Executive Summary

The National Antimicrobial Resistance Monitoring System (NARMS) is a national public health surveillance system through which the U.S. Department of Agriculture (USDA) Food Safety and Inspection Service's (FSIS) partners with state and local public health departments, the Centers for Disease Control and Prevention (CDC), and the Food and Drug Administration (FDA) to track changes in antimicrobial susceptibility of select foodborne bacteria found in ill people (CDC), retail meats (FDA), and food animals (FSIS).

This FSIS NARMS Multi-Year Report evaluates trends in *Salmonella* serotypes and antimicrobial resistance (AMR) in certain food animal species and products sampled from 2014 through 2019 as part of FSIS NARMS sampling. This is the first multi-year *Salmonella* trend analysis of NARMS data to focus on samples collected by FSIS.

Samples analyzed included cecal (intestinal content) samples from food-producing animals at slaughter and product samples tested as part of Pathogen Reduction/Hazard Analysis Critical Control Point (PR/HACCP) sampling (henceforth stated as product sampling). *Salmonella* isolates were analyzed by serotyping and antimicrobial susceptibility testing (AST)[1] to evaluate differences in sample source and slaughter class (chicken, turkey, cattle, and swine).

This report is intended to highlight certain data trends to identify emerging areas of concern in antimicrobial resistance and *Salmonella* serotypes of public health concern. This report is focused on *Salmonella* findings only.

Key Findings

Salmonella Serotypes

- The overall top three *Salmonella* serotypes in FSIS NARMS cecal and product sampling were Enteritidis, Infantis and Kentucky, with differing distributions by slaughter class and sample source.

- The top *Salmonella* serotypes in the cecal (intestinal) and product[2] samples for each slaughter class remained the same over the period of the study: Kentucky (chicken), Reading (turkey), Montevideo (cattle) and Anatum (swine).

- Serotype Infantis emerged as one of the top serotypes in chicken in both cecal (21%) and product samples (15%).

Antimicrobial Resistance

- Most of the *Salmonella* from cecal samples among all slaughter classes were not resistant to any of the antimicrobials tested (i.e., they were pan-susceptible) over the 6-year period.

- The proportion of *Salmonella* isolates that were pan-susceptible differed among slaughter classes and by sample sources (cecal/product samples, respectively): cattle (83%/71%), swine (65%/64%), chicken (35%/43%) and turkey (34%/32%).

[1] See Glossary
[2] Product sample sources can include carcass swabs, rinsates, intact muscle, and comminuted samples.

- Multidrug resistant (MDR) *Salmonella* gradually increased over time in both cecal and product samples, with a significant increase in product samples from 2016 to 2019.

- Serotype Infantis emerged as a major contributor to the increase in MDR *Salmonella* in chicken.

Resistance to Critically Important Antimicrobial Drug Classes[1]

- Increased resistance to at least one critically important antimicrobial drug class was observed in at least one *Salmonella* serotype isolated from cattle, swine, and chicken.

- *Salmonella* susceptibility to ciprofloxacin (DSC)[1] significantly decreased among isolates from cecal and product samples overall.

- Cephalosporin-resistant *Salmonella* increased over time in product samples from cattle and swine.

- *Salmonella* isolates showed a significant increase in resistance to the critically important antimicrobial drugs ciprofloxacin (DSC), ceftriaxone, and trimethoprim-sulfamethoxazole.

Impact and Significance

The continuous tracking of *Salmonella* serotypes and AMR trends in cecal and product samples serves as an early indicator of potential threats to public health. FSIS also uses NARMS data to explore opportunities to continually reduce *Salmonella* contamination in FSIS regulated products and to further reduce illnesses. The differences observed in *Salmonella* in cecal and product samples highlight the importance of understanding *Salmonella* from farm to slaughter.

Collaboration and Communication

FSIS continues to engage with NARMS partners, stakeholders, academia, and industry to bridge AMR information gaps. FSIS NARMS collaborations help identify opportunities for combating the emergence and spread of AMR pathogens during pre- and post-slaughter. Since December 2020, FSIS has made its AMR data publicly available in its quarterly data tables to promote communication and collaboration with its NARMS partners and stakeholders.

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Distribution of *Salmonella* in FSIS-collected samples

From 2014 through 2019, a total of 32,798 cecal samples yielded 7,908 *Salmonella* isolates from chicken (1,487), turkey (291), cattle (beef and dairy) (2,435) and swine (market swine and sows) (3,695) (**Table 1**). Recovery of *Salmonella* isolates (% positive) from swine ceca was consistently higher than other slaughter categories (49% in 2019). A rising trend in *Salmonella* recovery was observed in chicken ceca from 2016 (23.6%) to 2019 (49%) (**Figure 1)**.

During the same time frame, a total of 226,741 meat and poultry samples yielded 15,780 *Salmonella* isolates from chicken (10,269), turkey (1,328), beef (1,669) and pork (2,514) (**Table 2**).

Annual NARMS datasets are available on the FDA's NARMS website as interactive dashboards that allow users to explore the data in different ways. The data are also available as a raw dataset. Users of these public datasets who create their own estimates should exercise caution when analyzing and interpreting these data in this manner.

Salmonella recovery was positively impacted in 2016 when FSIS switched its sampling media from buffered peptone water (BPW) to neutralizing BPW (nBPW) for chicken carcass and parts sampling (Williams, 2018). This contributed to increased recovery of *Salmonella* in chicken carcass samples (**Table 2**). The change to nBPW did not impact cecal sample testing**.**

Table 1: Number of Cecal Samples Screened and *Salmonella* Isolates Tested for Antimicrobial Resistance, 2014 - 2019[a]

Year		Chickens (n)	Turkeys (n)	Cattle (n)	Swine (n)
2014	Samples	575	264	2858	1295
	Isolates	101	44	318	606
2015	Samples	553	266	2733	1179
	Isolates	130	25	359	494
2016	Samples	569	266	2824	1299
	Isolates	134	49	367	610
2017	Samples	835	307	3330	1337
	Isolates	314	42	419	687
2018	Samples	869	437	3577	1398
	Isolates	399	66	469	693
2019	Samples	811	428	3554	1234
	Isolates	407	64	500	605

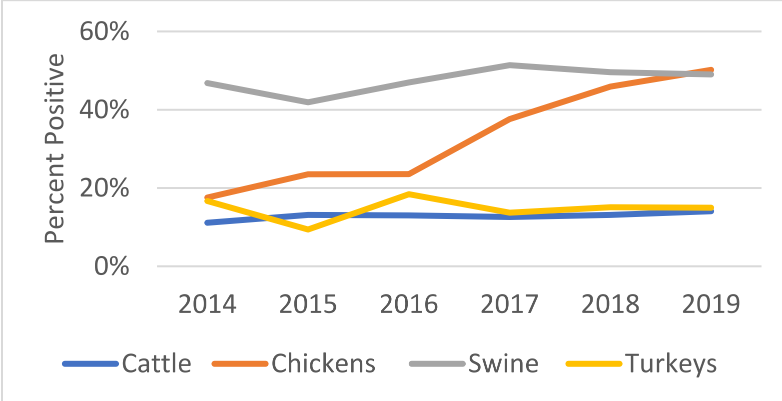
[a] Source: FSIS Laboratory Information Management System (LIMS)

Table 2: Number of Product Samples Screened and *Salmonella* Isolates Tested for Antimicrobial Resistance, 2014 - 2019[a,b]

Year		Chicken (n)	Turkey (n)	Beef (n)	Pork (n)
2014	Samples	11906	3501	16710	NT*
	Isolates	936	299	344	NT*
2015	Samples	12019	2565	14825	1544
	Isolates	1491	185	291	200
2016	Samples	16968	2737	15257	3296
	Isolates	1859	135	286	598
2017	Samples	18392	3016	14776	3931
	Isolates	2098	149	235	647
2018	Samples	18909	3399	14617	4085
	Isolates	1956	264	298	541
2019	Samples	22377	3292	15062	3557
	Isolates	1929	296	215	528

[a] Source: FSIS Laboratory Information Management System (LIMS)
[b] The number of product samples and isolates only include those that are part of the NARMS datasets except for exploratory pork product sample isolates
*NT – not tested

Figure 1: *Salmonella* in Cecal Samples by Animal Slaughter Class, 2014 - 2019 (percent positive)[a]



[a] Source: FSIS Laboratory Information Management System (LIMS)

Salmonella Serotypes

During the 6-year sampling period, the leading *Salmonella* serotypes isolated by slaughter class were the same in both cecal and product samples: Kentucky in chicken, Reading in turkey, Montevideo in cattle and Anatum in swine (**Appendix A**). However, the distribution of the top serotypes varied when slaughter class data were aggregated and analyzed by sample source. When serotype data for the slaughter classes were combined, the overall top three *Salmonella* serotypes were Kentucky (16.7%), Enteritidis (10.6%) and Infantis (10.3%) (**Table 3**). These three serotypes accounted for over 60% of all *Salmonella* in chicken cecal and product samples (**Appendix A, Table A1**). Among the other slaughter classes, these serotypes comprised less than 20% in cecal and product samples **(Appendix A, Tables A2-A4)**. Serotype changes observed over time in turkey, cattle and swine did not show the emergence of any distinct or new serotypes, or any statistically significant changes.

In this report, statistically significant findings are referred to as "significant" while other important findings that are not statistically significant are referred to as "notable."

Unless otherwise stated, percent changes (increase/decrease) stated indicate a net difference in data points from 2014 to 2019.

Table 3: *Salmonella* Serotype Distribution in Cecal and Product Samples, Combined Slaughter Classes, 2014 - 2019[a]

	FSIS NARMS Samples					
Serotype	**Rank**	**Overall** (N = 23,693)	**Rank**	**Cecal** (N = 7,908)	**Rank**	**Product** (N = 15,785)
Kentucky	1	3,958 (16.7%)	5	527 (6.7%)	1	3431 (21.7%)
Enteritidis	2	2,502 (10.6%)	8	253 (3.0%)	2	2249 (14.2%)
Infantis	3	2,447 (10.3%)	2	590 (7.5%)	3	1857 (11.8%)
Typhimurium	4	1,514 (6.4%)	8	390 (4.9%)	4	1124 (7.1%)
Anatum	5	1,442 (6.1%)	1	911 (11.5%)	7	531 (3.4%)
Schwarzengrund	6	1,075 (4.5%)	12	190 (2.4%)	5	885 (5.6%)
Montevideo	7	1,066 (4.5%)	3	587 (7.5%)	8	479 (3.0%)
I 4,[5],12:i:-	8	707 (3.0%)	7	269 (3.4%)	9	438 (2.8%)
Cerro	9	665 (2.8%)	4	536 (6.8%)	20	129 (0.8%)
Derby	10	662 (2.8%)	6	428 (5.4%)	13	234 (1.5%)

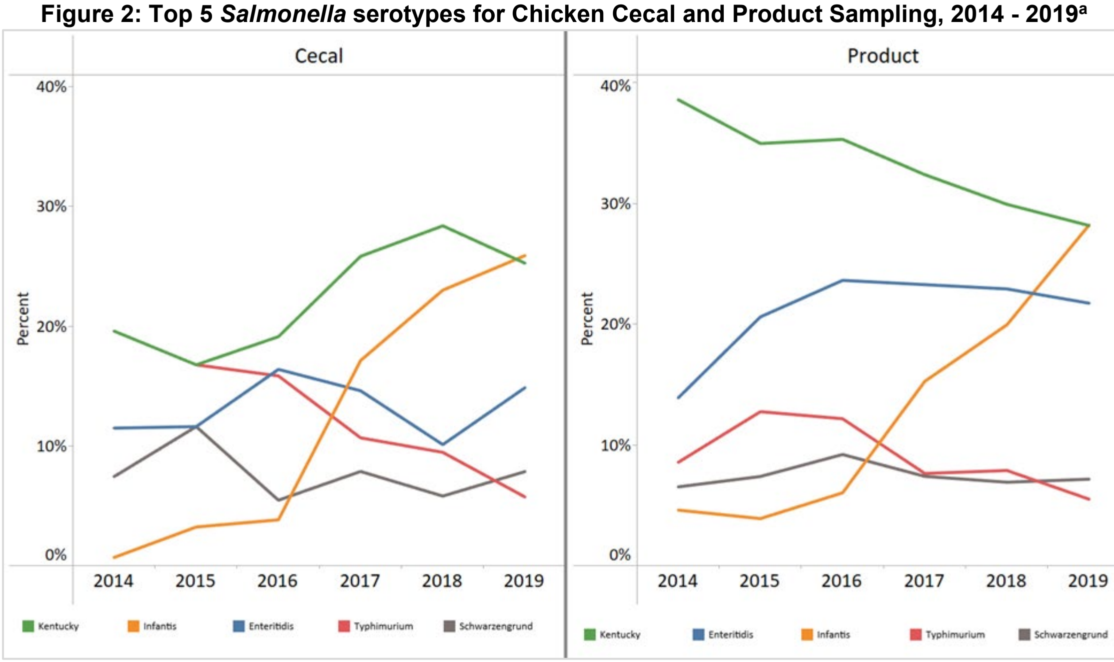
Others below top 10		7,655 (32.%)		3,227 (41.0%)		4428 (28.1%)

[a] Source: FSIS Laboratory Information Management System (LIMS)

Chicken

Infantis was one of the top serotypes in both cecal (ranked second) and product samples (ranked third) over the 6-year period (cumulative data) (**Figure 2 and Appendix A, Table A1**). Infantis significantly increased 25.2% in cecal and 23.6% in product samples from 2016 – 2019, making Infantis a co-dominant serotype with Kentucky in both sample sources in 2019 (**Appendix B, Table B1**). Typhimurium (ranked fourth) decreased 13.9% in cecal and 3.0% in product samples. Kentucky (ranked first) decreased 10.4% in product samples. Enteritidis increased 3.4% in cecal (ranked second) and 7.8% in product samples (ranked third).

Figure 2: Top 5 *Salmonella* serotypes for Chicken Cecal and Product Sampling, 2014 - 2019[a]

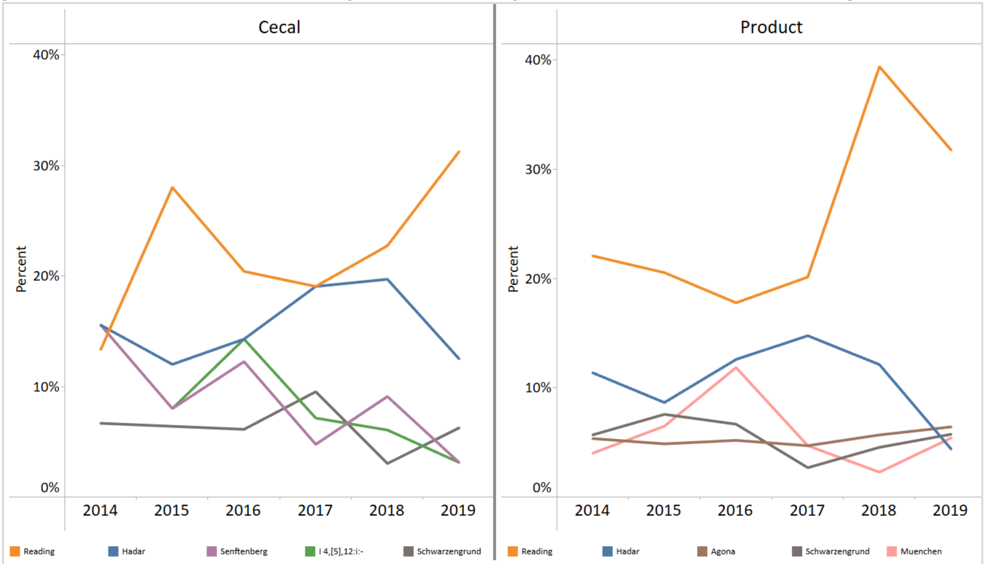


[a] Source: FSIS Laboratory Information Management System (LIMS)

Turkey

Reading was the top-ranked serotype in both cecal and product samples over the 6-year period (cumulative data). Reading increased 11% and constituted one-third of all serotypes recovered from both turkey cecal and product samples. (**Figure 3 and Appendix A, Table A2**). Interestingly, the increasing trends in Reading (turkey) and Infantis (chicken) began during the same period (2016–2017).

Figure 3: Top 5 *Salmonella* serotypes for Turkey Cecal and Product Sampling, 2014 - 2019[a]



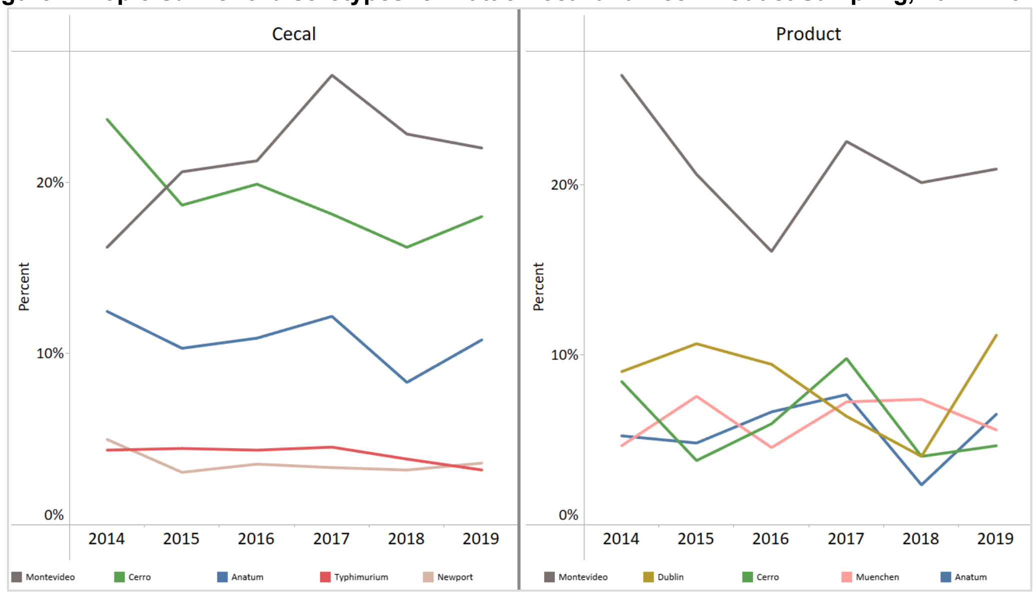
[a] Source: FSIS Laboratory Information Management System (LIMS)

Cattle

Montevideo was the top-ranked serotype in both cattle cecal and beef product samples over the 6-year period (cumulative data). Serotype differences were seen among *Salmonella* from cattle cecal and product samples and between beef and dairy cattle cecal samples. (**Figure 4 and Appendix A, Tables A3a and A3b**). Dublin ranked 30th or lower in both beef and dairy cattle cecal samples but ranked second in beef product samples (8%)[3]. Muenchen ranked tenth in cattle cecal samples but ranked fourth in beef cow, steer, and heifer cecal and product samples. Newport ranked fifth in cattle cecal and seventh in product samples. Muenchen and Newport varied in their top ten rankings in cecal samples among the slaughter subclasses (beef and dairy cow, steer and heifer). Muenchen did not rank among the top 10 serotypes in dairy cow cecal samples[2]. Newport did not rank among the top 10 serotypes in steer and heifer cecal samples.

[3] Appendix B tables include rankings for only for the top 10 *Salmonella* serotypes for each slaughter class and sample source.

Figure 4: Top 5 *Salmonella* serotypes for Cattle Cecal and Beef Product Sampling, 2014 - 2019[a]

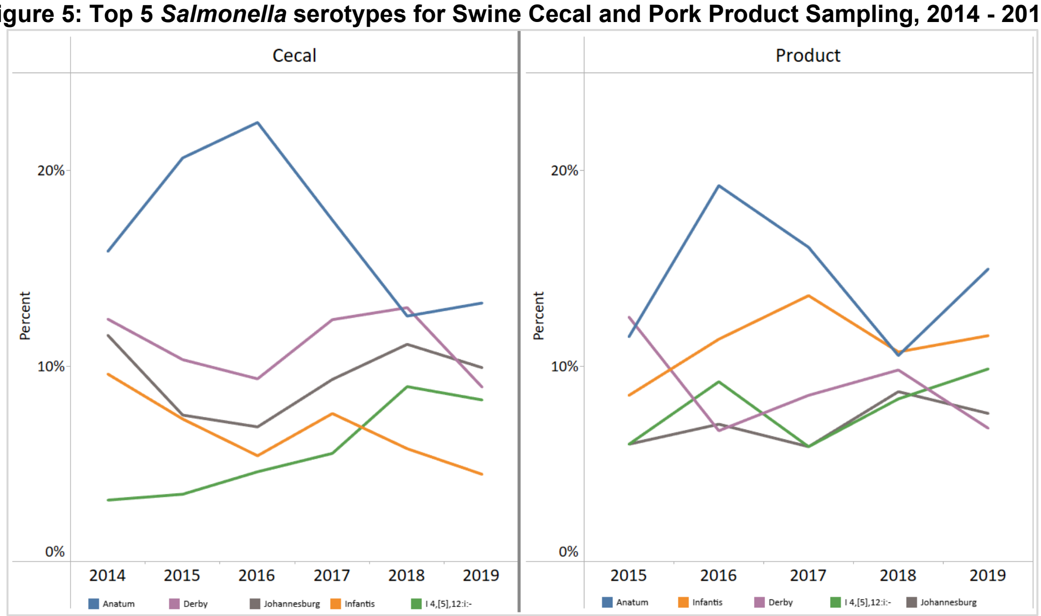


[a] Source: FSIS Laboratory Information Management System (LIMS)

Swine

Anatum was the top-ranked serotype in both swine cecal and pork product samples over the 6-year period (cumulative data) (**Figure 5 and Appendix A, Tables A4a and A4b**). Anatum was among the dominant serotypes in sow and market swine cecal samples (ranked first and second, respectively). In sow cecal samples, Anatum was almost two-fold higher (23%) compared to the next ranked serotype, Johannesburg (12%). I 4,[5],12:i:- increased 8% in market swine cecal and 4% in pork product samples but decreased 2% in sow cecal samples.

Figure 5: Top 5 *Salmonella* serotypes for Swine Cecal and Pork Product Sampling, 2014 - 2019[a]



[a] Source: FSIS Laboratory Information Management System (LIMS)

2019 Top 10 Serotypes of Public Health Significance

The distribution of CDC's 2019 top 10 *Salmonella* serotypes of public health significance (Tack, et al, 2020) was compared to the 2019 data for combined FSIS cecal and product samples (**Table 4**) and by individual slaughter classes (chicken, turkey, cattle and swine) (**Appendix B, Tables B1-B4**). It showed that the CDC top serotypes of public health significance differed from the top serotypes recovered from FSIS cecal and product samples. It should be noted that these observations are not informed by attribution; the *Salmonella* serotypes reported through CDC reflect human infections resulting from exposures reported through the Foodborne Diseases Active Surveillance Network (FoodNet). These exposure include foods that are not under FSIS jurisdiction.

Table 4: Top 10 *Salmonella* serotypes for Combined FSIS NARMS Product and Cecal Sampling (2019)[a] and the Centers for Disease Control and Prevention (CDC) Clinical Isolates (2019)[b]

	FSIS NARMS Sampling (chicken, turkey, cattle and swine combined)				CDC[1,2]
Serotype	**Rank**	**Product** (N = 2968)	**Rank**	**Cecal** (N = 1,576)	**Rank**
Infantis	1	627 (21%)	1	157 (10%)	6
Kentucky	2	555 (19%)	2	139 (9%)	*
Enteritidis	3	423 (14%)	6	72 (5%)	1
Schwarzengrund	4	165 (6%)	11	54 (3%)	*
Typhimurium	5	140 (5%)	8	60 (4%)	3
Anatum	6	110 (4%)	3	137 (9%)	*
Reading	7	110 (4%)	16	30 (2%)	*
I 4,[5],12:i:-	8	83 (3%)	9	56 (4%)	5
Montevideo	9	58 (2%)	4	117 (7%)	10
Johannesburg	10	56 (2%)	7	62 (4%)	*
Others below top 10		641 (22%)		692 (44%)	N/A

[a] Source: FSIS Laboratory Information Management System (LIMS)
[b]Tack, et al, 2020

[1] 2019 CDC *Salmonella* serotypes of public health significance – clinical samples (incidence rate greater than or equal to 0.20 per 100,000).
[2] The 2019 CDC ten most common fully serotyped *Salmonella* isolates included #1 – Enteriditis, #2 – Newport, #3 – Typhimirium, #4 – Javiana, #5 – I 4,[5],12:i-, #6 – Infantis, #7 – Saintpaul, #8 – Braenderup, #9 – Muenchen and #10 – Montevideo.

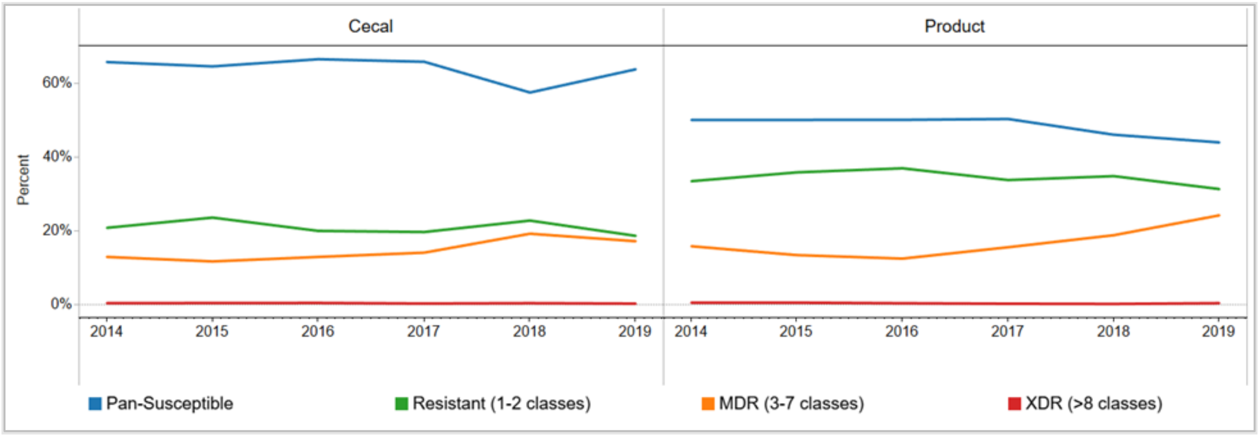
* Serotypes not reported as one of the top 10 *Salmonella* isolates in CDC clinical samples.

Antimicrobial Susceptibility and MDR

AMR Overall

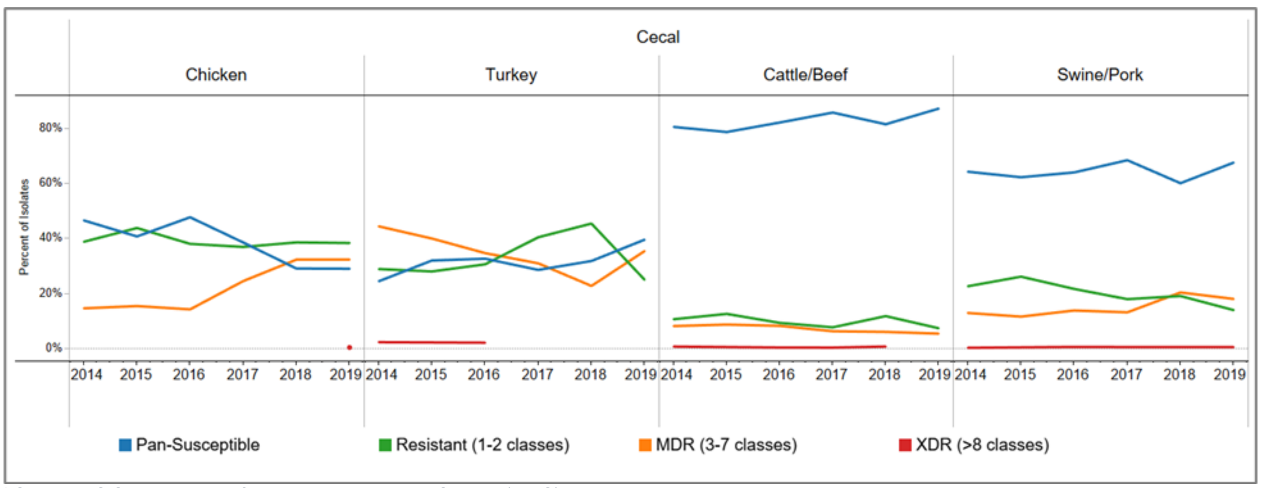
To determine overall AMR, *Salmonella* results in all slaughter classes were combined for 2014-2019. Pansusceptibility (no antimicrobial resistance) in *Salmonella* isolates recovered from food animals during 2014-2019 was 64% in cecal and 45% in product samples. Resistance to less than 3 classes decreased 2% in cecal (2.2%) and product (2.1%). MDR increased by 4% overall in both cecal (4.1%) and product (8.3%) samples. MDR in product showed a consistent increase from 2016 to 2019. Trends in extreme drug resistance (XDR) remained very low across all slaughter classes and sample sources (**Figure 6 and Appendix C, Table C1 and C2**).

Figure 6: Trends in Antimicrobial Susceptibility, Cecal and Product Samples, Combined Slaughter Classes, 2014 - 2019[a,b]



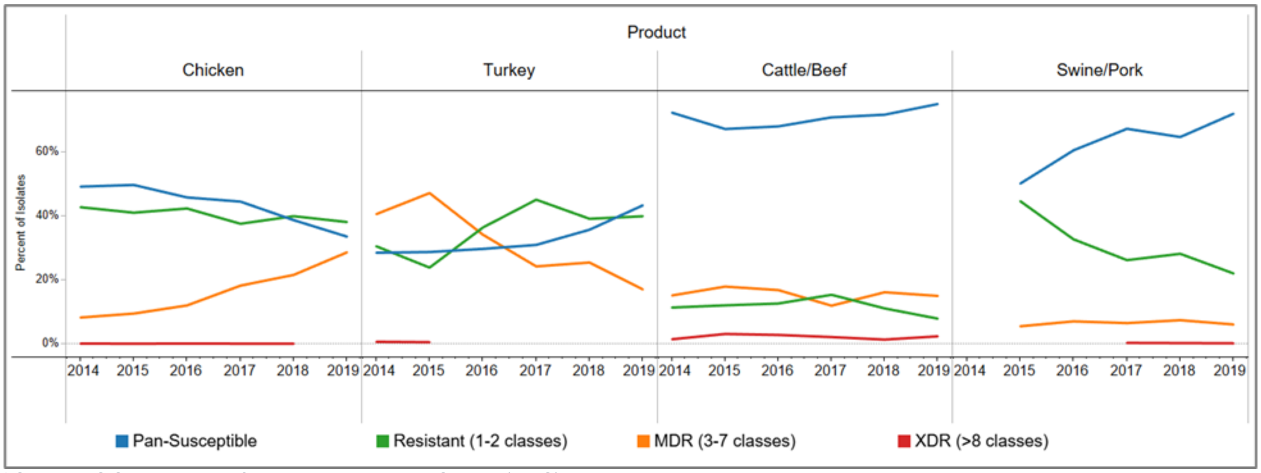
[a] Source: FSIS Laboratory Information Management System (LIMS)
[b] Includes chicken, turkey, cattle, and swine (cecal samples) and chicken, turkey, beef, and pork (product samples)

Figure 7: Distribution of Antimicrobial Resistant *Salmonella* in Cecal Samples by Animal Slaughter Class, 2014 - 2019[a]



[a] Source: FSIS Laboratory Information Management System (LIMS)

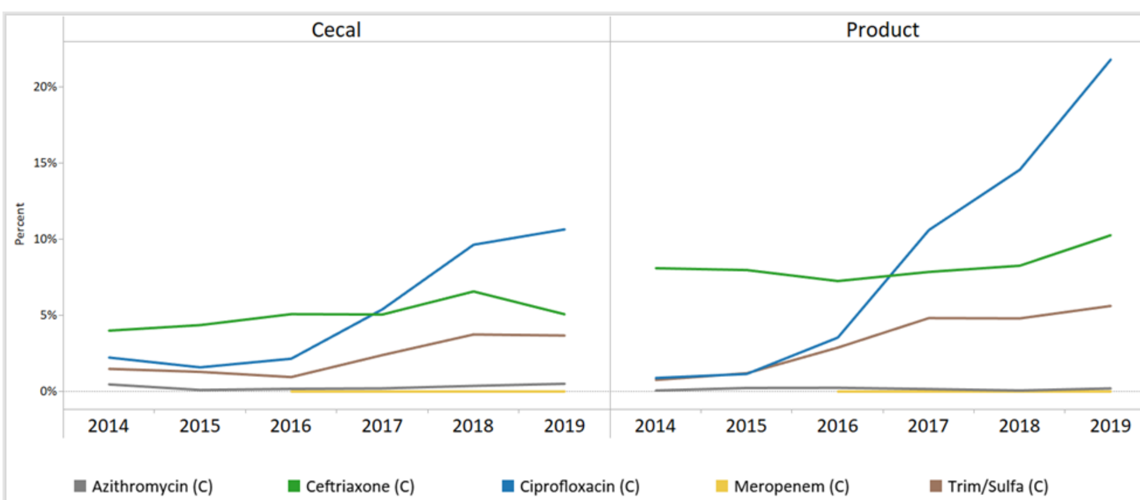
Figure 8: Distribution of Antimicrobial Resistant *Salmonella* in Product Samples by Animal Slaughter Class, 2014 - 2019[a]



[a] Source: FSIS Laboratory Information Management System (LIMS)

A significant increase in the numbers of ciprofloxacin-nonsusceptible *Salmonella* (also referred to as decreased susceptibility to ciprofloxacin or DSC *Salmonella*)[1] was observed in cecal (8.5%) and product (20.9%) samples overall (**Figure 9**). An overall increasing trend was observed in product samples in both cattle (4.9%) and swine (4.9%)(**Figures 12 and 13**). Resistance to meropenem (carbapenem drug class)[4] was not seen in *Salmonella* from cecal or product samples in all slaughter classes over the 6-year period.

Figure 9: Trends in *Salmonella* Resistance to Selected Critically Important Antimicrobial Drugs, Cecal and Product Samples, Combined Slaughter Classes, 2014 - 2019[a]



[a] Source: FSIS Laboratory Information Management System (LIMS)

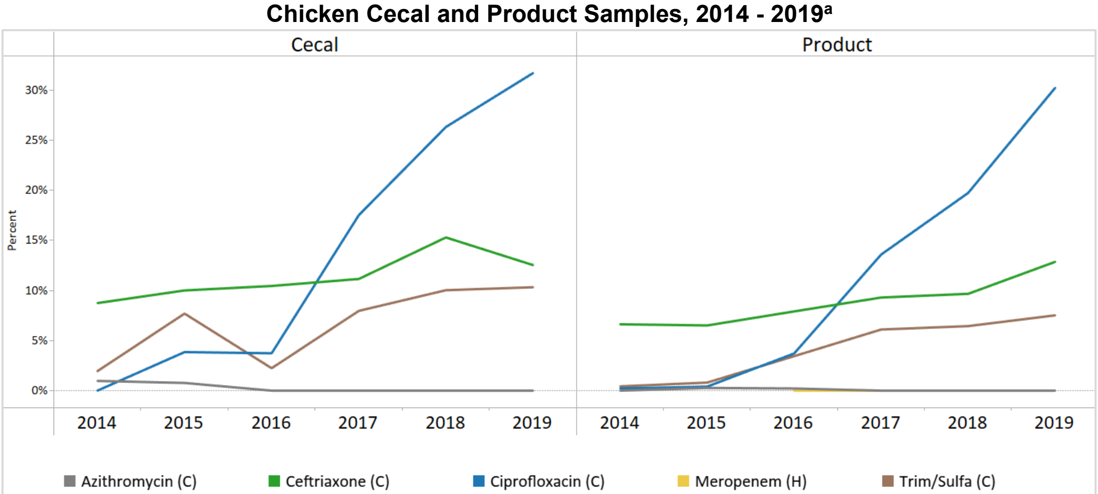
[4] Draft Guidance for Industry (GFI) #152, Food and Drug Administration, 2022.

Chicken

Pansusceptibility decreased 17% in cecal and 16% product samples **(Figure 7 and 8)**. MDR increased 17.7% in cecal samples and 20.3% in product samples (**Figures 10**). In product samples, this trend was significant. These changes were primarily driven by the emergence of serotype Infantis. Resistance to less than 3 classes increased 17% in cecal and 21% in product.

Resistance to the critically important antimicrobials increased in cecal and product samples (respectively) for ciprofloxacin[5] (31.7%/30%), ceftriaxone (3.8%/6.2%), and trimethoprim-sulfamethoxazole (8.4%/7.1%) (**Figure 10 and Appendix E**). The increase in ciprofloxacin-nonsusceptibility (DSC) *Salmonella* was significant in both cecal and product samples. This is noteworthy since the DSC phenomenon, relatively uncommon before 2014, was seen in almost 30% of all chicken cecal and product samples in 2019.

Figure 10: Trends in *Salmonella* Resistance to Selected Critically Important Antimicrobial Drugs, Chicken Cecal and Product Samples, 2014 - 2019[a]



[a] Source: FSIS Laboratory Information Management System (LIMS)

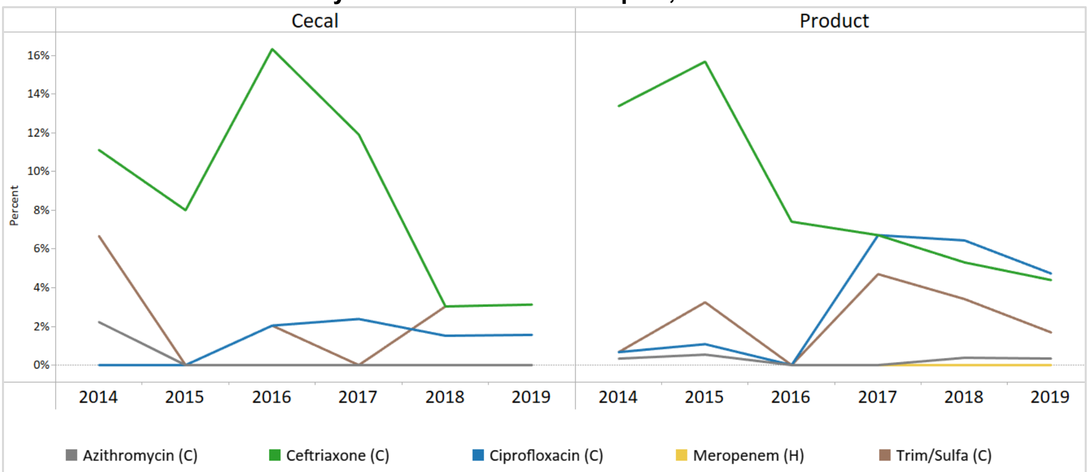
Turkey

Pansusceptibility increased 15% in cecal and 17% in product samples (**Figure 7 and 8** and **Appendix C, Table C2**). MDR decreased 13% in cecal samples and 23% in product samples The change in cecal samples was significant. Resistance to less than 3 classes increased 1% in cecal and 8% in product samples.

Resistance to the critically important antimicrobial drug ceftriaxone decreased 8% in cecal and 9% in product samples (**Figure 11 and Appendix E**). The small number of resistant isolates recovered from turkey samples limited the trend analysis.

[5] Expressed as DSC (decreased susceptibility to ciprofloxacin)

Figure 11: Trends in *Salmonella* Resistance to Selected Critically Important Antimicrobial Drugs, Turkey Cecal and Product Samples, 2014 - 2019[a]

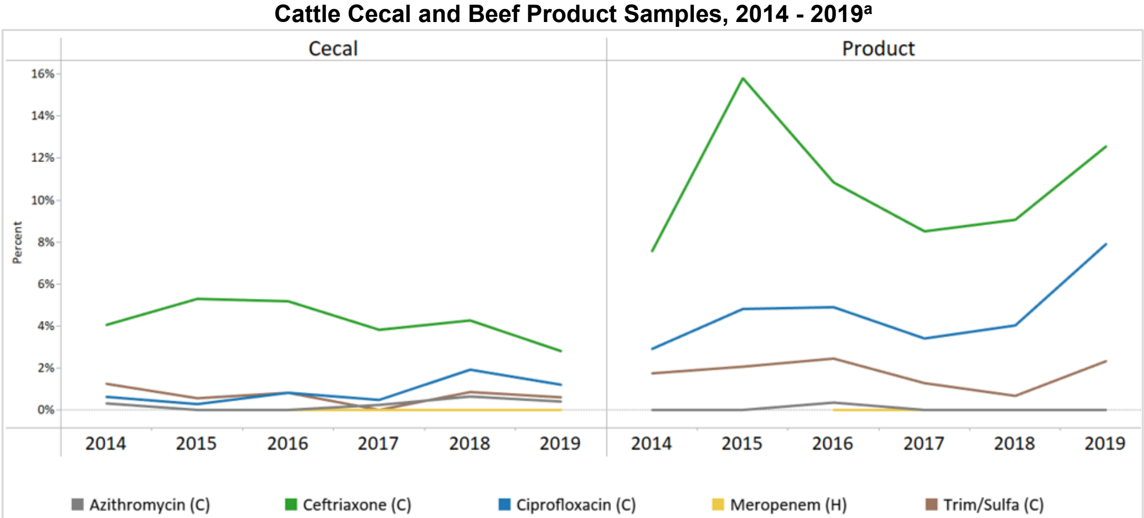


[a] Source: FSIS Laboratory Information Management System (LIMS)

Cattle/Beef

Pansusceptibility increased 7% in cecal and 4% in product samples (**Figures 7 and 8 and Appendix C, Table C2**). MDR decreased 3% in both cattle cecal and product samples. In comparison, MDR fluctuated between 5% and 9% in beef cattle cecal samples and significantly decreased from 10% to 4% in dairy cattle cecal samples. In product samples, MDR fluctuated over time (between 12% and 18%) but showed an overall net reduction. Resistance to less than 3 classes decreased 4% in both cecal and product samples.

Figure 12: Trends in *Salmonella* Resistance to Selected Critically Important Antimicrobial Drugs, Cattle Cecal and Beef Product Samples, 2014 - 2019[a]



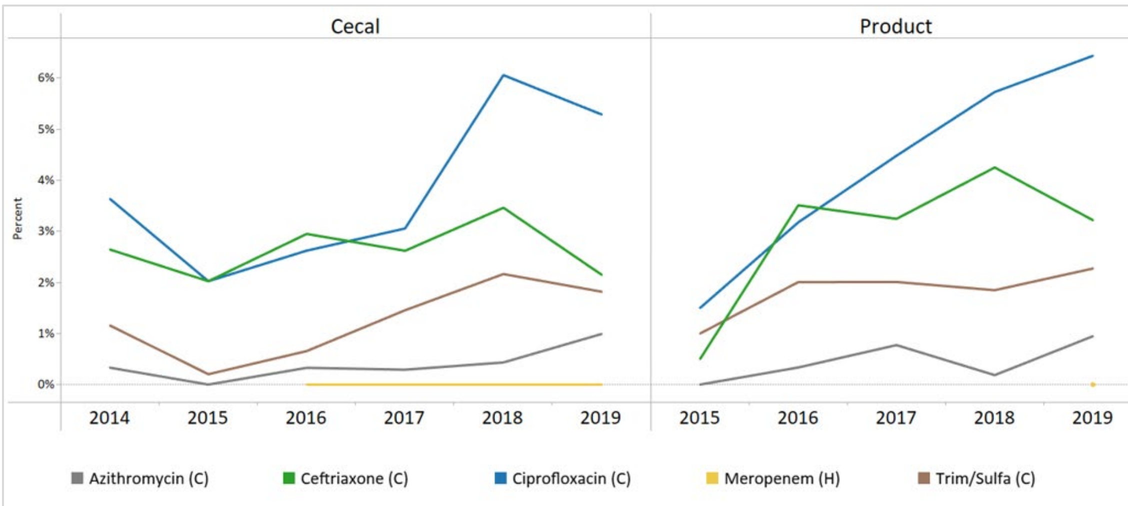
[a] Source: FSIS Laboratory Information Management System (LIMS)

Resistance to critically important antimicrobial drugs showed marked differences between cattle cecal and product samples over the 6-year period: resistance to ceftriaxone decreased 1.2% in cecal samples and increased 4.8% in product samples. From 2018-2019, increased resistance to ceftriaxone (3.3%), trimethoprim-sulfamethoxazole (1.6%) and ciprofloxacin[5] (3.8%) was seen in product samples (**Figure 12 and Appendix E**). Azithromycin resistance was observed in a small number of beef cattle cecal samples from 2017–2019.

Swine/Pork

Pansusceptibility increased 6% in cecal and 20% in product samples (**Figures 7** and **8** and **Appendix C, Table C2**). MDR significantly increased 3% in swine cecal samples and increased 9% in pork product samples. In comparison, MDR trends in cecal samples were relatively low in sows (range of 3-10%) and relatively high in market swine (range of 17-24%). Resistance to less than 3 classes decreased 9% in cecal and 29% in product samples.

Figure 13: Trends in *Salmonella* Resistance to Selected Critically Important Antimicrobial Drugs, Swine Cecal and Pork Product Samples, 2014 - 2019[a,b]



[a] Source: FSIS Laboratory Information Management System (LIMS)
[b] Pork product exploratory sampling began in 2015

Resistance to the critically important antimicrobial drugs increased in pork product samples for ceftriaxone (2.7%), ciprofloxacin[5] (4.9%), trimethoprim-sulfamethoxazole (1.3%), and azithromycin (0.9%) (**Figure 13 and Appendix E)**. In cecal samples, resistance to critically important antimicrobial drugs increased for ciprofloxacin[5] (2.2%), azithromycin (0.6%) and trimethoprim-sulfamethoxazole (0.9%).

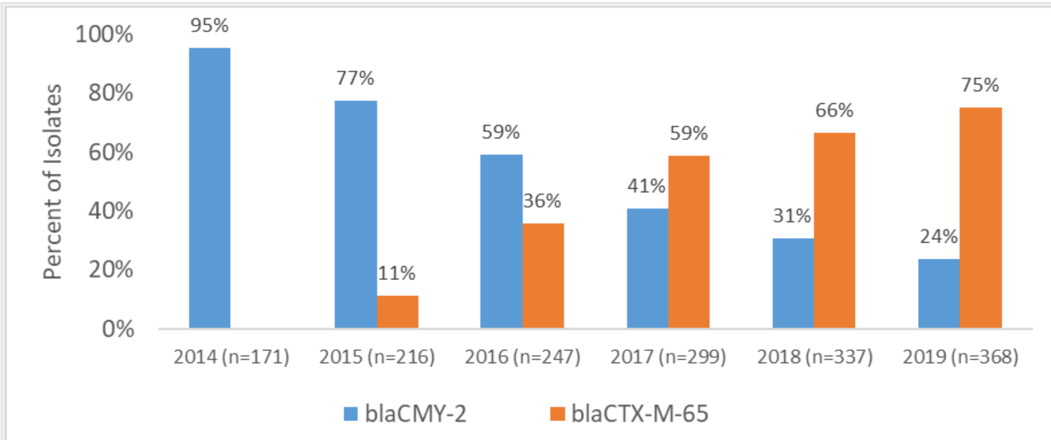
Antimicrobial Resistance and Whole Genome Sequencing (WGS)

WGS provides a deeper insight into the genetic information necessary to characterize *Salmonella* isolates and identify AMR mechanisms and emerging resistance patterns. Between 2014 and 2016, NARMS added genotypic methods to its AMR testing. Unlike earlier phenotypic antimicrobial tests (e.g., the minimum inhibitory concentration (MIC) test), WGS provides information on both resistance and the underlying genes, location of the genes and potential genetic insertions, deletions, shifts and drifts. A shift was observed in genes responsible for extended spectrum beta lactamase (responsible for resistance to third-generation cephalosporins) and ciprofloxacin resistance/decreased susceptibility. FSIS NARMS *Salmonella* isolates that were phenotypically resistant to critically important antimicrobials and contained specific genetic determinants for antimicrobial resistance (ARGD) are further described below.

Cephalosporin-resistance

Ceftriaxone is a critically important, third-generation cephalosporin antimicrobial drug. Different types of cephalosporin-resistance genes were detected in ceftriaxone resistant *Salmonella* isolates (**Figure 14**). Among those with genetic determinants (n=1,638), two types of cephalosporin-resistance genes — $bla_{CMY\text{-}2}$ and $bla_{CTX\text{-}M\text{-}65}$ —showed opposite trends from 2015 to 2019. The $bla_{CTX\text{-}M\text{-}65}$ gene, which was nonexistent among FSIS *Salmonella* isolates before 2015, largely replaced the once predominant *bla*$_{CMY-2}$. While the *bla*$_{CMY-2}$ gene was seen in several serotypes (including Typhimurium, Kentucky and Newport) isolated from various animal commodities, the majority of *bla*$_{CTX-M-65}$ gene occurrence was in Infantis isolated from chicken (**Appendix F, Table F1**).

Figure 14: Distribution of Ceftriaxone-resistance Genes blaCMY-2 and blaCTX-M-65 in *Salmonella* Serotypes from Cecal and Product Samples in Combined Slaughter Classes, 2014 - 2019[a]



[a] Source: FSIS Laboratory Information Management System (LIMS)

Azithromycin-resistance

The number of phenotypically azithromycin-resistant *Salmonella* (n=51) in FSIS NARMS sources have remained low. While most of the phenotypic azithromycin-resistance in *Salmonella* was due to the *mph(A)* genes, other azithromycin-resistance genes including *mph(E)*, *erm(42)* and *msr(E)* were observed. All the azithromycin-resistance genes were located on mobile genetic elements/structures called plasmids, which are known to spread horizontally among bacteria.

Quinolone-resistance

Quinolone resistance in *Salmonella* can be due to mutational gyrase (*gyrA*) genes or acquired (plasmid-mediated) *qnr* genes. Of the DSC *Salmonella* isolates reported (n=1,646), the majority were from chicken sources. More than 90% of DSC in *Salmonella* was attributable to mutations in *gyrA* and remained relatively stable over time (93–100%) (**Appendix F, Figure F1**). The plasmid-mediated quinolone resistance (PMQR) was mostly associated with presence of variants of quinolone- resistance (*qnr*) genes. In contrast to mutational *gyrA* in chicken *Salmonella*, the plasmid-mediated *qnr* genes were predominantly seen in swine (market swine and sows) *Salmonella* and fluctuated over time (market swine: 37–75%; sows: 6–33%)(**Appendix F, Figure F2**). Additionally, a few *Salmonella* also showed both mutational *gyrA* and acquired, plasmid-mediated *qnr* genes. Unlike the mutational resistance, resistance located on plasmids is generally known to spread horizontally among bacteria.

Impact and Significance

FSIS NARMS sampling provides reliable data for the surveillance of AMR *Salmonella*. It is essential to have an in-depth understanding of AMR *Salmonella* trends along the farm-to-slaughter continuum, to develop effective strategies to reduce AMR *Salmonella* in food. Some of these strategies and considerations are described in FSIS' proposed framework for reducing *Salmonella* in poultry[6] as well

[6] Reducing *Salmonella* in Poultry, USDA Food Safety and Inspection Service, 2022.

as FDA's Draft Guidance for Industry (GFI) #152, and GFI #213[7]. Although the leading *Salmonella* serotypes in cecal and product samples over the 6-year period were the same *within* slaughter classes, the trends in AMR *Salmonella* were not. Differences and similarities observed in the AMR and *Salmonella* serotypes between cecal and food product samples highlight the importance of these discrete sampling points.

From 2016–2019, the dominant serotypes in chicken cecal and product samples were Infantis, Kentucky, Enteritidis and Typhimurium. MDR Infantis was first detected in chicken in 2015 and showed a marked increase beginning in 2016. Despite mixed serotype trends over time between chicken cecal and product samples, the sustained and pronounced increase in Infantis from 2016 to 2019 suggests that genetic changes in Infantis continue to provide this serotype a competitive advantage in both cecal and product environments. A recent NARMS publication showed that close to 93% of Infantis from chicken contained the pESI plasmid (McMillan et al., 2020). This plasmid is known for its transmissibility and multidrug resistance; it contains several genes that improve survival and adaptability in product or cecal environments. The emergence of Infantis underscores the rapid manner in which the profile of *Salmonella* can shift over time given certain environmental and host factors.

The rationale for the NARMS program is to examine if the antimicrobials used in food production could lead to increased resistance to antimicrobials in pathogenic and indicator bacteria. Antibiotic use on farms and AMR bacteria found in food do not have a one-to-one relationship. While some believe antibiotic use in agriculture is one of the primary drivers for AMR emergence, the fact is we have an incomplete understanding of the factors that contribute to AMR in various settings[8]. It is noteworthy that observations of bacterial resistance to certain antimicrobial drugs do not automatically indicate antimicrobial drug use in animals (Baker-Austin, 2006). This may be due to a process called co-selection, which can lead to the development of non-specific antimicrobial resistance. Several non-specific triggers can facilitate the development and/or spread of co-resistance to antimicrobial drugs. Some of these triggers include acquired AMR/MDR through mobile genetic elements on plasmids, use of antimicrobials outside of food-producing animal systems, and environmental factors (e.g., heavy metals and AMR association) (Baker-Austin, 2006; Yu, 2017). The resulting AMR bacteria can spread geographically to regions where certain antimicrobial drugs may not be in use.

Examining the connections between AMR and the related genes or genetic sequences helps the NARMS partners understand the types of AMR genes and resistance mechanisms, their location (whether chromosomal or plasmid), their potential for spread, pertinent evolutionary and geographic relationships, potential factors for genetic changes and trends over time. FSIS routinely engages with NARMS partners and the food production industry to bridge information gaps between the NARMS findings and pre-slaughter changes. This report shows how the analysis of both cecal and product samples provides a more complete picture of changes in *Salmonella* AMR and continually serves as an early indicator of emerging AMR *Salmonella* threats to public health. AMR monitoring at a genomic level has helped FSIS, public health partners and stakeholders understand the specific genomic events or changes in *Salmonella*. This information is crucial in our efforts to develop appropriate solutions to prevent and contain AMR.

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[7] Draft Guidance for Industry (GFI) #213, Food and Drug Administration, 2022.

[8] What is the relationship between antibiotic use in agriculture and AMR bacteria? USDA Antimicrobial Resistance Overview (AMR) www.usda.gov/topics/animals/one-health/antimicrobial-resistance-overview-amr.

About NARMS

NARMS is a national public health surveillance system that monitors enteric bacteria and select animal pathogens to determine if they are resistant to antimicrobial agents used in human and veterinary medicine. NARMS is a collaboration of agencies within the U.S. Department of Health and Human Services (Food and Drug Administration (FDA) and Centers for Disease Control and Prevention (CDC) and USDA (FSIS, Animal and Plant Health Inspection Service (APHIS), and Agricultural Research Service).

The NARMS program tracks trends in antimicrobial resistance over time, identifies new types and patterns of resistance, and helps measure the impact of interventions designed to limit the spread of resistance. NARMS data are used by FDA in the regulatory review of new animal antimicrobial drugs and in the development of policies on judicious antimicrobial use in animals. To minimize potential consumer exposure to pathogens and antimicrobial resistance thereof, the CDC and FSIS use NARMS information on a case-by-case basis in foodborne illness and outbreak investigations.

> FSIS Quarterly Sampling Reports on Antimicrobial Resistance can be found on FSIS' Science and Data webpage, under Data Sets and Visualizations > Microbiology.
>
> Data sets for FSIS NARMS cecal and product sampling programs can be found on the FDA's Integrated Reports/Summaries webpage.

The FSIS NARMS sampling program provides data on selected enteric bacteria and their AMR profiles from slaughter classes. The FSIS NARMS program can detect AMR trends and novel findings of public health concern in real-time. Consequently, FSIS can use NARMS findings[9] as early warning indicators to inform the NARMS partners, industry and other stakeholders.

Under FSIS' verification sampling (PR/HACCP sampling), FSIS routinely collects samples from meat and poultry products at regulated facilities across the United States. Prior to 2013, these meat and poultry samples were tested to study antimicrobial resistance using the phenotypic (or observable characteristics) antimicrobial susceptibility testing (AST) approach. After that, genomic sequencing was implemented to identify and understand the genes and mechanisms involved in AMR. AST is still used in cecal samples to monitor for novel phenotypic changes.

In March 2013, FDA and FSIS added cecal (intestinal) sampling, thereby providing insight into AMR of the microbial population in the animal coming to slaughter. The food animal species in this program included young chickens, young turkeys, swine (market swine and sow) and cattle (beef cow and dairy cow). Over time, additional animal classes have been added (e.g., bob veal calves, Siluriformes fish). More information on the transition and subsequent developments in FSIS' NARMS program is available on FSIS' NARMS webpage.

Data and Analytical Considerations

The FSIS NARMS samples[10] are collected from two distinct sources: cecal samples and product samples. There are differences between the cecal sampling program and product sampling program, including the sampling design, sampling sources, laboratory methodologies and analytic approaches.

Product samples are collected post-interventions/processing and the number of samples collected are based on the planned number of samples to analyze as published in FSIS' Annual Sampling Plan. Cecal sampling is conducted using a statistical design based on establishment production volume and predicted positive rates to reach a target number of bacterial isolates for antimicrobial susceptibility

[9] See NARMS Interim Data Updates
[10] See FSIS Annual Sampling Plan

testing. These samples provide industry-wide data on antimicrobial susceptibility among four targeted bacteria (*Salmonella, Campylobacter,* generic *Escherichia coli* and *Enterococcus*) at a point in the slaughter process prior to the application of antimicrobial interventions.

For the sampling period 2014-2019, no separate swine/pork product sampling program existed. Therefore, data from the Raw Pork Products Exploratory Sampling Program (conducted 2015-2018) was used to compare trends under the product sampling program.

In FSIS NARMS data sets there are differences in sample collection points (cecal vs. finished product) and the number of samples collected from the various sampling projects. These differences necessitate caution when interpreting these data.

Sampling Program Design

The laboratory methods used to retrieve and isolate *Salmonella* from samples are described in the FSIS Microbiology Laboratory Guidebook. The laboratory methods used for antimicrobial susceptibility testing are described in the FDA NARMS Manual of Laboratory Methods. As a part of bacterial characterization, FSIS routinely conducts WGS on *Salmonella* isolates from cecal and product (PR/HACCP) sampling programs. Sampling information and isolate characterization results have been linked in this report to facilitate further analysis. Additional information on design of the sampling program and analytical methods used can be found on the FSIS NARMS webpage.

It is important to note that FSIS regulations require the entire digestive track, including the cecum, be removed during slaughter. FSIS verification activities include sampling and testing for microbial pathogens and indicator organisms. FSIS conducts these activities to monitor the effectiveness of procedures to prevent contamination of carcasses with digestive tract contents, including pathogenic bacteria, and thus prevent such contamination from entering the food supply.

GLOSSARY

Antimicrobial resistance: when bacteria develop the ability to defeat the drugs designed to kill them.

Antimicrobial resistance patterns:
- **Pan-susceptible:** bacterial isolates that are susceptible to all antimicrobial drugs that are represented by the nine antimicrobial drug classes included in the NARMS testing panel.
- **Resistant:** bacterial isolates resistant to one or two drug classes.
- **Multidrug-resistant (MDR):** bacterial isolates resistant to three to seven drug classes.
- **Extreme drug resistant (XDR):** MDR bacterial isolates that are resistant to eight or all nine drug classes.

Antimicrobial drugs: drugs that treat infections by killing or slowing the growth of bacteria or other microbial organisms that cause infections, including antibiotics.

Antimicrobial susceptibility testing (AST): Laboratory testing performed on bacteria to find out if they are susceptible or resistant to one or more antimicrobial drugs. The antimicrobial drugs selected for testing are based on their importance in human and veterinary medicine. AST is used to guide options for antimicrobial drug selection and potential for effective patient treatment.

Decreased Susceptibility to Ciprofloxacin (DSC) *Salmonella*: *Salmonella* with MIC ≥ 0.12 ug/ml. Because even small increases in quinolone MICs can negatively impact the response to treatment, the DSC classification which includes *Salmonella* with lower-level resistance helps to decrease the likelihood of inadvertent ciprofloxacin treatment failures (see the NARMS Interpretive Criteria for Susceptibility Testing of *Salmonella* and *E. coli* - Breakpoints, Table 1 footnote, accessible at www.fda.gov/media/108180/download).

Isolate: pure sample of bacteria.

Medically important antimicrobial drugs (antibiotics): drugs that are commonly needed to treat infections in people.

Pathogen: an organism, such as a bacterium, that can cause infections.

Plasmid: a small, often circular DNA molecule found in bacteria and other cells. Plasmids are separate from bacterial chromosomes and replicate independently of it. They generally carry only a small number of genes, notably some associated with antibiotic resistance. Plasmids are mobile genetic elements that may be passed between different bacterial cells.

REFERENCES

Baker-Austin, C., Wright, M., Stepanauskas, R., McArthur, J. (2006). Co-selection of antibiotic and metal resistance. Trends in Microbiology 14(4), 176-182. doi.org/10.1016/j.tim.2006.02.006.

Foley, S.L., Nayak, R., Hanning, I. B., Johnson, T.J., Han, J., Ricke, S.C. (2011). Population Dynamics of *Salmonella* enterica Serotypes in Commercial Egg and Poultry Production. Applied and Environmental Microbiology, 77(13), 4273-4279. doi:doi:10.1128/AEM.00598-11.

Gilbert, R.O. (1987). Statistical methods for environmental pollution monitoring. New York: Van Nostrand Reinhold Co.

Karp, B.E., Tate, H., Plumbee, J.R., Dessai, U., Whichard, J.M., et al. (2017). National Antimicrobial Resistance Monitoring System: Two Decades of Advancing Public Health Through Integrated Surveillance of Antimicrobial Resistance. Foodborne Pathogens and Disease 14(10), 545-557. doi.org/10.1089/fpd.2017.2283.

Kendall, M.G. (1970). Rank correlation methods. London: Griffin.

Mann, H.B. (1945). Nonparametric Tests Against Trend. Econometrica, 13(3), 245-259. doi:10.2307/1907187.

McMillan, E., Wasilenko, J., Tagg, K., Chen, J., Simmons, M., Gupta, S., Frye, J. (2020). Carriage and Gene Content Variability of the pESI-Like Plasmid Associated with *Salmonella* Infantis Recently Established in United States Poultry Production. Genes, 11, 1516. doi:10.3390/genes11121516.

O'Bryan, C.A., Ricke, S.C., Marcy, J.A. (2022). Public health impact of *Salmonella* spp. on raw poultry: Current concepts and future prospects in the United States. Food Control, 132, 108539. doi:https://doi.org/10.1016/j.foodcont.2021.108539.

Rabsch, W., Hargis, B.M., Tsolis, R.M., Kingsley, R.A., Hinz, K.H., Tschäpe, H., et al. Competitive exclusion of *Salmonella enteritidis* by *Salmonella gallinarum* in poultry. Emerging Infect Dis (2000) 6(5):443–8. doi:10.3201/eid0605.000501.

Sen, P.K. (1968). Estimates of the Regression Coefficient Based on Kendall's Tau. Journal of the American Statistical Association, 63(324), 1379-1389. doi:10.1080/01621459.1968.10480934.

Tableau (version. 9.1). (2016). Journal of the Medical Library Association: JMLA, 104(2), 182-183. doi:10.3163/1536-5050.104.2.022.

Tack, D.M., et al. (2020). Preliminary Incidence and Trends of Infections with Pathogens Transmitted Commonly Through Food - Foodborne Diseases Active Surveillance Network, 10 U.S. Sites, 2016-2019. MMWR. Morbidity and Mortality Weekly Report, 69(17), 509-514. doi: http://dx.doi.org/10.15585/mmwr.mm6917a1.

U.S. Department of Agriculture, Food Safety and Inspection Service. Reducing *Salmonella* in Poultry. Accessed December 20, 2022. (available at www.fsis.usda.gov/inspection/inspection-programs/inspection-poultry-products/reducing-salmonella-poultry)

U.S. Department of Health and Human Services, Food and Drug Administration. (2022). Draft Guidance for Industry: Evaluating the Safety of Antimicrobial New Animal Drugs with Regards to Their Microbiological Effects on Bacteria of Human Health Concern (GFI #152) (available at ww.fda.gov/regulatory-information/search-fda-guidance-documents/cvm-gfi-152-evaluating-safety-antimicrobial-new-animal-drugs-regard-their-microbiological-effects).

U.S. Department of Health and Human Services, Food and Drug Administration. (2013). Guidance for Industry New Animal Drugs and New Animal Drug Combination Products Administered in or on Medicated Feed or Drinking Water of Food Producing Animals: Recommendations for Drug Sponsors for Voluntarily Aligning Product Use Conditions with GFI #209 (GFI #213) (available at www.fda.gov/regulatory-information/search-fda-guidance-documents/cvm-gfi-213-new-animal-drugs-and-new-animal-drug-combination-products-administered-or-medicated-feed).

U.S. Department of Health and Human Services, Food and Drug Administration. The National Antimicrobial Resistance Monitoring System: NARMS Integrated Reports. Accessed March 25, 2022. (available at www.fda.gov/animal-veterinary/national-antimicrobial-resistance-monitoring-system/integrated-reportssummaries).

Williams, M.S., Ebel, E.D., Hretz, S.A., Golden, N.J. (2018). Adoption of Neutralizing Buffered Peptone Water Coincides with Changes in Apparent Prevalence of *Salmonella* and *Campylobacter* of Broiler Rinse Samples. Journal of Food Protection, 81(11), 1851-1863. doi:10.4315/0362-028x.Jfp-18-124.

Williams, M.S., Ebel, E.D., Saini, G., Nyrabagizi, E. (2020). Changes in *Salmonella* Contamination in Meat and Poultry Since the Introduction of the Pathogen Reduction and Hazard Analysis and Critical Control Point Rule. Journal of Food Protection, 83(10), 1707-1717. doi:10.4315/jfp-20-126.

Yu, Z., Gunn, L., Wall, P., Fanning, S.(2017). Antimicrobial resistance and its association with tolerance to heavy metals in agriculture production. Food Microbiology 64, 23-32. doi.org/10.1016/j.fm.2016.12.009.

APPENDIX A – Top Ten *Salmonella* Serotype Rankings by Slaughter Class and Sample Source, 2014 – 2019

Table A1. *Salmonella* Serotype Distribution in Chicken Cecal and Product Samples, 2014 - 2019

	Cecal Sampling				Product Sampling		
Serotype	Rank.	%	No.	**Serotype**	Rank.	%	No.
Kentucky	1	29%	429	Kentucky	1	32%	3,345
Infantis	2	21%	301	Enteritidis	2	22%	2,231
Enteritidis	3	16%	234	Infantis	3	15%	1,467
Typhimurium	4	12%	187	Typhimurium	4	9%	916
Schwarzengrund	5	8%	115	Schwarzengrund	5	8%	770
Heidelberg	6	2%	38	Heidelberg	6	4%	449
Senftenberg	7	1%	20	Thompson	7	2%	211
Braenderup	8	1%	18	I 4,[5],12:i:-	8	1%	146
Mbandaka	9	1%	14	Braenderup	9	1%	117
Anatum	10	1%	13	Montevideo	10	1%	76

Table A2. *Salmonella* Serotype Distribution in Turkey Cecal and Product Samples, 2014 - 2019

	Cecal Sampling				Product Sampling		
Serotype	Rank.	%	No.	**Serotype**	Rank.	%	No.
Reading	1	23%	66	Reading	1	27%	356
Hadar	2	16%	46	Hadar	2	10%	134
Senftenberg	3	8%	25	Agona	3	6%	73
I 4,[5],12:i:-	4	7%	18	Schwarzengrund	4	5%	73
Schwarzengrund	5	6%	16	Muenchen	5	6%	69
Agona	6	6%	15	Heidelberg	6	4%	59
Anatum	7	5%	15	I 4,[5],12:i:-	7	4%	58
Saintpaul	8	3%	12	Senftenberg	8	4%	54
Albany	9	4%	11	Uganda	9	4%	49
Muenchen	10	4%	11	Infantis	10	4%	47

Table A3a. *Salmonella* Serotype Distribution in Cattle Cecal[a] and Product Samples, 2014 - 2019

	Cecal Sampling				Product Sampling		
Serotype	Rank.	%	No.	**Serotype**	Rank.	%	No.
Montevideo	1	22%	531	Montevideo	1	21%	355
Cerro	2	19%	458	Dublin	2	8%	140
Anatum	3	11%	261	Cerro	3	6%	102
Typhimurium	4	4%	99	Muenchen	4	6%	102
Newport	5	4%	87	Anatum	5	6%	90
Kentucky	6	3%	81	Typhimurium	6	5%	81
Muenster	7	3%	78	Newport	7	4%	72
Agona	8	3%	76	Muenster	8	4%	62
Mbandaka	9	3%	73	Kentucky	9	3%	59
Muenchen	10	3%	73	6,7:g,m,s:e,n,z15	10	3%	51

[a] Cattle cecal sampling includes beef cow, dairy cow, steers and heifers

Table A3b. *Salmonella* Serotype Distribution in Beef and Dairy Cow Cecal Samples, 2014 - 2019

	Beef Cow Cecal Sampling				Dairy Cattle Cecal Sampling		
Serotype	Rank.	%	No.	**Serotype**	Rank.	%	No.
Montevideo	1	18%	37	Cerro	1	29%	408
Anatum	2	10%	19	Montevideo	2	25%	346
Typhimurium	3	7%	14	Anatum	3	5%	72
Cerro	4	6%	12	Newport	4	4%	61
Meleagridis	5	6%	12	Typhimurium	5	4%	58
Muenster	6	5%	10	Kentucky	6	4%	51
Newport	7	4%	8	Muenster	7	3%	48
I 4,[5],12:i:-	8	4%	7	Agona	8	3%	45
Mbandaka	9	4%	7	Mbandaka	9	3%	43
Muenchen	10	3%	6	Meleagridis	10	3%	39

Table A3c. *Salmonella* Serotype Distribution in Steer and Heifer Cecal Samples, 2014 – 2019

	Steer Cecal Sampling		
Serotype	Rank.	%	No.
Anatum	1	22%	103
Montevideo	2	20%	91
6,7:g,m,s:e,n,z15	3	5%	25
Cerro	4	5%	24
Muenchen	5	5%	22
Kentucky	6	4%	21
Agona	7	3%	15
Typhimurium	8	3%	14
Mbandaka	9	3%	13
Infantis	10	2%	11

	Heifer Cecal Sampling		
Serotype	Rank.	%	No.
Anatum	1	21%	67
Montevideo	2	19%	57
6,7:g,m,s:e,n,z15	3	7%	20
Cerro	4	4%	14
Typhimurium	5	4%	13
Agona	6	4%	12
Muenchen	7	4%	11
Mbandaka	8	2%	10
Meleagridis	9	3%	9
Muenster	10	3%	9

Table A4a. *Salmonella* Serotype Distribution in Swine Cecal[a] and Product Samples, 2014 - 2019

	Cecal Sampling		
Serotype	Rank.	%	No.
Anatum	1	17%	622
Derby	2	11%	412
Johannesburg	3	9%	350
Infantis	4	6%	246
I 4,[5],12:i:-	5	6%	214
London	6	5%	155
Uganda	7	3%	117
Adelaide	8	3%	111
Agona	9	3%	109
Eko	10	3%	106

	Product Sampling		
Serotype	Rank.	%	No.
Anatum	1	15%	378
Infantis	2	12%	292
Derby	3	8%	209
I 4,[5],12:i:-	4	8%	202
Johannesburg	5	7%	179
Ohio	6	4%	110
London	7	4%	107
Adelaide	8	4%	106
Typhimurium	9	3%	82
Uganda	10	3%	77

[a] Swine cecal sampling includes market swine and sows

Table A4b. *Salmonella* Serotype Distribution in Sow and Market Hog Cecal Samples, 2014 - 2019

Serotype	Sow Cecal Sampling Rank.	%	No.
Anatum	1	24%	330
Johannesburg	2	12%	168
Infantis	3	6%	103
Derby	4	7%	100
London	5	5%	60
Uganda	6	4%	59
Muenchen	7	3%	53
Agona	8	3%	43
Saintpaul	9	3%	41
Adelaide	10	3%	39

Serotype	Market Swine Cecal Sampling Rank.	%	No.
Derby	1	13%	312
Anatum	2	13%	292
I 4,[5],12:i:-	3	9%	188
Johannesburg	4	8%	182
Infantis	5	6%	143
London	6	4%	95
Typhimurium	7	3%	78
Eko	8	3%	74
Adelaide	9	3%	72
Agona	10	3%	66

APPENDIX B – Top 10 *Salmonella* serotypes for FSIS NARMS Cecal and Product Sampling by Slaughter Class (2019)[a] and the Centers for Disease Control and Prevention (CDC) Clinical Isolates (2019)[a,b]

Table B1: Chicken

	2019 FSIS NARMS Sampling - Chicken				CDC[1,2]
Serotype	Rank	Product (N = 1929)	Rank	Cecal (N = 407)	Rank
Infantis	1	544 (28.2%)	1	121 (29.7%)	6
Kentucky	2	543 (28.1%)	2	119 (29.2%)	*
Enteritidis	3	419 (21.7%)	3	70 (17.2%)	1
Schwarzengrund	4	138 (7.2%)	4	33 (8.1%)	*
Typhimurium	5	106 (5.5%)	5	26 (6.4%)	3
I 4,[5],12:i:-	6	25 (1.3%)	12	2 (0.5%)	5
Braenderup	7	24 (1.2%)	6	6 (1.5%)	8
Heidelberg	8	24 (1.2%)	7	5 (1.2%)	*
Thompson	9	22 (1.1%)	NA	NA	*
Rough_O:r:1,5	10	16 (0.8%)	14	2 (0.5%)	*

Table B2: Turkey

	2019 FSIS NARMS Sampling - Turkey				CDC[1,2]
Serotype	Rank	Product (N = 296)	Rank	Cecal (N = 64)	Rank
Reading	1	94 (31.8%)	1	20 (31.3%)	*
Uganda	2	23 (7.8%)	3	6 (9.4%)	*
Agona	3	19 (6.4%)	4	4 (6.3%)	*
Typhimurium	4	18 (6.1%)	20	1 (1.6%)	3
Schwarzengrund	5	17 (5.7%)	6	4 (6.3%)	*
Muenchen	6	16 (5.4%)	8	2 (3.1%)	9
Anatum	7	15 (5.1%)	12	1 (1.6%)	*
Infantis	8	15 (5.1%)	15	1 (1.6%)	6
Hadar	9	13 (4.4%)	2	8 (12.5%)	*
Senftenberg	10	12 (4.1%)	10	2 (3.1%)	*

Table B3: Cattle

	2019 FSIS NARMS Sampling - Cattle						CDC[1,2]
Serotype	**Rank**	**Product** (N = 215)	**Rank**	**Beef Cattle Cecal** (N = 275)	**Rank**	**Dairy Cattle Cecal** (N = 275)	**Rank**
Montevideo	1	45 (20.9%)	2	71 (25.8%)	2	71 (25.8%)	10
Dublin	2	24 (11.2%)	NA	NA	NA	NA	*
Anatum	3	14 (6.5%)	7	11 (4.0%)	7	11 (4.0%)	*
Muenchen	4	12 (5.6%)	8	9 (3.3%)	8	9 (3.3%)	9
Newport	5	12 (5.6%)	6	12 (4.4%)	6	12 (4.4%)	2
Cerro	6	10 (4.7%)	1	80 (29.1%)	1	80 (29.1%)	*
Kentucky	7	9 (4.2%)	4	12 (4.4%)	4	12 (4.4%)	*
Muenster	8	9 (4.2%)	5	12 (4.4%)	5	12 (4.4%)	*
Give	9	8 (3.7%)	14	3 (1.1%)	14	3 (1.1%)	*
Typhimurium	10	8 (3.7%)	9	7 (2.5%)	9	7 (2.5%)	3

Table B4: Swine

	2019 FSIS NARMS Sampling - Swine						CDC[1,2]
Serotype	**Rank**	**Product** (N= 528)	**Rank**	**Market Swine Cecal** (N = 433)	**Rank**	**Sows Cecal** (N = 172)	**Rank**
Anatum	1	79 (15%)	3	39 (9.0%)	1	41 (23.8%)	*
Infantis	2	61 (12%)	7	22 (5.1%)	11	5 (2.9%)	6
I4,[5],12:i:-	3	52 (9.9%)	1	47 (10.9%)	13	3 (1.7%)	5
Johannesburg	4	40 (7.6%)	4	36 (8.3%)	2	24 (4.0%)	*
Derby	5	36 (6.8%)	2	42 (9.7%)	4	12 (7.0%)	*
Adelaide	6	32 (6.1%)	5	26 (6.0%)	5	10 (5.8%)	*
London	7	26 (4.9%)	6	25 (5.8%)	3	13 (7.6%)	*
Ohio	8	18 (3.4%)	10	13 (3.0%)	24	1 (0.6%)	*
Uganda	9	15 (2.8%)	16	9 (2.1%)	6	9 (5.2%)	*
Agona	10	13 (2.5%)	12	12 (2.8%)	9	5 (2.9%)	*

[a] Data sources: FSIS Laboratory Information Management System (LIMS) and CDC FoodNet (https://wwwn.cdc.gov/foodnetfast/)
[b] *Tack, et al, 2020*
[1] 2019 CDC *Salmonella* serotypes of public health significance – clinical samples (incidence rate greater than or equal to 0.20 per 100,000).
[2] The 2019 CDC ten most common fully serotyped *Salmonella* isolates included #1 – Enteriditis, #2 – Newport, #3 – Typhimirium, #4 – Javiana, #5 – I 4,[5],12:i-, #6 – Infantis, #7 – Saintpaul, #8 – Braenderup, #9 – Muenchen and #10 – Montevideo.
* Serotypes not reported as one of the top 10 *Salmonella* isolates in CDC clinical samples.
[NA] Serotypes not reported in FSIS cecal samples

APPENDIX C – *Salmonella* Antimicrobial Susceptibility Trends and Distribution of the Top-ranked FSIS *Salmonella* Serotype by Major Animal Commodities, Sample Sources and Year, 2014 – 2019

Table C1: *Salmonella* Antimicrobial Susceptibility in Cecal and Product Samples, Combined Slaughter Classes, 2014 - 2019[a,b,c]

	Cecal Sampling							Product Sampling						
Resistance pattern	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**Total**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**Total**
Pan-susceptible (0)	66% (708)	65% (652)	67% (773)	66% (964)	58% (937)	64% (1,007)	**64% (5,041)**	50% (792)	50% (1,087)	50% (1,444)	50% (1,577)	46% (1,411)	44% (1,309)	**48% (7,620)**
Resistant (1 or 2)	21% (224)	24% (238)	20% (232)	20% (288)	23% (371)	19% (294)	**21% (1,647)**	34% (529)	36% (778)	37% (1,065)	34% (1,058)	35% (1,067)	31% (934)	**34% (5,431)**
MDR (3 or more)	13% (143)	12% (118)	13% (155)	14% (210)	20% (319)	17% (275)	**15% (1,220)**	16% (258)	14% (302)	13% (369)	16% (494)	19% (581)	25% (730)	**17% (2,734)**
Total (N)	**1,075**	**1,008**	**1,160**	**1,462**	**1,627**	**1,576**	**7,908**	**1,579**	**2,167**	**2,878**	**3,129**	**3,059**	**2,973**	**15,785**

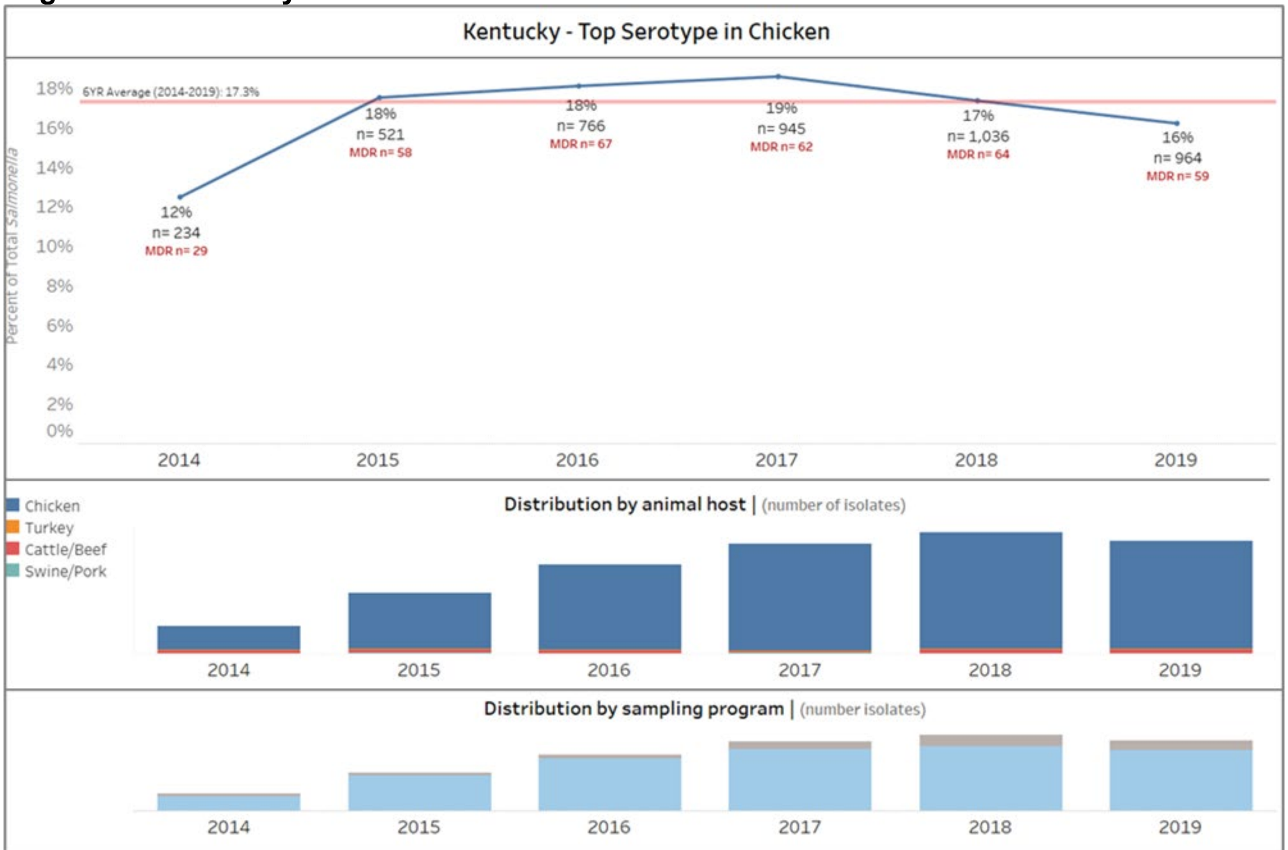
[a] Source: FSIS Laboratory Information Management System (LIMS)
[b] Includes chicken, turkey, cattle, and swine (cecal samples) and chicken, turkey, beef, and pork (product samples)
[c] XDR data not shown in the table; comprised less than 1% of the total

Table C2: *Salmonella* Antimicrobial Susceptibility in Cecal and Product Samples by Slaughter Class, 2014 – 2019 Aggregate Data[a,b]

	Cecal Sampling							Product Sampling				
Resistance pattern	**Chicken**	**Turkey**	**Beef Cattle**	**Dairy Cattle**	**Market Swine**	**Sows**	**Total**	**Chicken**	**Turkey**	**Beef**	**Pork**	**Total**
Pan-susceptible (0)	35% (523)	32% (93)	80% (804)	85% (1,223)	58% (1,310)	75% (1,088)	**64% (5,041)**	43% (4,373)	34% (452)	71% (1,182)	64% (1,613)	**46% (7,620)**
Resistant (1 - 2)	39% (573)	35% (101)	12% (124)	7.8% (112)	21% (474)	18% (263)	**21% (1,647)**	40% (4,085)	35% (467)	12% (195)	27% (684)	**34% (5,431)**
MDR (3 or more)	26% (391)	33% (97)	7.4% (74)	6.8% (98)	21% (462)	6.8% (98)	**15% (1,220)**	18% (1,814)	31% (409)	18% (294)	8.6% (217)	**17% (2,734)**
Total (N)	**1,487**	**291**	**1,002**	**1,433**	**2,246**	**1,449**	**7,908**	**10,272**	**1,328**	**1,671**	**2,514**	**15,785**

[a] Source: FSIS Laboratory Information Management System (LIMS)
[b] XDR data not shown in the table; comprised less than 1% of the total

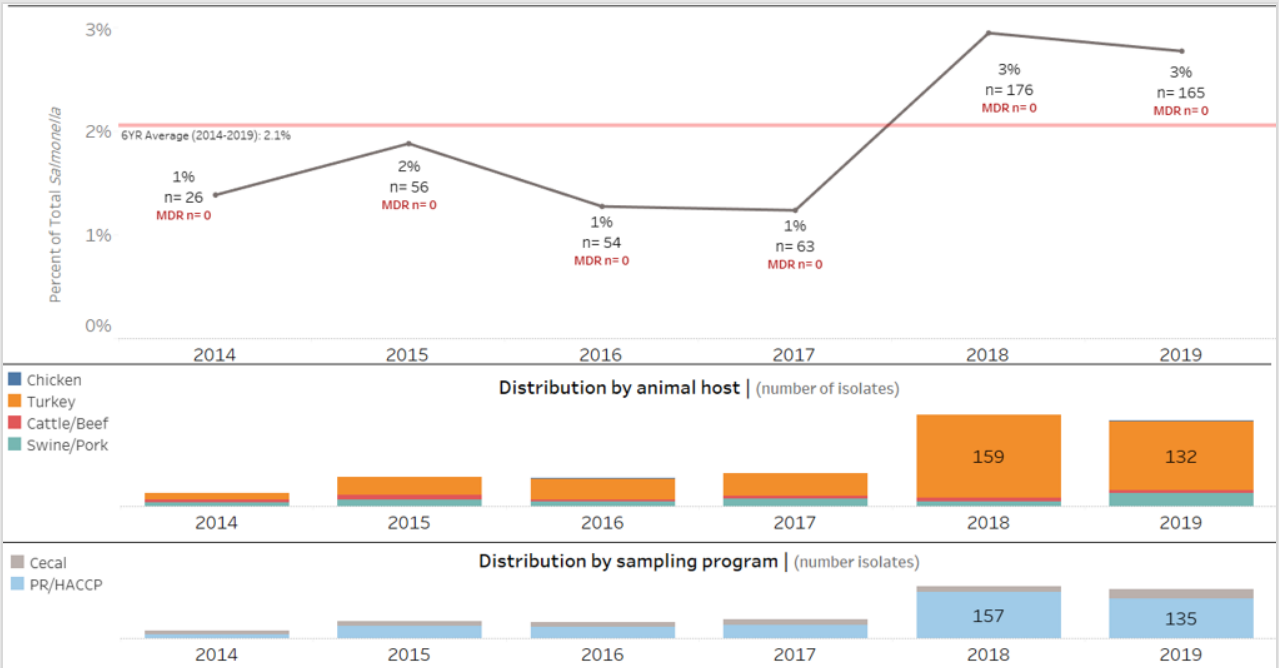
Figure C1: Kentucky



Serotype	Animal Host	2014	2015	2016	2017	2018	2019
Kentucky	Chicken	205	483	735	922	993	927
	Turkey	5	3	1	1	4	2
	Cattle/Beef	22	24	27	17	38	32
	Swine/Pork	2	11	3	5	1	3

Serotype	Sample Source	2014	2015	2016	2017	2018	2019
Kentucky	Cecal	41	41	50	105	151	138
	PR/HACCP	193	480	716	840	885	826

Figure C2: Reading



Serotype	Animal Host	2014	2015	2016	2017	2018	2019
Reading	Chicken			1			2
	Turkey	13	34	41	43	159	132
	Cattle/Beef	5	10	3	5	8	5
	Swine/Pork	8	12	9	15	9	26

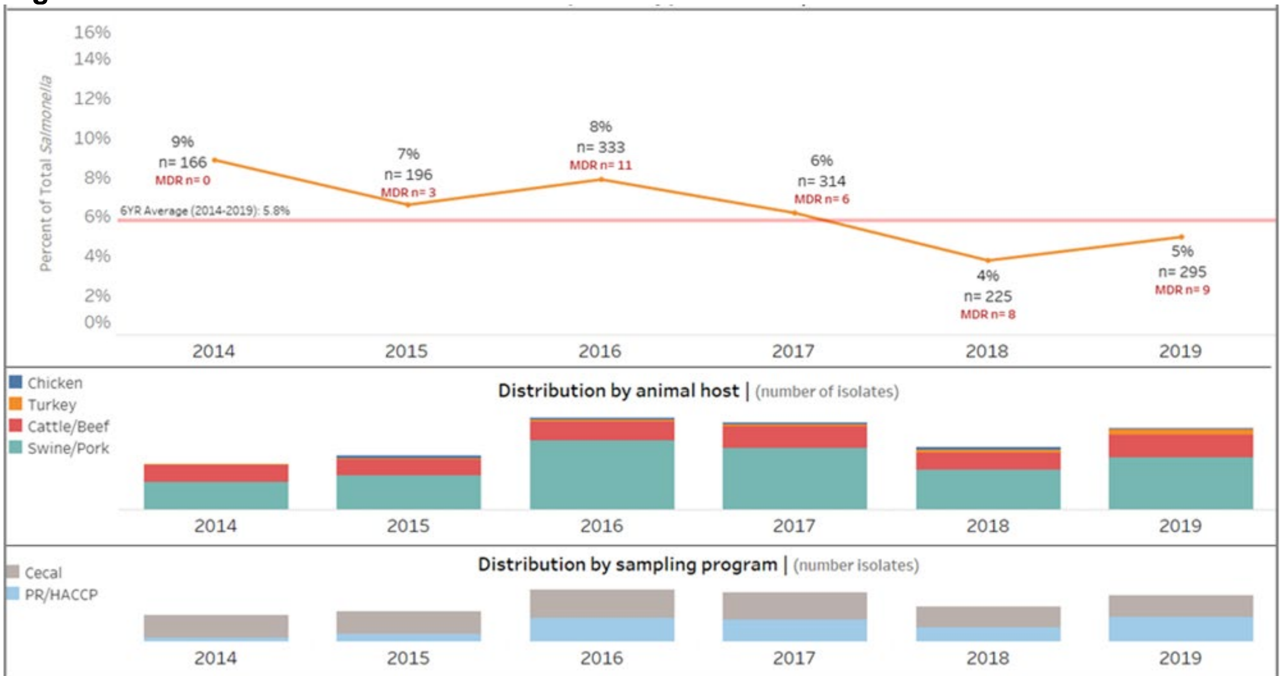
Serotype	Sample Source	2014	2015	2016	2017	2018	2019
Reading	Cecal	14	16	16	17	19	30
	PR/HACCP	12	40	38	46	157	135

Figure C3: Montevideo

Serotype	Animal Host	2014	2015	2016	2017	2018	2019
Montevideo	Chicken	1	17	16	14	31	10
	Turkey	2	3	3	7	7	7
	Cattle/Beef	153	154	142	173	202	178
	Swine/Pork	7	5	14	12	16	10

Serotype	Sample Source	2014	2015	2016	2017	2018	2019
Montevideo	Cecal	60	81	87	121	123	119
	PR/HACCP	103	98	88	85	133	86

Figure C4: Anatum



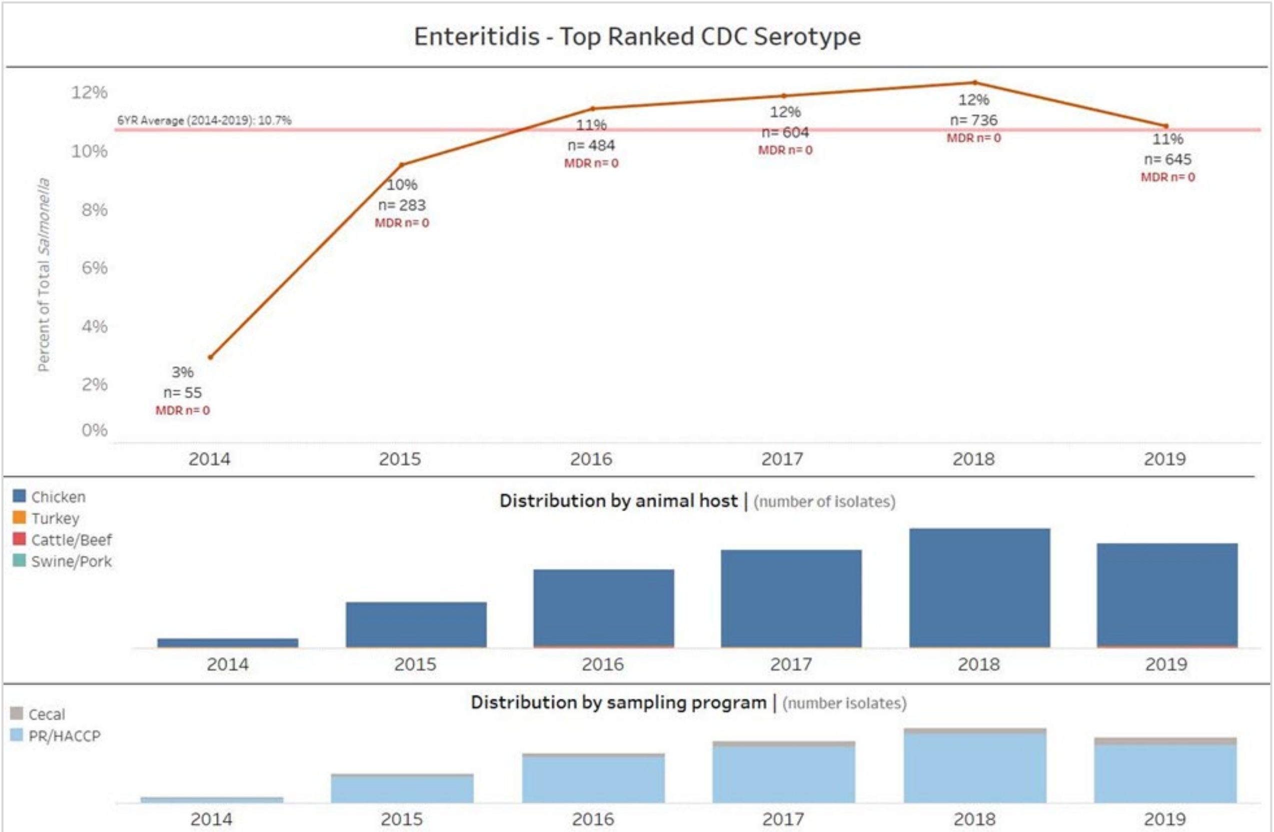
Serotype	Animal Host	2014	2015	2016	2017	2018	2019
Anatum	Chicken		9	7	6	10	5
	Turkey	4	3	8	7	8	20
	Cattle/Beef	64	59	66	77	63	82
	Swine/Pork*	98	125	252	224	144	188

Serotype	Sample Source	2014	2015	2016	2017	2018	2019
Anatum	Cecal	142	145	181	175	133	137
	PR/HACCP*	24	51	152	139	92	158

*Exploratory pork sampling started in May 2015

APPENDIX D – Distribution of the Top Three Ranked 2019 CDC *Salmonella* Serotype and MDR Trends by Major Animal Commodities, Sample Source and Year, 2014 - 2019

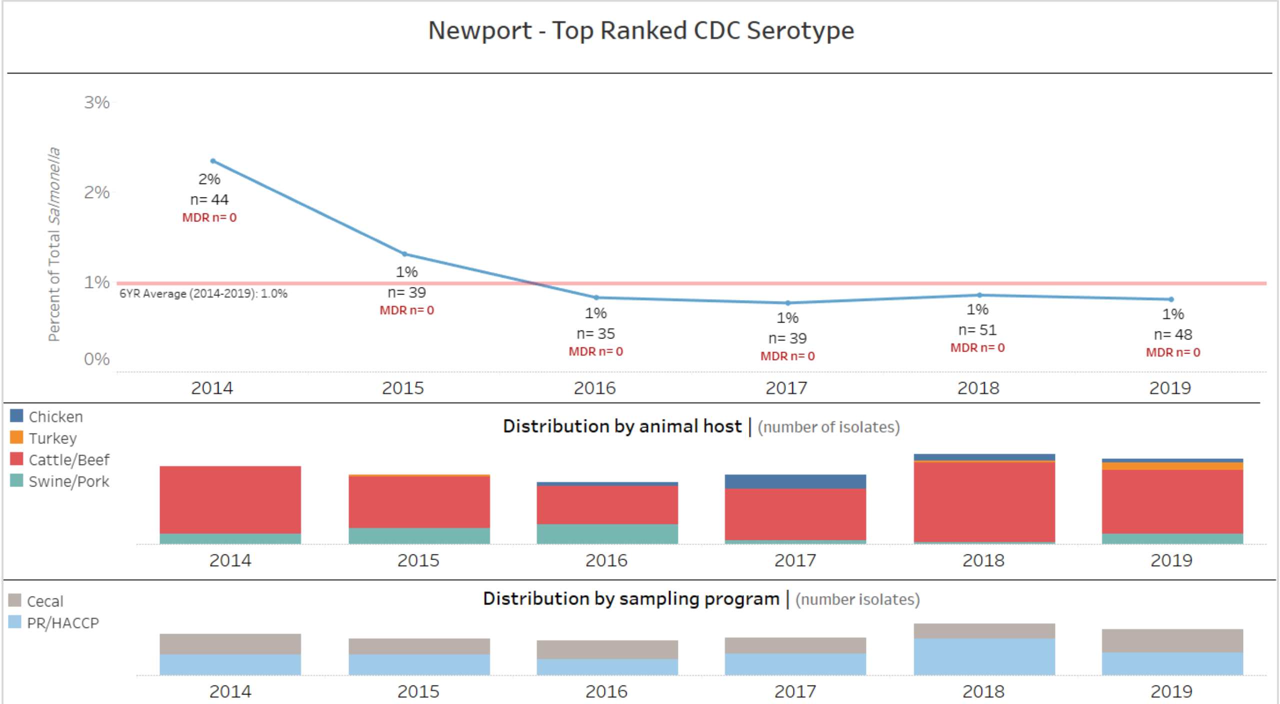
Figure D1: Enteriditis



Serotype	Animal Host	2014	2015	2016	2017	2018	2019
Enteritidis	Chicken	52	278	475	597	730	633
	Turkey	1	1	1	1	1	5
	Cattle/Beef	1	1	4	2	4	2
	Swine/Pork	1	3	4	4	1	5

Serotype	Sample Source	2014	2015	2016	2017	2018	2019
Enteritidis	Cecal	19	21	33	55	52	72
	PR/HACCP	36	262	451	549	684	573

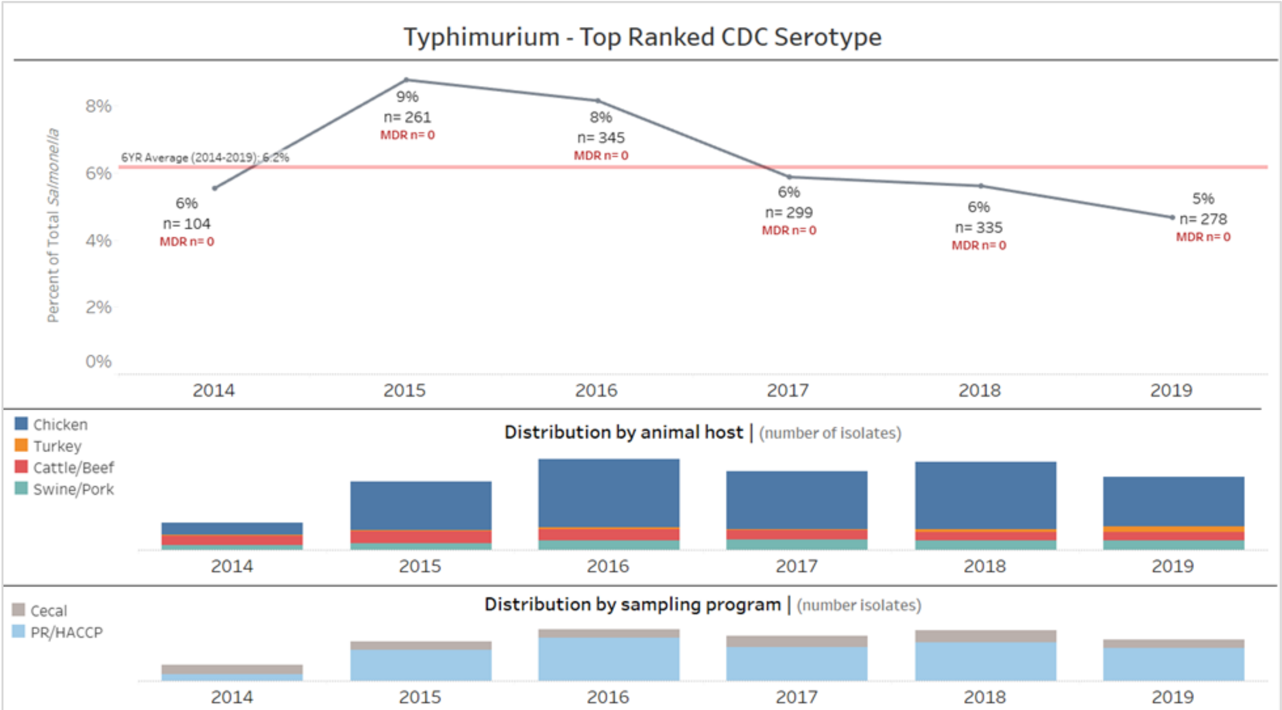
Figure D2: Newport



Serotype	Animal Host	2014	2015	2016	2017	2018	2019
Newport	Chicken			2	8	4	2
	Turkey		1			1	4
	Cattle/Beef	38	29	22	29	45	36
	Swine/Pork	6	9	11	2	1	6

Serotype	Sample Source	2014	2015	2016	2017	2018	2019
Newport	Cecal	22	17	20	17	16	25
	PR/HACCP	22	22	15	22	35	23

Figure D3: Typhimurium



Serotype	Animal Host	2014	2015	2016	2017	2018	2019
Typhimurium	Chicken	48	186	258	221	257	189
	Turkey	3	4	9	4	12	22
	Cattle/Beef	34	46	43	35	29	32
	Swine/Pork	19	25	35	39	37	35

Serotype	Sample Source	2014	2015	2016	2017	2018	2019
Typhimurium	Cecal	62	57	57	75	80	61
	PR/HACCP	42	204	288	224	255	217

APPENDIX E – Critically Important Antimicrobial Drugs

Table E1. *Salmonella* Resistance to Selected Critically Important Antimicrobial Drugs[a,b] by Animal Host, Sample Source and Year (2014 - 2019)

Animal Host	Year	Isolates (n)	Cecal (%)					Isolates (n)	Product (%)				
			Azi	Axo	Cip	Mer	Cot		Azi	Axo	Cip	Mer	Cot
Chicken	2014	101	1.0	8.7	0.0	0.0	1.9	936	0.0	6.6	0.2	0.0	0.4
	2015	130	0.8	10.0	3.8	0.0	7.7	1491	0.3	6.5	0.4	0.0	0.8
	2016	134	0.0	10.4	3.7	0.0	2.2	1859	0.2	7.9	3.7	0.0	3.4
	2017	314	0.0	11.1	17.5	0.0	8.0	2098	0.0	9.3	13.6	0.0	6.1
	2018	399	0.0	15.3	26.3	0.0	10.0	1956	0.0	9.7	19.7	0.0	6.4
	2019	407	0.0	12.5	31.7	0.0	10.3	1929	0.0	12.8	30.2	0.0	7.5
Turkey	2014	44	2.2	11.1	0.0	0.0	6.7	299	0.3	13.4	0.7	0.0	0.7
	2015	25	0.0	8.0	0.0	0.0	0.0	185	0.5	15.7	1.1	0.0	3.2
	2016	49	0.0	16.3	2.0	0.0	2.0	135	0.0	7.4	0.0	0.0	0.0
	2017	42	0.0	11.9	2.4	0.0	0.0	149	0.0	6.7	6.7	0.0	4.7
	2018	66	0.0	3.0	1.5	0.0	3.0	264	0.4	5.3	6.4	0.0	3.4
	2019	64	0.0	3.1	1.6	0.0	3.1	296	0.3	4.4	4.7	0.0	1.7
Cattle/Beef	2014	318	0.3	4.0	0.6	0.0	1.2	344	0.0	7.6	2.9	0.0	1.7
	2015	359	0.0	5.3	0.3	0.0	0.6	291	0.0	15.8	4.8	0.0	2.1
	2016	367	0.0	5.2	0.8	0.0	0.8	286	0.3	10.8	4.9	0.0	2.4
	2017	419	0.2	3.8	0.5	0.0	0.0	235	0.0	8.5	3.4	0.0	1.3
	2018	469	0.6	4.3	1.9	0.0	0.9	298	0.0	9.1	4.0	0.0	0.7
	2019	500	0.4	2.8	1.2	0.0	0.6	215	0.0	12.4	7.8	0.0	2.3
Swine/Pork	2014	606	0.3	2.6	3.6	0.0	1.2	*	*	*	*	*	*
	2015	494	0.0	1.6	1.9	0.0	0.4	200	0.0	0.5	1.5	0.0	1.0
	2016	610	0.3	3.2	2.9	0.0	1.3	598	0.3	3.5	3.2	0.0	2.0
	2017	687	0.5	2.9	3.7	0.0	1.7	647	0.8	3.2	4.5	0.0	2.0
	2018	693	0.3	3.8	5.9	0.0	2.0	541	0.2	4.3	5.7	0.0	1.8
	2019	605	1.0	2.6	5.8	0.0	2.0	528	0.9	3.2	6.4	0.0	2.3
Overall	2014	1069	0.5	4.0	2.2	0.0	1.5	1579	0.1	8.1	0.9	0.0	0.8
	2015	1008	0.1	4.4	1.6	0.0	1.3	2167	0.2	8.0	1.2	0.0	1.2
	2016	1160	0.2	5.1	2.2	0.0	0.9	2878	0.2	7.3	3.5	0.0	2.9
	2017	1462	0.2	5.1	5.4	0.0	2.4	3129	0.2	7.9	10.6	0.0	4.8
	2018	1627	0.4	6.6	9.6	0.0	3.7	3059	0.1	8.3	14.6	0.0	4.8
	2019	1576	0.5	5.1	10.7	0.0	3.7	2968	0.2	10.3	21.8	0.0	5.6

[a] Critically important antimicrobials include azithromycin (Azi), ceftriaxone (Axo),ciprofloxacin (Cip), meropenem (Mer) and trimethoprim-sulfamethoxazole (Cot).
[b] Draft Guidance for Industry (GFI) #152, Food and Drug Administration, 2022.
[*] Data not available.

APPENDIX F – Whole Genome Sequencing

Table F1. Distribution of the genetic determinants bla_{CMY-2} and $bla_{CTX-M-65}$ by animal host, sample source and *Salmonella* serotypes (2014 - 2019)

Animal Host	*bla*CMY-2								*bla*CTX-M-65		
	Typhimurium (n)	Kentucky (n)	Newport (n)	Dublin (n)	Agona (n)	Heidelberg (n)	Others (n)	Total (n)	Infantis (n)	Others (n)	Total (n)
Beef Cattle[C]	8		11	4			6	29			
Cattle[P]	10	1	23	29		3	7	73	3		3
Chickens[C,P]	78	84	1			13	6	182	614	15	629
Dairy Cattle[C]	18		34	1	1		6	60	1		1
Market Swine[C]	1	2	1		16	2	37	59	2		2
Sows[C]	2				6		14	22			
Turkeys[C,P]	2				5	8	22	37	23		23
Grand Total (n, %)	119 25.8%	87 18.8%	70 15.2%	34 7.3%	28 6.1%	26 5.6%	98 21.2%	462 100%	643 97.7%	15 2.3%	658 100%

[C] Cecal sampling, [P] Product sampling

Figure F1: Distribution of DSC *Salmonella* isolates with mutational resistance (gyrA) by animal host, 2014 - 2019

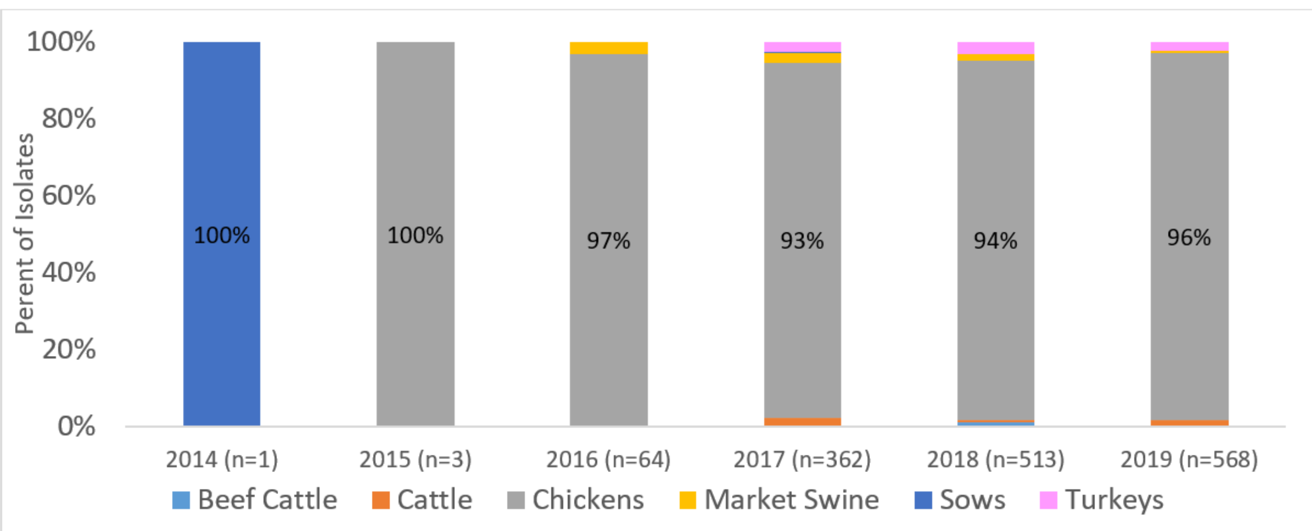


Figure F2: **Distribution of DSC *Salmonella* isolates with acquired resistance by animal host, 2014 - 2019**