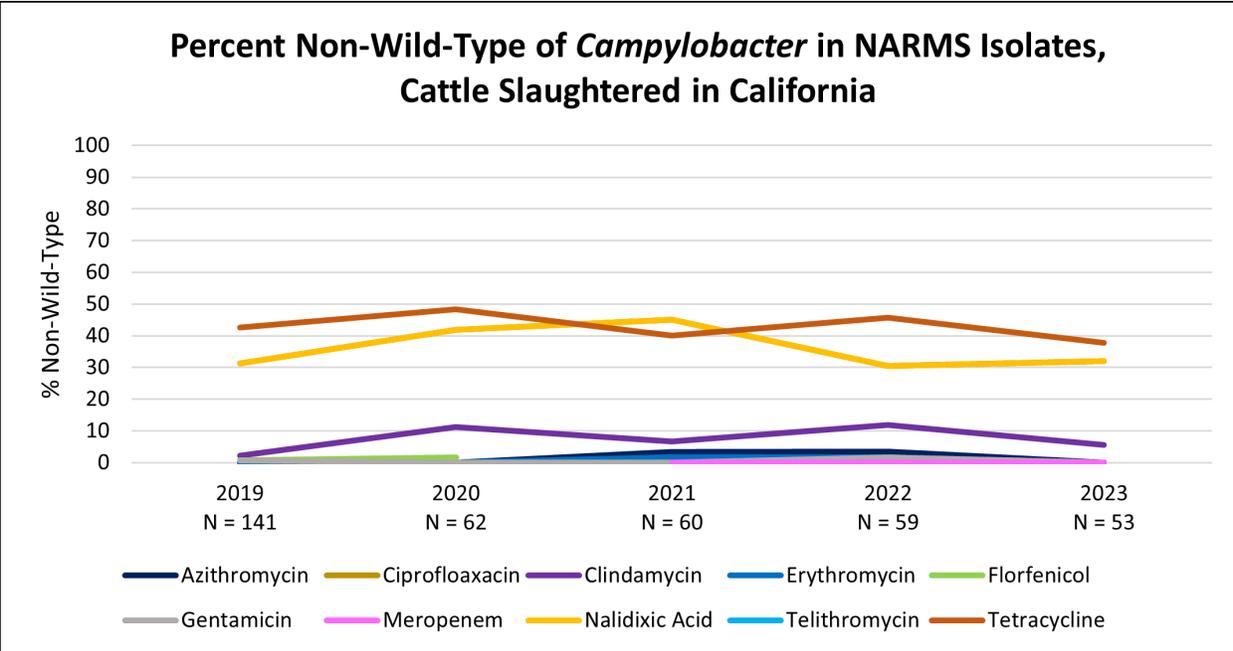
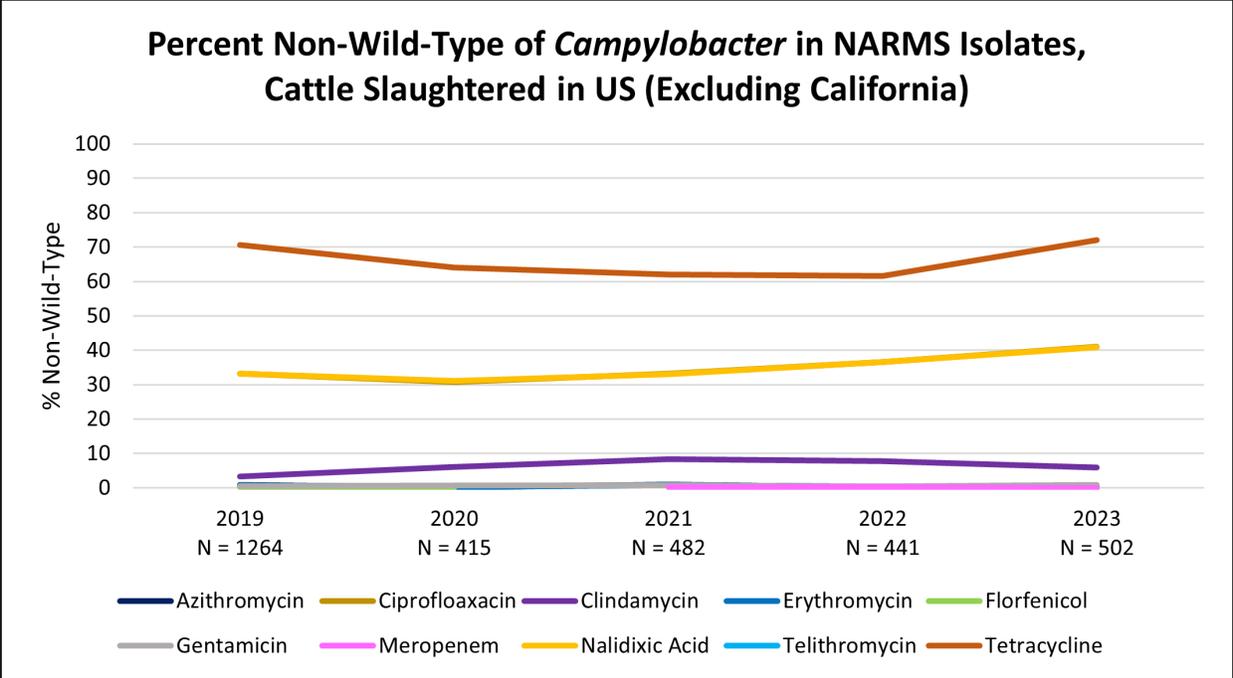


Figure 9. Comparison of Trends in Non-Wild-Type *Campylobacter* Isolates from US NARMS Cattle Data (excluding California) and Cattle Slaughtered in California Data, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2019-2023.

N indicates the number of isolates tested in a given year.

Figure 10 is a heat map comparison of NARMS cecal isolates from cattle. This comparison graph illustrates the percentage difference in susceptibility of NARMS *Campylobacter* isolates to specific antibiotics in California-slaughtered food animals versus other participating states, by year. Red tones or positive differences indicate higher percent non-wild-type isolates in California-slaughtered animals, while blue tones or negative differences reflect lower percent wild-type isolates in California-slaughtered animals compared to other states participating in the NARMS program. **Figure 10** shows that non-wild-type isolates with reduced susceptibility to tetracycline were consistently lower in California-slaughtered cattle compared to other states participating in the NARMS Cecal Sampling Program across all years from 2019 to 2023. The largest difference was observed in 2023, with California reporting 37.7% non-wild-type isolates versus 72.1% across other NARMS-participating states - a gap of over 34 percentage points. This pattern suggests a notably higher frequency of reduced susceptibility of isolates to tetracycline in NARMS cecal samples from other participating states compared to cattle slaughtered in California.

Heat Map of Non-Wild-Type Difference in *Campylobacter* NARMS Cecal Isolates Cattle Slaughtered in California vs. US NARMS Data (excluding CA), 2019-2023

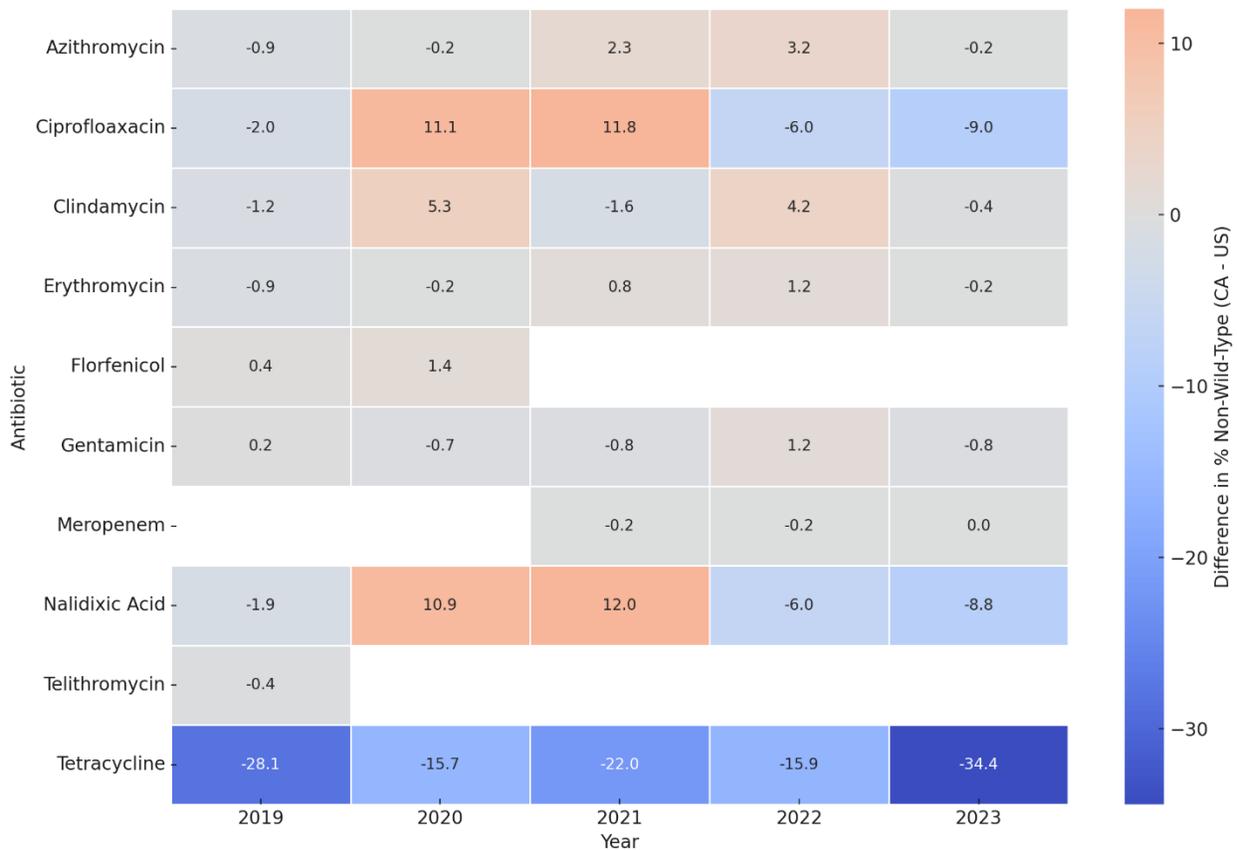


Figure 10. Heat Map of Non-Wild-Type Difference of *Campylobacter* Isolates from US NARMS Cattle Data (excluding California) and Cattle Slaughtered in California Data, NARMS Cecal Isolates Tested with the NARMS Antibiotic Panel, 2019-2023.

The *Campylobacter* susceptibility data for chickens, turkeys, and swine slaughtered in California, as compared to other states participating in the NARMS program, excluding California, are presented in **Figures 11, 12, and 13**. However, the number of California-specific bacterial isolates that underwent AST per year remained below the recommended threshold of 30 isolates necessary to compare trends in resistance. As a result, the interpretation of these data cannot be provided.

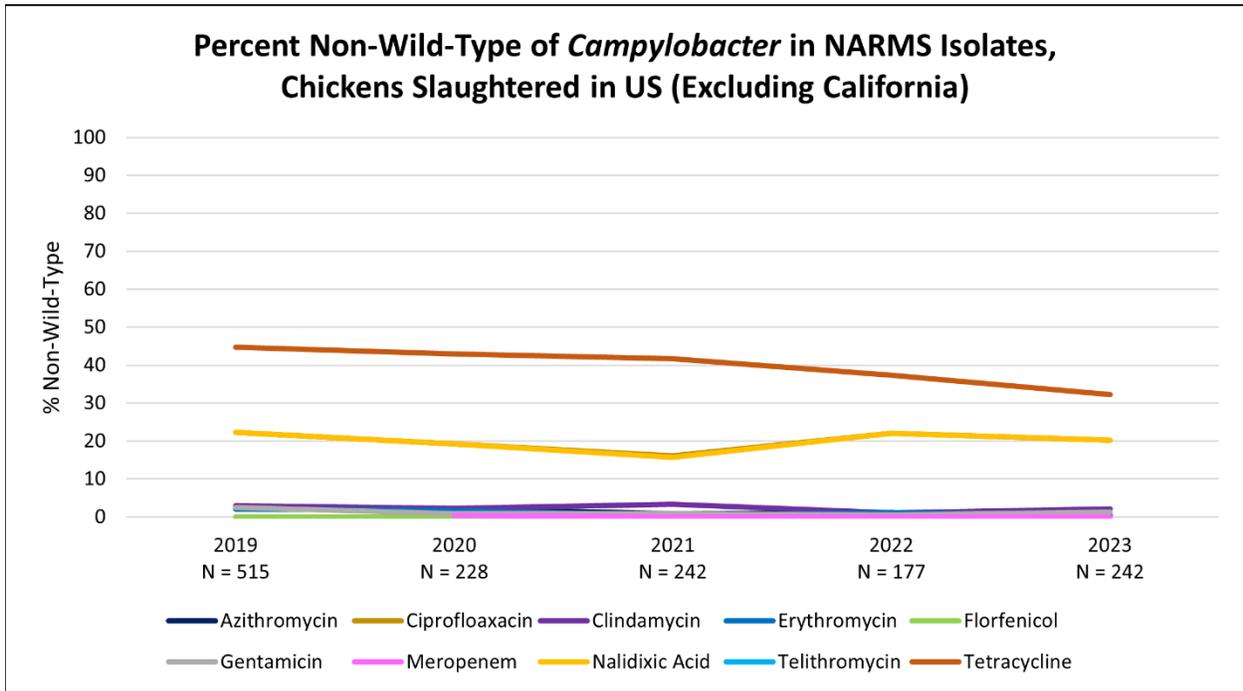


Figure 11. Non-Wild-Type *Campylobacter* Isolates in Chickens, US NARMS Data (excluding California), Cecal Isolates, 2019-2023

Percent Non-Wild-Type of *Campylobacter* in NARMS Isolates, Turkeys Slaughtered in US (Excluding California)

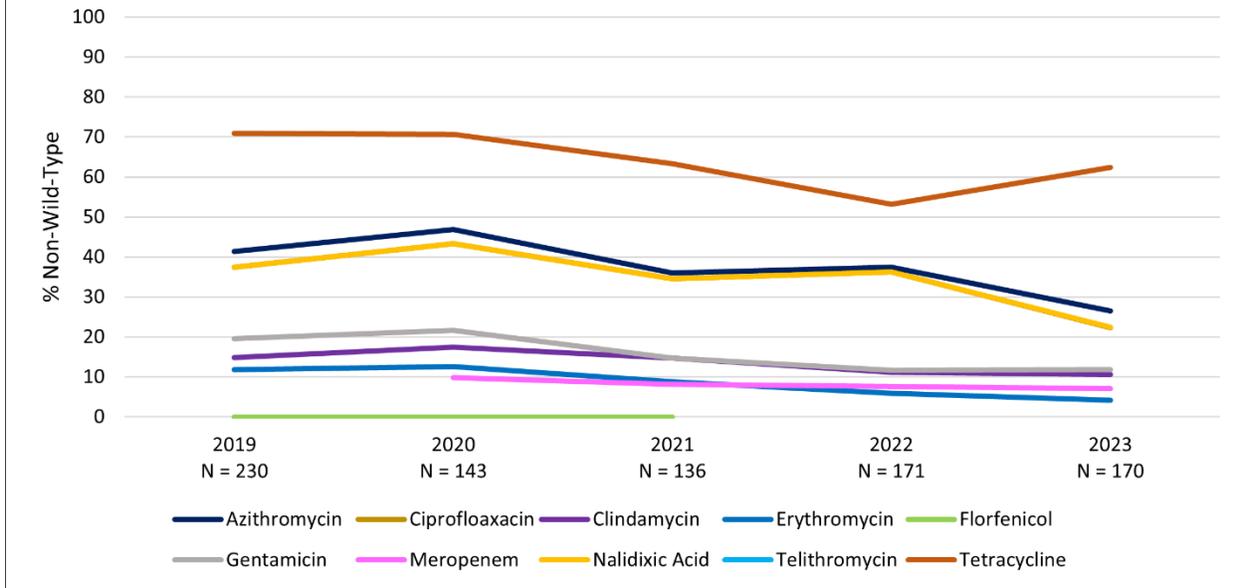


Figure 12. Non-Wild-Type *Campylobacter* Isolates in Turkeys, US NARMS Data (excluding California), Cecal Isolates, 2019-2023

Percent Non-Wild-Type of *Campylobacter* in NARMS Isolates, Swine Slaughtered in US (Excluding California)

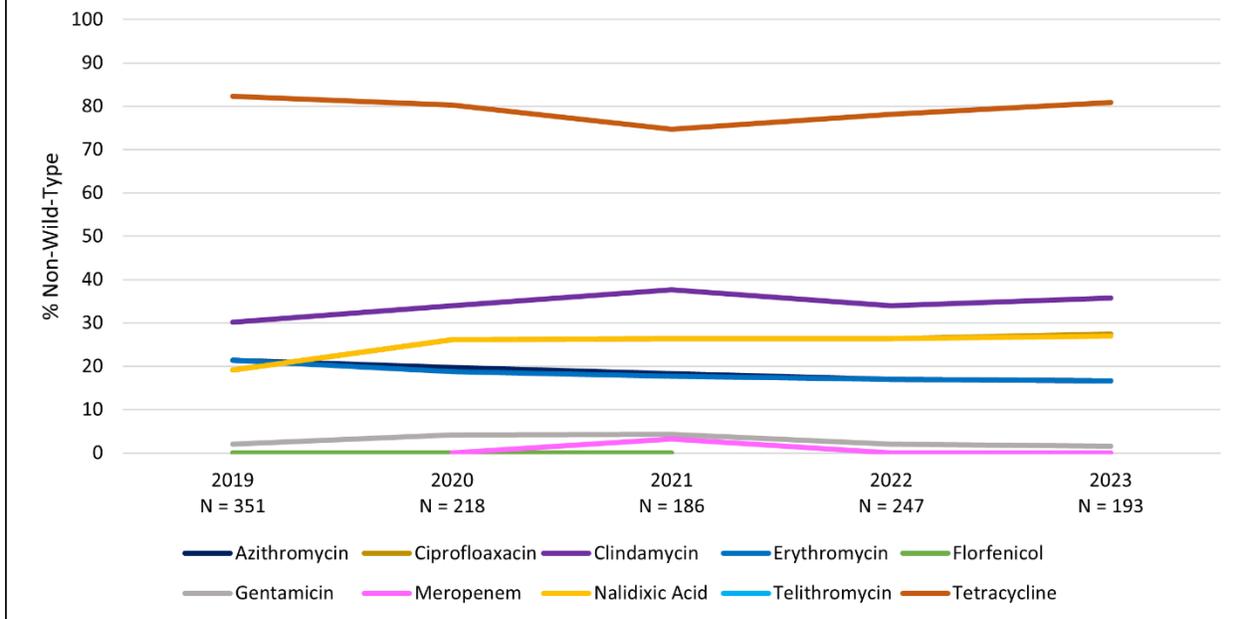


Figure 13. Non-Wild-Type *Campylobacter* Isolates in Swine, US NARMS Data (excluding California), Cecal Isolates, 2019-2023



Future Directions

NARMS continues to expand its usage of WGS to predict antimicrobial resistance profiles and has transitioned toward using whole genome sequencing (WGS) to predict antimicrobial susceptibility in most non-cecal isolates, moving away from traditional phenotypic AST.²⁷ As a result, future NARMS reports may present susceptibility data based on genomic prediction models rather than interpretations of laboratory-derived MICs. This shift may lead to changes in how susceptibility classifications are reported, potentially affecting trend comparisons over time.

In the future, AUS plans to publish California-specific pathogen reports for NARMS data on *Salmonella*, *E. coli*, and *Enterococcus* cecal isolates. While these reports will present comparable information, the format and specific content may differ by pathogen due to variations in NARMS AST methodology and interpretive criteria, and the number of isolates obtained from California. Additionally, AUS intends to release a cattle-focused report that will include data on all four enteric pathogens monitored in the NARMS database. Finally, AUS is committed to overcoming the inherent challenges of static reports and is actively exploring innovative solutions to provide stakeholders with an interactive dashboard. This user-driven experience will ensure that all data is easily accessible and readily available, empowering our stakeholders to make informed and timely decisions.



Acknowledgements

CDFA AUS would like to thank USDA-FSIS and NARMS for providing access to these valuable data specific to California and general consultation on the dataset organization and NARMS program procedures.

Appendix A

Table A1. Antimicrobial Agents and Antimicrobial Susceptibility Testing Methods for *Campylobacter* Isolates from Humans and Chickens, 1997-2024

Antimicrobial Class	Method	E-Test®		Broth Microdilution Sensititre® Plate: CAMPY	Broth Microdilution Sensititre® Plate: CAMPY2	Broth Microdilution Sensititre® Plate: CMVCAMPY
	Year	1997	1998-2004	2005-2019 ²	2019 (last quarter)	2020-Current
	Antimicrobial Agent					
Aminoglycosides	Gentamicin		√	√	√	√
Ketolides	Telithromycin			√		
Lincosamides	Clindamycin	√	√	√	√	√
Macrolides	Azithromycin		√	√	√	√
	Erythromycin	√	√	√	√	√
Penems	Meropenem					√
Phenicol	Chloramphenicol	√	√			
	Florfenicol			√	√	√
Quinolones	Ciprofloxacin	√	√	√	√	√
	Nalidixic acid	√	√	√	√	√
Tetracyclines	Doxycycline					
	Tetracycline	√	√	√	√	√

¹ Testing of *Campylobacter* isolates from humans and chickens began in 1997 and 1998, respectively

² Telithromycin was removed from the panel during the last quarter of CY2018

Appendix B

USDA NARMS interpretive criteria used for AST for *Campylobacter*.²⁸

Table B1. Interpretive Criteria Used for Susceptibility Testing of *Campylobacter*¹

Antimicrobial Class	Antimicrobial Agent	Profile Abbreviation	Breakpoints (µg/ml)			
			<i>C. jejuni</i>		<i>C. coli</i>	
			Susceptible	Resistant	Susceptible	Resistant
Aminoglycosides	Gentamicin	Gen	≤ 2	≥ 4	≤ 2	≥ 4
Carbapenems	Meropenem	Mer	2	≥ 4	2	≥ 4
Ketolides	Telithromycin	Tel	≤ 4	≥ 8	≤ 4	≥ 8
Lincosamides	Clindamycin	Cli	≤ 0.5	≥ 1	≤ 1	≥ 2
Macrolides	Azithromycin	Azi	≤ 0.25	≥ 0.5	≤ 0.5	≥ 1
	Erythromycin	Ery	≤ 4	≥ 8	≤ 8	≥ 16
Phenicols	Chloramphenicol	Chl	≤ 16	≥ 32	≤ 16	≥ 32
	Florfenicol	Ffn	≤ 4	≥ 8	≤ 4	≥ 8
Quinolones	Ciprofloxacin	Cip	≤ 0.5	≥ 1	≤ 0.5	≥ 1
	Nalidixic acid	Nal	≤ 16	≥ 32	≤ 16	≥ 32
Tetracyclines	Tetracycline	Tet	≤ 1	≥ 2	≤ 2	≥ 4

¹ Breakpoints were adopted from EUCAST (European Committee on Antimicrobial Susceptibility Testing) epidemiological cut off values.

Appendix C

Table C1. NARMS *Campylobacter* AST Panel and Uses in Food Animal

Antimicrobial Class	Antimicrobial Formulation	FDA GFI 152 Classification	Human or Food Animal Use	Approved Animal Use
Aminoglycoside	Gentamicin	Highly Important	Both	Water (swine), Oral solution (swine), IM (swine), SC (swine, chickens, turkeys), OU (calves)
Carbapenems	Meropenem	Critically Important	Human	Not approved for use in food animals
Ketolides	Telithromycin ⁽¹⁾	Not Classified	Human	Not approved for use in food animals
Lincosamides	Clindamycin	Highly Important	Human	Not approved for use in food animals
Macrolides	Azithromycin	Critically Important	Both	Not approved for use in food animals
	Erythromycin	Critically Important	Both	IM (cattle), IMM (cattle), Water (chickens, turkeys), Feed (chickens, turkeys)
Phenicol	Chloramphenicol	Highly Important	Humans	Not approved for use in food animals
	Florfenicol	Not Classified	Both	Feed (swine), Water (swine), IM (cattle, swine), SC (cattle)
Quinolones	Ciprofloxacin	Critically Important	Humans	Not approved for use in food animals
	Nalidixic acid	Important	Humans	Not approved for use in food animals
Tetracyclines	Tetracycline	Highly Important	Both	Water (cattle, swine, chickens, turkey), IM (cattle, swine), PO (cattle), TOP (cattle, swine)

*Antibiotics above are those included in the NARMS antibiotic panel for *Campylobacter* AST. Food animal approved use of these drugs and other drug formulations within the antibiotic class approved for use in food animals are listed. Classification of these drugs under GFI #152 is listed.

(1) Telithromycin was effectively withdrawn from human use in the U.S. and is no longer marketed.

Feed: medicated feed

Water: medicated water

PO: oral bolus

IM: intramuscular

IV: intravenous

SC: subcutaneous

SCi: subcutaneous implant

TOP: topical

OU: ocular

AU: otic



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