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## A Multidrug-Resistant *Salmonella* Infantis Clone Is Spreading and Recombining in the United States

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### Abstract

Recently, there have been reports worldwide of a multidrug-resistant, emergent *Salmonella* Infantis (ESI) clone with a large megaplasmid (pESI), often containing the extended-spectrum beta-lactamase gene *bla*<sub>CTX-M-65</sub>. This clone also has a *gyrA* mutation conferring fluoroquinolone resistance, further limiting treatment options. In the United States, this clone has also been found in poultry sources, indicating a likely source of human illnesses. We conducted short-read sequencing of *Salmonella enterica* isolated from retail meats as part of routine surveillance by the National Antimicrobial Resistance Monitoring System (NARMS). We analyzed the resulting data temporally and geographically to determine when and where the ESI clone has spread in the United States. We found the ESI clone was first found in retail meats in Tennessee in 2014, but by 2019 was throughout the United States and comprised 29% of all *Salmonella* isolated from retail chickens, and 7% from retail turkey. Of these isolates, 85.0% were within 20 single nucleotide polymorphisms (SNPs) of those causing human illnesses. Long-read sequencing data indicated substantial recombination in the pESI plasmid resulting in the presence of 0–10 resistance genes, despite all their chromosomes being within 31 SNPs of one another. This work demonstrates the

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#### Disclosure Statement

No competing financial interests exist.

#### Supplementary Material

Supplementary Table S1

Supplementary Table S2

rapid spread of this clone of *Salmonella* Infantis in poultry in the United States, with the potential for increased burden of human illness attributed to this multidrug-resistant pathogen.

## Keywords

*Salmonella enterica*; antibiotic resistance; plasmids; poultry

## Introduction

*Salmonella enterica* is a major cause of foodborne illness in the United States.<sup>1</sup> Although most infections resolve on their own without need for treatment, severe infections may need antimicrobial therapy, usually with cephalosporins or fluoroquinolones.<sup>2</sup> *S. enterica* serovar Infantis has been among the top 10 serotypes causing human illness in the United States every year since 2010.<sup>3</sup> Poultry is the most common source of *Salmonella* Infantis,<sup>4</sup> although it has also been found in swine and other sources.<sup>5</sup> In the United States, the National Antimicrobial Resistance Monitoring System (NARMS) conducts routine surveillance for antimicrobial resistance in *Salmonella* and other foodborne pathogens, including in retail meats. Historically, we have found ~2–4% of retail meat *Salmonella* are of serovar Infantis, with most being pansusceptible to antimicrobials on the NARMS panel.<sup>6</sup>

In 2014, there was the first report of a multidrug-resistant, emergent *Salmonella* Infantis (ESI) in Israel, with subsequent findings in Italy, Japan, and Russia, among others.<sup>7–10</sup> Subsequent reports and retrospective sequencing tracked the origins of this clone to South America.<sup>11,12</sup> This clone carried a large plasmid ESI (pESI) that carried several antimicrobial resistance, metal, and virulence genes. This plasmid could transfer to other *Salmonella* and *Escherichia coli* and conferred increased adhesion and virulence in cell and mammalian models, likely owing to the presence of fimbrial genes.<sup>7</sup> In 2017, we identified this clone of *Salmonella* Infantis in a retail chicken isolate in the United States as part of NARMS sampling.<sup>13</sup> Additional surveillance identified this clone in poultry animals, and in several human cases of illness in the United States. Characterization of the pESI megaplasmid found it was ~300 kb and contained a variety of resistance genes.<sup>13</sup> The most prominent of these was *bla*<sub>CTX-M-65</sub>, an extended-spectrum beta-lactamase (ESBL) gene, which confers resistance to third-generation cephalosporins.<sup>13</sup> This was the first reported instance of *bla*<sub>CTX-M-65</sub> in *Salmonella* from retail meats in the United States. Additional resistance genes were found in some isolates, including those conferring resistance to tetracycline, aminoglycosides, sulfonamides, phenicols, and fosfomycin, and all resistance genes were found on elements flanked by transposases or integrases.<sup>13</sup> This clone also had a GyrA (D87Y) amino acid change conferring resistance to fluoroquinolones, a drug class not used in U.S. poultry production since 2005.<sup>14</sup>

An additional epidemiological study further characterized the rise of this *Salmonella* Infantis clone in the United States, where it accounted for nearly 10% of all *Salmonella* Infantis human cases by 2017.<sup>15</sup> Initially most human illnesses were associated with international travel to South America, but domestically acquired cases began in 2014. These human isolates were highly related to those from chicken sources.<sup>15</sup>

Owing to the resistant nature of this pathogen and its contribution to human infections, we sought to determine whether this clone has spread further in the food supply. We used long-read DNA sequencing to understand the genetics underlying the evolution of the megaplasmid as a reference point for tracking its spread, as we attempt to further understand this important pathogenic clone.

## Methods

### Bacterial isolates and sequencing

As part of routine NARMS surveillance 3,934 *Salmonella* isolates were collected from retail meat sampling in 21 states from 2014 to 2019. A total of 453 of these were of the *Salmonella* Infantis ESI clone. Each of these isolates was sequenced by short-read sequencing on the Illumina MiSeq as previously described.<sup>16</sup> In brief, genomic DNA was extracted with QIAmp 96 DNA QIAcube HT kits (Qiagen, Germantown, MD) on the automated QIAcube HT machine per the manufacturer's instructions. Libraries were prepared with Nextera XT kits and sequenced with v3 reagent kits 2 × 300 bp on the Illumina MiSeq (Illumina, San Diego, CA). Illumina sequences were submitted to the sequence read archive (SRA) in National Center for Biotechnology Information (NCBI), where they were assembled by SKESA.<sup>17</sup> SRA accessions are listed in Supplementary Table S1, with all sequences in BioProject PRJNA292661.

### Data mining

The NCBI Isolates Browser ([www.ncbi.nlm.nih.gov/pathogens/isolates](http://www.ncbi.nlm.nih.gov/pathogens/isolates)) was analyzed for the ESI clone as of January 10, 2020. The isolates browser automatically assigns each sequence within 50 single nucleotide polymorphisms (SNPs) of one another into a single SNP cluster, generating phylogenetic trees based on the maximum compatibility method.<sup>18</sup> This clone was identified by searching for the NCBI SNP cluster PDS000003955.782, which included 4,699 isolates. Isolates specific to NARMS retail meat sampling were identified from BioProject PRJNA292661.

### Geographic analysis

We used the Geographic Information System (GIS) program ArcGIS 10.7 (Environmental Systems Research Institute, Redlands, CA) to input state-level metadata information and overlay geographic and temporal metadata onto a map of the United States. These included all 453 NARMS retail meat isolates with state and year information.

### Long-read sequencing

Thirty-one isolates were selected for long-read sequencing, to represent isolates with diverse combinations of resistance genes. This sequencing was conducted as previously described using the 10-kb template preparation protocol using the Pacific Biosciences Sequel sequencer with Sequel sequencing kit v 3.0 (Pacific Biosciences, Menlo Park, CA).<sup>19</sup> The long reads were assembled to contigs by HGAP4 or Microbial Assembly and contigs were circularized by Circlator.<sup>20,21</sup> PacBio genome assemblies were submitted to GenBank with nucleotide accession numbers and BioSample numbers as listed in Supplementary

Table S2. All sequences are under the same BioSamples as those associated with the short-read sequences and are in BioProject PRJNA292661.

### Sequencing analysis

Resistance genes were identified in the Isolates Browser by using AMRFinder under default settings.<sup>22</sup> The relatedness of retail meat ESI clones to human ESI clones was identified with the NCBI SNP tree, using information from the Min-diff column in the NCBI Isolates Browser.

SNP analysis from long-read sequencing data was conducted with kSNP version 3.1, and kmer size chosen by kChooser.<sup>23</sup> A maximum likelihood tree was constructed by MEGA7.0 with support values estimated through 500 bootstraps.<sup>24</sup> Plasmids were removed before conducting phylogenetic analysis. This tree included 31 ESI clones and three non-ESI *Infantis* as an outgroup.

## Results

### Prevalence of ESI clone

To have an all-encompassing definition of the ESI clone that was not limited by pulsed-field gel electrophoresis (PFGE) patterns or the presence of specific resistance genes such as *bla*<sub>CTX-M-65</sub>, we relied on phylogenetic analysis. We used the Isolates Browser housed at the NCBI website, which partitions sequences into distinct clusters within 50 SNPs. We analyzed the presence of isolates in the SNP cluster PDS000003955.782 in the Isolates Browser (<https://www.ncbi.nlm.nih.gov/pathogens/isolates/#PDS000003955.782>), containing 4,669 isolates at the time of analysis. We defined this cluster as isolates of the ESI clone, regardless of the presence of individual resistance genes.

In this SNP cluster, we found isolates in retail meats and humans as far back as 2009, with all from before 2012 isolated in Peru. There were no isolates from any NARMS sampling of U.S. retail meat before 2014, but by 2019, 29.2% of retail chicken *Salmonella* were of the ESI clone, and 6.7% of retail turkey isolates (Fig. 1). From 2014 to 2019, there were also two isolates from ground beef, among 67 total isolates from this source during this time. Further geographic analysis points to the rapid spread of the ESI clone. It was first identified in Tennessee and subsequently emerged in the northeastern United States before being found in all NARMS sampling states (Fig. 2). The largest number of retail meat isolates were in Maryland and Tennessee, although it is worth noting that NARMS does not sample in all 50 states.

### Resistance gene analysis and relatedness to human isolates

Among the 453 total isolates of the ESI clone collected from NARMS retail meat surveillance, there were 57 different combinations of resistance genes (Supplementary Table S1). Although most isolates had three to seven resistance genes (293/453, 64.7%), 32.9% had eight or more resistance genes, including 7.7% of isolates having 10 resistance genes (Fig. 3A). Five isolates had no resistance genes. The most common resistance genotype, in 19.2% of isolates (87/453), was with *aadA1*, *sull1*, and *te(A)*, which confer resistance to

streptomycin, sulfisoxazole, and tetracycline, respectively. The most common pattern with *bla*<sub>CTX-M-65</sub> was in 9.9% of isolates (45/453) and included *aac(3)-IV*, *aadA1*, *aph(4)-Ia*, *bla*<sub>CTX-M-65</sub>, *floR*, *sul1*, and *tet(A)*, conferring resistance to various aminoglycosides, beta-lactams, chloramphenicol, sulfisoxazole, and tetracycline.

Although the combinations of resistance genes varied widely among the isolates, they always comprised different combinations of a set of 10 resistance genes (Fig. 3B). These resistance genes are across several different drug classes, including tetracyclines (*tet(A)*), folate synthesis inhibitors (*sul1*, *dfrA14*), aminoglycosides (*aadA1*, *aac(3)-IV*, *aph(4)-Ia*, *aph(3')-Ia*), beta-lactams (*bla*<sub>CTX-M-65</sub>), and phenicols (*floR*), and fosfomycin (*fosA3*). Each gene was in at least 20% of ESI clones. Based on GIS analysis, there was no clear geographic or temporal trend for the presence of specific resistance genes.

In the large ESI SNP cluster, there were 1,241 isolates from human illnesses collected as part of PulseNet surveillance, in BioProject PRJNA230403. Analysis from the NCBI Isolates Browser showed that 85.0% (385/453) of the retail meat isolates were within 20 SNPs of human cases, the threshold typically used for outbreak investigations.<sup>25</sup> Furthermore, 62 of our retail meat isolates were within 5 SNPs of human isolates, with 45 having *bla*<sub>CTX-M-65</sub> (72.6%). Only 49.7% of all the retail meat ESI clones had this gene.

### Long-read sequencing

To characterize differences in plasmid content and resistance genes, we sequenced 31 isolates using PacBio long-read sequencing technologies. The 31 isolates were closely related and formed a separate clade from three *Infantis* from other NCBI SNP clusters, as expected (Fig. 4). This figure also depicts the complement of resistance genes in each isolate, illustrating the high level of recombination occurring within the pESI plasmid. All ESI clones were within 31 SNPs of each other, indicating a high degree of relatedness. Nevertheless, isolates in the same subclusters often had different combinations of resistance genes on their plasmids. This was particularly evident with closely related isolates such as N17S1234 and N17S1598, which were adjacent on the phylogenetic tree. Although some resistance genes were the same in both plasmids, N17S1234 had *dfrA14* and *aph(3')-Ia*, whereas N17S1598 had *aadA1*, *sul1*, and *tet(A)*. Of interest, the isolate N19S0949 did not have any resistance genes, but still possessed the pESI plasmid, simply missing the regions containing resistance genes (Table 1). Isolate-level accession numbers and plasmid length and source information are given in Table 1.

In one isolate, N18S2039, the pESI plasmid was only 168 kb long, and had no resistance genes. The rest of the plasmid was integrated into the chromosome, including the region containing the *bla*<sub>CTX-M-65</sub> and *tet(A)* genes. An 80-kb portion of this integrated plasmid aligned with >99% identity to the IncII plasmid pC193 from an *E. coli* in Bolivia.<sup>26</sup> Because the pESI plasmid is thought to have come from South America, this *E. coli* plasmid may have been an original component that helped form the megaplasmid. The N18S2039 isolate was the only one with long-read sequencing data that had any chromosomal resistance genes.

## Discussion

The emergence of the ESI clone of *Salmonella* Infantis is concerning, as its sudden rise in retail meats and contributions to human illnesses is combined with a propensity for multidrug-resistance. This is particularly a problem when a greater proportion of ESI clones closely related to those causing human infections have the ESBL gene *bla*<sub>CTX-M-65</sub> than the overall proportion. Combined with fluoroquinolone resistance resulting from a *gyrA* mutation in the ESI clone, this can make infections caused by this clone difficult to treat, because fluoroquinolones and cephalosporins are the most commonly used drugs to treat severe salmonellosis.<sup>2</sup>

In this work, we used SNP clusters from NCBI's Isolates Browser to identify the ESI clone, which has dramatically risen in prevalence in retail meats as it has spread across the United States. We believe the use of SNP trees, such as those produced in NCBI's Isolates Browser, are an ideal method for identifying these emerging bacterial clones. This provides a more inclusive and forward-looking definition than methods such as PFGE clusters, which have previously excluded related isolates of the ESI clone.<sup>13</sup> AMRFinder results from this approach also agreed with prior work finding two sites within the pESI plasmid with resistance genes, with *bla*<sub>CTX-M-65</sub>, *fosA3*, *floR*, *aph(4)-Ia*, *aac(3)-VI*, *dfrA14*, and *aph(3)-Ia* at one site and *sulI*, *tet(A)*, and *aadA1* at the other site.<sup>13</sup>

We believe long-read sequencing is an essential component of understanding the emergence and epidemiology of this clone, as it helped us determine the complement of resistance genes and their variability among highly related isolates. Long-read sequencing also identified an IncX4 plasmid with the *bla*<sub>TEM-1</sub> gene in one isolate. This indicates the pESI plasmid was not restrictive in preventing acquisition or maintenance of additional plasmids, at least of this incompatibility type.

The unusual genotype and early epidemiological linkages highlight that the ESI clone originated outside the United States, likely in South America.<sup>15</sup> After having arrived, the ESI clone has risen quickly and continuously, but why it has successfully spread in food animals and retail meats in the United States remains unknown. Since fluoroquinolone use was banned in poultry in 2005 and cephalosporin use has been restricted since 2012,<sup>14</sup> the use of other antimicrobials may help select for the range of plasmid structures seen in the different isolates, including those with *bla*<sub>CTX-M-65</sub>. In fact, >90% of isolates had the *tet(A)* gene, conferring tetracycline resistance, and tetracyclines are the antimicrobial with highest annual sales in food animals in the United States.<sup>27</sup> Thus, use of antimicrobials such as tetracycline has the potential to co-select for the continued presence of the pESI plasmid.

Another factor potentially contributing to the success of the ESI clone and its pESI plasmid are its association with virulence. Prior reports demonstrated that the pESI plasmid confers increased adhesion and invasion in cell culture models and increased virulence in a mouse model of infection.<sup>7</sup> This adhesion and increased virulence are proposed to be mediated by two chapterone-usher fimbria gene clusters encoded by *fea* and *ipf* genes found on the pESI plasmid.<sup>7</sup> Given that ESI clones without resistance genes are successfully spreading, it is likely that these other factors are also contributing to its increased dissemination. Why it has



successfully spread in poultry sources, and not others such as cattle, where this clone has also been found,<sup>13</sup> remains unknown.

Typing of the pESI plasmid is still difficult, given that it is a megaplasmid that appears to have arisen from multiple recombination events. PlasmidFinder classifies this as an IncFIB-type plasmid, as has been previously described.<sup>13,28</sup> However, as a megaplasmid, it appears to have resulted from integration of an IncFIB and IncI1 plasmid. For isolate N18S2039, the IncI1 portion containing *bla*<sub>CTX-M-65</sub> integrated into the chromosome, resulting in a much smaller IncFIB plasmid. A potential contribution from an IncP plasmid has also been postulated.<sup>7</sup> Together, these findings indicate the difficulties in applying conventional plasmid typing methods to megaplasms.

Despite the significance of our findings, there are some limitations to this study. For instance, not all states perform NARMS retail meat sampling, so our information on the prevalence and geographic distribution of the ESI clone is limited to ~20 states. In addition, for SNP cluster information we rely upon NCBI's Isolates Browser, which includes sequences that are heavily biased toward those from the United States and United Kingdom, which have the most public data. Despite these limitations, robust NARMS sequencing efforts have included all retail meat *Salmonella* since sampling began in 2002. Although there may have been ESI clones in retail meats before 2014, when it was first detected, this probably would have been rare based on our sampling of thousands of retail meats for *Salmonella* each year.

In summary, the ESI clone has continued to increase among retail poultry in the United States, now accounting for almost one-third of all *Salmonella* isolates from retail chicken. Given the association of this clone and the pESI plasmid with multidrug-resistance and increased virulence, it is likely to have an increased burden on human health. There is the potential for similar spread in the European Union, where *Salmonella* Infantis is the number one *Salmonella* serotype from food animals, and number three from humans.<sup>29</sup> The ESI clone, including the pESI plasmid and associated resistance and virulence genes, have been found in Europe and Asia,<sup>9,10</sup> and accounted for a majority of pediatric *Salmonella* cases in a study in Peru.<sup>30</sup>

Furthermore, the potential spread of the pESI plasmid is of concern, as it has been successfully transferred to other enteric organisms, including other types of *Salmonella*.<sup>31</sup> Thus, the ESI clone and its associated pESI plasmid pose a continued public health problem deserving of further attention and study.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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### Funding Information

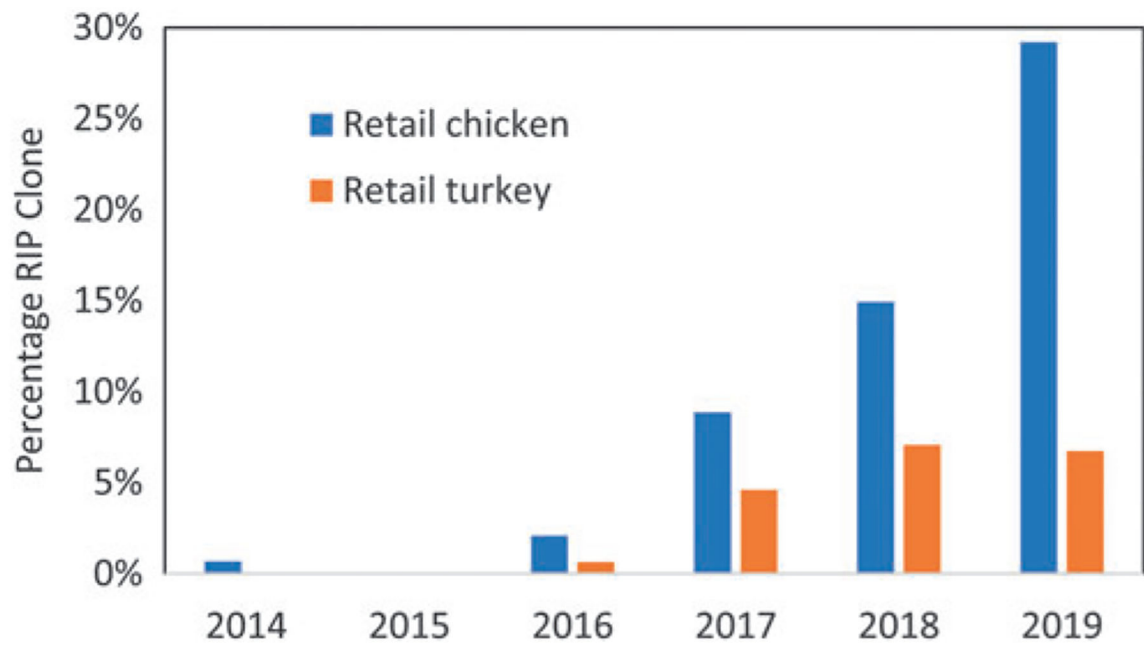
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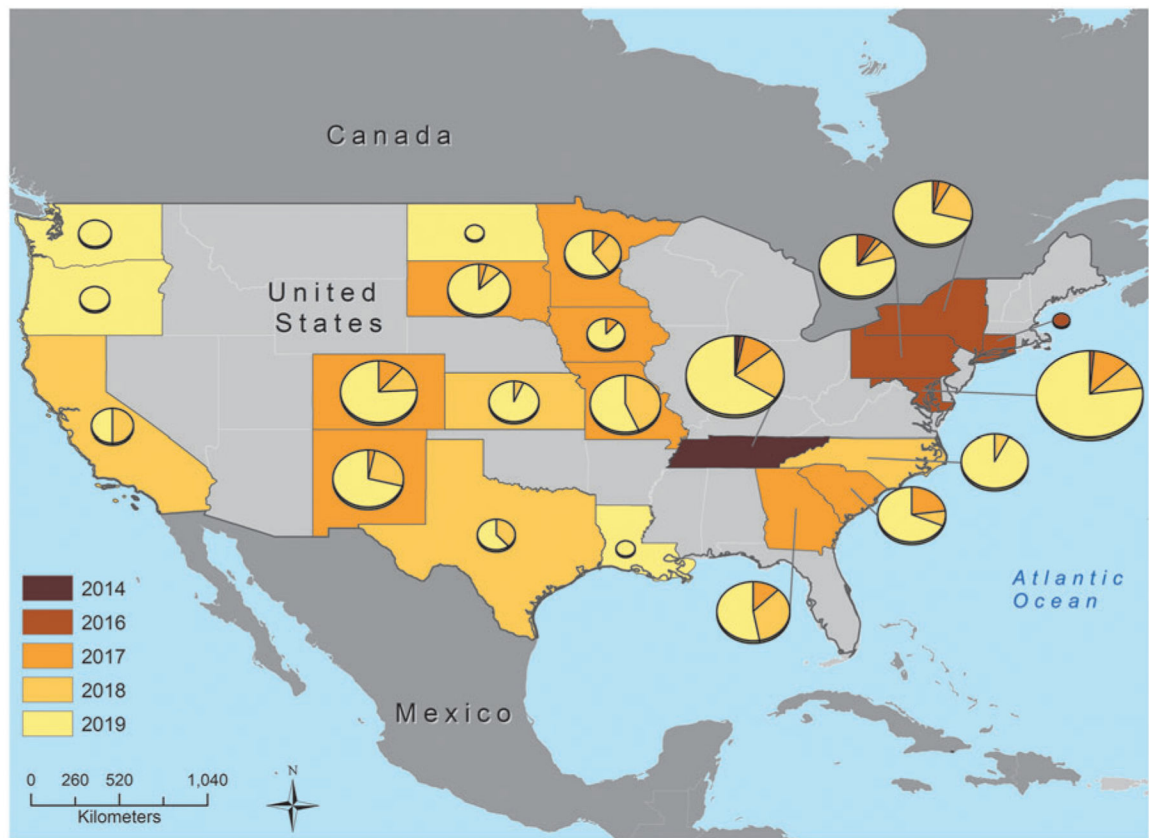
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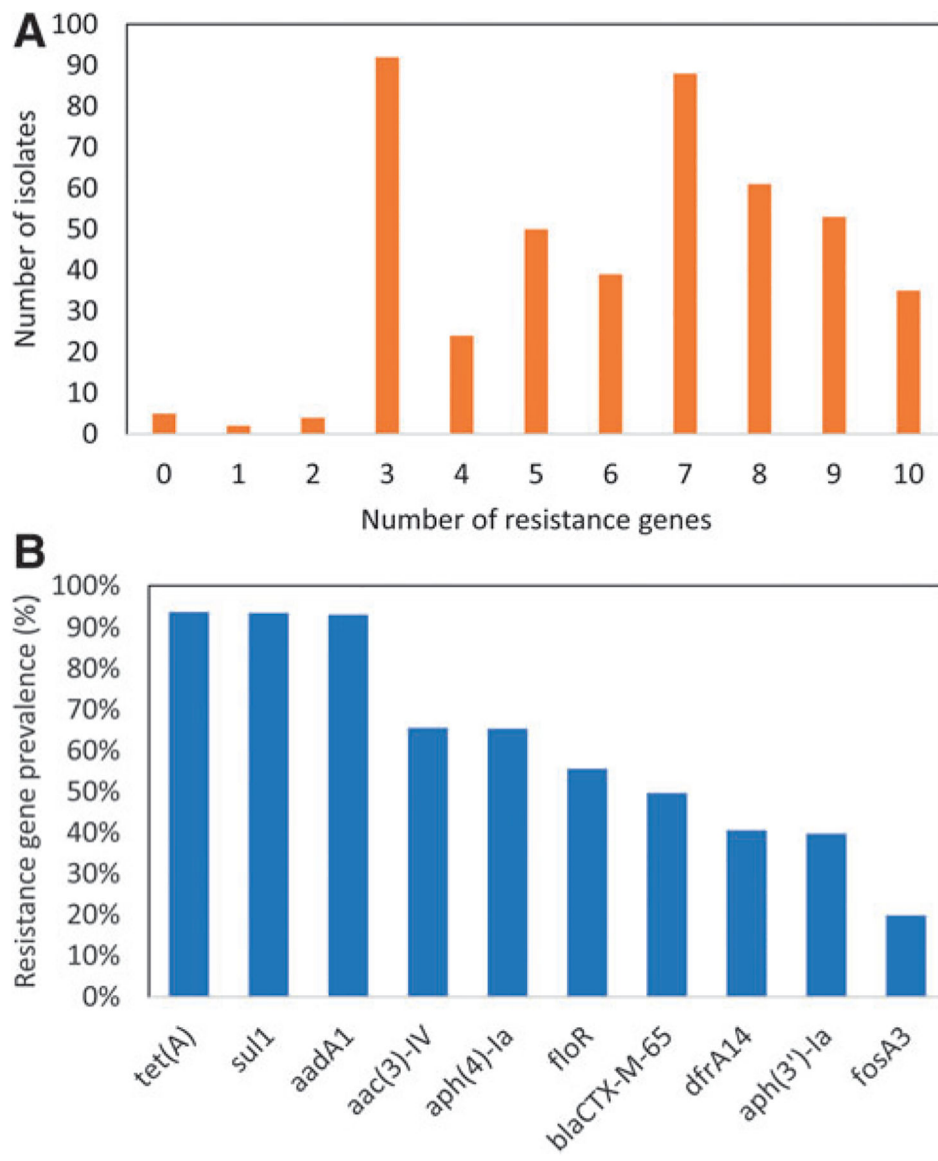


**FIG. 1.** Prevalence of ESI clone from 2014 to 2019 from NARMS sampling among retail meat sources. ESI, emergent *Salmonella* Infantis; NARMS, National Antimicrobial Resistance Monitoring System.

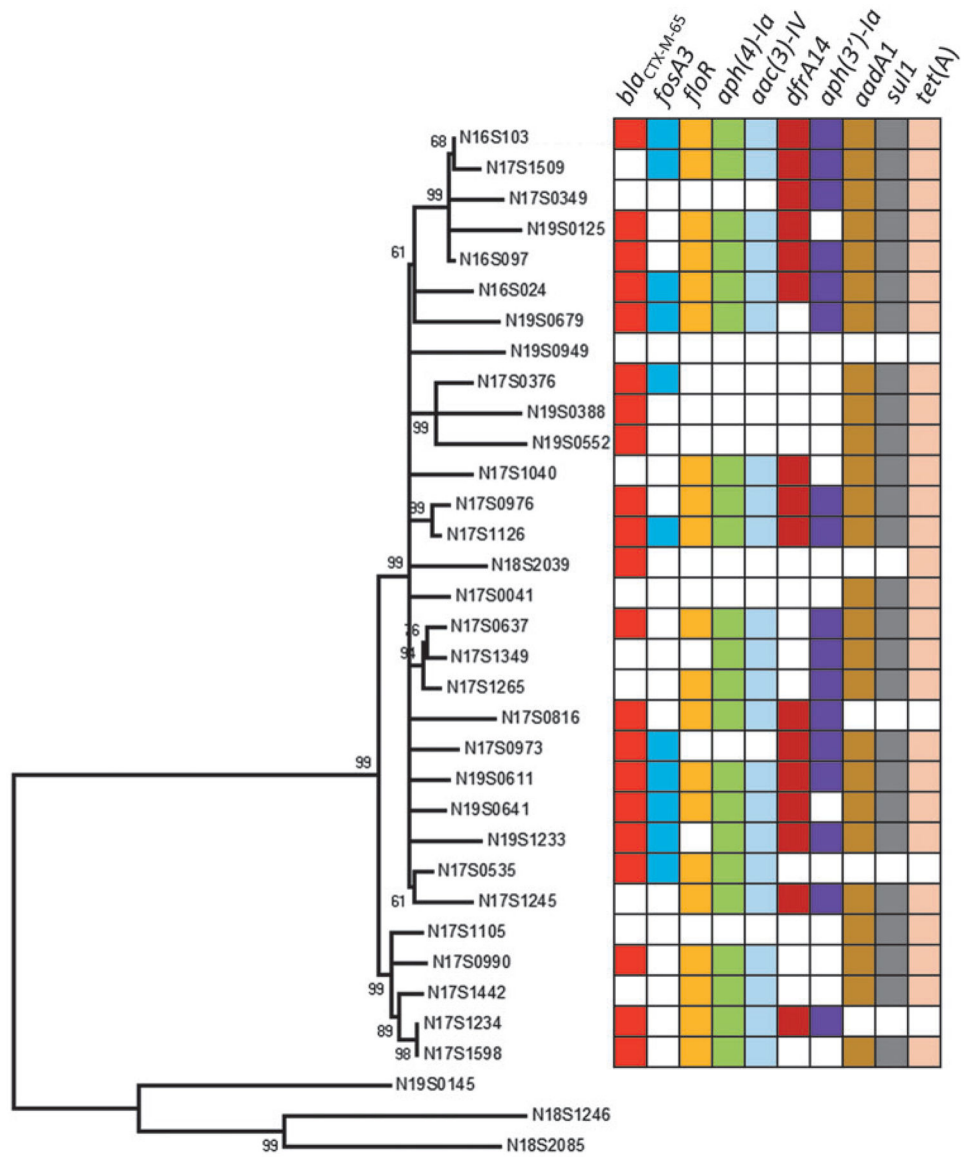


**FIG. 2.**

Geographic representation of ESI clone emergence. States are colored by the year the clone was first identified in retail meats, with pie charts representing the proportion of isolates from each year. The size of the pie chart is proportional to the number of isolates from each state. Note: not all states were part of surveillance for all years of this study, and states colored *gray* are not part of NARMS surveillance.



**FIG. 3.** (A) Number of resistance genes among ESI clones, and (B) prevalence of each resistance gene among them.



**FIG. 4.** Phylogenetic tree of 31 ESI clones with closed genomes, including resistance gene information. Numbers in the figure are bootstrap values. The *bottom* three sequences are non-ESI clone *Infantis* included as an outgroup.

Plasmid Resistance Genes and Accession Numbers from Long-Read Sequencing of 31 Isolates

Table 1.

NARMS ID	GenBank accession	Plasmid length	Source	Year	State	Plasmid genotype
N16S024	CP052840	322,506	Chicken	2016	CT	<i>aac(3)-IV aadA1 aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR fosA3 sul1 tet(A)</i>
N16S097	CP052838	318,524	Chicken	2016	PA	<i>aac(3)-IV aadA1 aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR sul1 tet(A)</i>
N16S103	CP052836	322,451	Chicken	2016	PA	<i>aac(3)-IV aadA1 aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR fosA3 sul1 tet(A)</i>
N17S041	CP052834	288,008	Turkey	2017	GA	<i>aadA1 sul1 tet(A)</i>
N17S1040	CP052832	306,079	Chicken	2017	NY	<i>aac(3)-IVa aadA1 aph(4)-Ia dftrA14 floR sul1 tet(A)</i>
N17S1105	CP052830	289,847	Chicken	2017	SC	<i>aadA1 sul1 tet(A)</i>
N17S1126	CP052828	322,509	Turkey	2017	TN	<i>aac(3)-IVa aadA1 aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR fosA3 sul1 tet(A)</i>
N17S1234	CP051676	297,707	Chicken	2017	CO	<i>aac(3)-IVa aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR</i>
N17S1245	CP052826	299,741	Chicken	2017	CO	<i>aac(3)-IVa aadA1 aph(3')-Ia aph(4)-Ia dftrA14 floR sul1 tet(A)</i>
N17S1265	CP052824	290,274	Chicken	2017	CO	<i>aac(3)-IVa aadA1 aph(3')-Ia aph(4)-Ia floR sul1 tet(A)</i>
N17S1349	CP052822	298,238	Chicken	2017	MD	<i>aac(3)-IVa aadA1 aph(3')-Ia aph(4)-Ia sul1 tet(A)</i>
N17S1442	CP052820	292,474	Chicken	2017	SC	<i>aac(3)-IVa aadA1 aph(4)-Ia floR sul1 tet(A)</i>
N17S1509	CP052818	306,853	Chicken	2017	GA	<i>aac(3)-IVa aadA1 aph(3')-Ia aph(4)-Ia dftrA14 floR fosA3 sul1 tet(A)</i>
N17S1598	CP052816	303,467	Chicken	2017	TN	<i>aac(3)-IVa aadA1 aph(4)-Ia bla<sub>CTX-M-65</sub>floR sul1 tet(A)</i>
N17S349	CP052814	300,799	Turkey	2017	SC	<i>aadA1 aph(3')-Ia dftrA14 sul1 tet(A)</i>
N17S376	CP052812	293,162	Chicken	2017	SD	<i>aadA1 bla<sub>CTX-M-65</sub>fosA3 sul1 tet(A)</i>
N17S535	CP052810	283,099	Chicken	2017	IA	<i>aac(3)-IVa aph(4)-Ia bla<sub>CTX-M-65</sub>floR fosA3</i>
N17S637	CP052808	312,913	Chicken	2017	MIN	<i>aac(3)-IVa aadA1 aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>floR sul1 tet(A)</i>
N17S816	CP052806	296,746	Chicken	2017	PA	<i>aac(3)-IVa aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR</i>
N17S973	CP052804	309,326	Chicken	2017	MD	<i>aadA1 aph(3')-Ia bla<sub>CTX-M-65</sub>dftrA14 fosA3 sul1 tet(A)</i>
N17S976	CP052802	319,023	Turkey	2017	MD	<i>aac(3)-IVa aadA1 aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR sul1 tet(A)</i>
N17S990	CP052799	310,270	Turkey	2017	MIN	<i>aac(3)-IVa aadA1 aph(4)-Ia bla<sub>CTX-M-65</sub>floR sul1 tet(A)</i>
N18S2039	CP052797	168,393	Turkey	2018	CA	None ( <i>bla<sub>CTX-M-65</sub>tet(A)</i> on chromosome)
N19S0125	CP052795	317,309	Chicken	2019	MD	<i>aac(3)-IV aadA1 aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR sul1 tet(A)</i>
N19S0388	CP052793	290,416	Chicken	2019	SD	<i>aadA1 bla<sub>CTX-M-65</sub>sul1 tet(A)</i>
N19S0552	CP052791	289,609	Turkey	2019	TX	<i>aadA1 bla<sub>CTX-M-65</sub>sul1 tet(A)</i>
N19S0611	CP052788	322,462	Turkey	2019	NC	<i>aac(3)-IV aadA1 aph(3')-Ia aph(4)-Ia bla<sub>CTX-M-65</sub>dftrA14 floR fosA3 sul1 tet(A)</i>



NARMS ID	GenBank accession	Plasmid length	Source	Year	State	Plasmid genotype
N19S0641	<a href="#">CP052786</a>	321,524	Chicken	2019	PA	<i>aac(3)-IV aadA1 aph(4)-Ia bla<sub>CTX-M-65</sub> dfrA14 floR fosA3 sul1 tet(A)</i>
N19S0679	<a href="#">CP052783</a>	312,779	Chicken	2019	NY	<i>aac(3)-IV aadA1 aph(3)-Ia aph(4)-Ia bla<sub>CTX-M-65</sub> floR fosA3 sul1 tet(A)</i>
N19S0949	<a href="#">CP052781</a>	265,507	Chicken	2019	TX	None
N19S1233	<a href="#">CP052779</a>	314,663	Turkey	2019	TN	<i>aac(3)-IV aadA1 aph(3)-Ia aph(4)-Ia bla<sub>CTX-M-65</sub> dfrA14 fosA3 sul1 tet(A)</i>

NARMS, National Antimicrobial Resistance Monitoring System.