A Comparison of Non-Typhoidal *Salmonella* from Humans and Food Animals Using Pulsed-Field Gel Electrophoresis and Antimicrobial Susceptibility Patterns

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Abstract

Salmonellosis is one of the most important foodborne diseases affecting humans. To characterize the relationship between *Salmonella* causing human infections and their food animal reservoirs, we compared pulsed-field gel electrophoresis (PFGE) and antimicrobial susceptibility patterns of non-typhoidal *Salmonella* isolated from ill humans in Pennsylvania and from food animals before retail. Human clinical isolates were received from 2005 through 2011 during routine public health operations in Pennsylvania. Isolates from cattle, chickens, swine and turkeys were recovered during the same period from federally inspected slaughter and processing facilities in the northeastern United States. We found that subtyping *Salmonella* isolates by PFGE revealed differences in antimicrobial susceptibility patterns and, for human *Salmonella*, differences in sources and invasiveness that were not evident from serotyping alone. Sixteen of the 20 most common human *Salmonella* PFGE patterns were identified in *Salmonella* recovered from food animals. The most common human *Salmonella* PFGE pattern, Enteritidis pattern JEGX01.0004 (JEGX01.0003ARS), was associated with more cases of invasive salmonellosis than all other patterns. In food animals, this pattern was almost exclusively (99%) found in *Salmonella* recovered from chickens and was present in poultry meat in every year of the study. Enteritidis pattern JEGX01.0004 (JEGX01.0003ARS) was associated with susceptibility to all antimicrobial agents tested in 94.7% of human and 97.2% of food animal *Salmonella* isolates. In contrast, multidrug resistance (resistance to three or more classes of antimicrobial agents) was observed in five PFGE patterns. Typhimurium patterns JPXX01.0003 (JPXX01.0003 ARS) and JPXX01.0018 (JPXX01.0002 ARS), considered together, were associated with resistance to five or more classes of antimicrobial agents: ampicillin, chloramphenicol, streptomycin, sulfonamides and tetracycline (ACSSuT), in 92% of human and 80% of food animal *Salmonella* isolates. The information from our study can assist in source attribution, outbreak investigations, and tailoring of interventions to maximize their impact on prevention.

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Introduction

In the United States, non-typhoidal *Salmonella enterica* subs. *enterica* cause an estimated one million episodes of salmonellosis each year [1] and are the leading cause of hospitalization and death from foodborne illness. The resulting annual economic burden, based on the costs of medical treatment, lost productivity and premature death, is estimated to be in the range of $3.3-4.4 billion [2,3].

PulseNet is the national molecular surveillance network for foodborne infections and includes in its network the laboratories of state, territorial, and local public health departments, federal food regulatory agencies, veterinary agencies, and agricultural agencies. PulseNet was established by the Centers for Disease Control and Prevention (CDC) and the Association of Public Health Laborato-

ories in 1996 to reduce the time needed to detect, investigate, and control multistate outbreaks caused by foodborne bacterial pathogens. PulseNet laboratories subtype these pathogens using pulsed-field gel electrophoresis (PFGE) and upload the PFGE patterns to a centralized database at CDC [4,5].

The National Antimicrobial Resistance Monitoring System (NARMS) is a national public health surveillance system that tracks antimicrobial resistance in foodborne bacteria. The NARMS program was established in 1996 as a partnership between the U.S. Food and Drug Administration (FDA), CDC, and the U.S. Department of Agriculture (USDA) and is described on the FDA website [6]. The animal arm of NARMS resides in the USDA-Agricultural Research Service (ARS) laboratory in Athens, GA. In addition to monitoring antimicrobial susceptibility, NARMS partners collaborate on epidemiologic and microbiologic...
research studies. NARMS also examines foodborne bacteria for genetic relatedness using PFGE, and PFGE patterns are entered into USDA’s VetNet database [7]. The food animal arm of NARMS is described on the USDA web site [8]. PulseNet and VetNet work synergistically to provide information that is important for public health. The PFGE protocols are highly standardized protocols developed by PulseNet to facilitate inter-laboratory comparisons [9].

As part of communicable disease control reporting requirements in Pennsylvania, clinical laboratories routinely submit Salmonella isolates to the Pennsylvania Department of Health Bureau of Laboratories (BOL). At BOL, Salmonella isolates are biochemically identified, serotyped and subtyped by PFGE. USDA’s Food Safety and Inspection Service (FSIS) samples food animals for Salmonella during slaughter and processing. Salmonella isolates from food animals are tested for susceptibility to antimicrobial agents and then subtyped via PFGE by the USDA-ARS Laboratory in Athens, Georgia.

Our objective was to compare clinical isolates of non-typhoidal Salmonella recovered from humans (human Salmonella) received as part of routine surveillance at the BOL in Pennsylvania from 2005 through 2011 with Salmonella isolates recovered during the same period from food animals (food animal Salmonella) at slaughter and processing facilities in the northeastern United States. The most common PFGE patterns observed in human Salmonella served as the reference set and included associated invasiveness and antimicrobial susceptibility profiles. Our hypothesis was that subtyping Salmonella isolates by PFGE could reveal differences within serotypes in terms of antimicrobial susceptibility patterns and, for human Salmonella, differences in food animal sources and invasiveness that were not evident from serotyping alone.

Materials and Methods

Sample Sources and Processing

Human and food animal non-typhoidal Salmonella isolates received between January 1, 2005 and December 31, 2011, were included in the study. At BOL, human Salmonella isolates received as part of the state’s routine operations were grown, identified, and serotyped by the Bacteriology Section, using standard procedures [10,11]. Food animal Salmonella isolates were recovered from carcass rinsates (chickens), carcass swabs (turkeys, cattle, and swine), and ground products (chicken, turkey, and beef) during slaughter and processing at federally inspected facilities in the northeast Pennsylvania, Maine, Vermont, New Hampshire, New York, Maryland, Connecticut, Rhode Island, Massachusetts, Delaware, New Jersey, Indiana, Ohio, Michigan and Washington, DC) as previously described [12].

PFGE testing of human Salmonella isolates was conducted by the BOL according to the CDC-standardized procedure used by all PulseNet-certified laboratories [9]. Gel images were analyzed using BioNumerics software Version 6.6 (Applied Maths, Saint-Martens-Latem, Belgium). All non-typhoidal human Salmonella isolated received at the BOL were evaluated by PFGE, except when the same serotype of Salmonella was recovered more than once from a patient within a six-month period. In this case, only the first isolate received was tested. PFGE testing of food animal Salmonella isolates was done by the animal arm of the NARMS, located in Athens, GA, as previously described [7].

PFGE Pattern Names

PFGE fingerprints of human Salmonella were maintained in a local Pennsylvania database and submitted to CDC’s PulseNet national Salmonella database where they were assigned pattern names [4,5]. The USDA maintains a similar database called USDA-VetNet for PFGE fingerprints of Salmonella isolated from food animals [7]. Food animal Salmonella pattern names were assigned by USDA-VetNet as previously described [7]. Isolates in the VetNet database were compared to the PulseNet database to capture matching PulseNet pattern names.

Common Human Salmonella Patterns and Shared Common Patterns

The 20 most frequently identified PFGE patterns among human Salmonella isolates and with at least two isolates in each year of the study were designated as the most common human Salmonella patterns. These 20 patterns included patterns that occurred both sporadically (n = 4,471) and linked to known outbreaks (n = 251). The USDA-VetNet database was then searched for matching patterns in Salmonella isolates recovered from food animals during slaughter and processing in northeastern U.S. facilities. The most common human patterns that were also identified in food animal Salmonella and are defined here as “shared common patterns.”

Antimicrobial Susceptibility Testing

Susceptibility to the following classes of antimicrobial agents was tested using the Sensititre semi-automated broth microdilution antimicrobial susceptibility system (Trek Diagnostic Systems Inc., Cleveland, Ohio), with minimum inhibitory concentrations evaluated according to Clinical Laboratory Standards Institute (CLSI) guidelines [13]: (antimicrobial agents in parentheses; resistance breakpoints in brackets): aminoglycosides (amikacin [≥ 64 μg/mL], gentamicin [≥ 16 μg/mL], kanamycin [≥ 64 μg/mL] and streptomycin [≥ 64 μg/mL]), β-lactam/β-lactamase inhibitor combinations (amoxicillin/clavulanic acid [≥ 32/16 μg/mL]), cephems (cefotaxim [≥ 32 μg/mL], ceftriaxone [≥ 1 μg/mL], and cefoxitin [≥ 8 μg/mL]) and ceftriaxone [≥ 1 μg/mL], penicillins (ampicillin [≥ 32 μg/mL]), quinolones (ciprofloxacin [≥ 8 μg/mL] and nalidixic acid [≥ 32 μg/mL]), folate pathway inhibitors (sulfadoxazole [≥ 512 μg/mL], trimethoprim/sulfamethoxazole [≥ 4/76 μg/mL], folic biosynthesis inhibitors (sulfamethoxazole [≥ 32 μg/mL], folate pathway inhibitors (sulfadoxazole [≥ 512 μg/mL], trimethoprim/sulfamethoxazole [≥ 4/76 μg/mL], folic biosynthesis inhibitors (sulfamethoxazole [≥ 32 μg/mL]), and tetracyclines (tetracycline [≥ 16 μg/mL]). For antimicrobial agents without CLSI approved standards, NARMS interpretive criteria as established by the NARMS working group were used and quality control strains were as previously described [8]. Multidrug resistance was defined as resistance to three or more classes of antimicrobial agents. Of the 4,235 human Salmonella isolates with common shared patterns, 467 (11%) were tested for susceptibility to antimicrobial agents. Limited resources precluded testing all of the isolates. The isolates chosen for susceptibility testing included 267 randomly selected isolates originating from Pennsylvania that were tested by the human arm of NARMS as part of its routine surveillance program [14]. The Pennsylvania Department of Agriculture tested an additional 200 human Salmonella isolates sampled from the 16 shared common patterns. NARMS tested all 275 of the food animal Salmonella isolates having shared common patterns for antimicrobial susceptibility as previously described [12].

Correlation of Invasiveness with PFGE Patterns

Isolation of Salmonella from human blood was used as an indicator of invasive disease [15]. The statistical association between each PFGE pattern and invasiveness was tested via a 2×2 contingency table and evaluated on the basis of the conditional maximum likelihood estimate of Odds Ratio (OR) and the mid-p test (two-tailed p value) [16]. PFGE patterns with OR≥1 and p≤0.05 were interpreted as associated with increased
invasiveness; patterns with OR ≤ 1 and p ≤ 0.05 were interpreted as associated with decreased invasiveness.

Correlation of Antimicrobial Resistance with Invasiveness

A two-tailed p value obtained with a Fisher’s exact test (GraphPad QuickCalcs, GraphPad Software, Inc., San Diego, CA) was used to evaluate the relationship between antimicrobial resistance and invasiveness.

Regarding data for Salmonella recovered from animals: ACUC approval was not needed as the isolates were obtained as part of the National Antimicrobial Resistance Monitoring System (NARMS) from the USDA Food Safety and Inspection Service (FSIS) as part of their Salmonella PR/HACCP verification testing program [http://www.ars.usda.gov/Main/docs.htm?docid=6750&page=2]. Accessed 2013 September 19.

Results

PFGE Patterns Found both in Human and Food Animal Salmonella Isolates

A total of 11,967 human Salmonella and 2,187 food animal Salmonella isolates were submitted for laboratory testing during the study period (2005–2011). The food animal Salmonella isolates were recovered from a total of 65,655 animals tested for Salmonella during slaughter and processing at federally inspected facilities in the northeastern U.S., and represented an overall yield of 3.3% (Table 1). The 65,655 animals tested for Salmonella included 42,368 (64.5%) cattle, 10,412 (15.9%) swine, 9,661 (14.7%) chickens and 3,214 (4.9%) turkeys. Salmonella was isolated from a total of 2,187 samples (Table 1). Of the 2,187 Salmonella-positive samples, 1,194 (54.6%) were recovered from chickens, 472 (21.6%) from cattle, 282 (12.9%) from turkeys and 239 (10.9%) from swine. A total of 2,083 of the 2,187 food animal Salmonella isolates were available to VetNet for PFGE, antimicrobial susceptibility testing and comparison with human Salmonella isolates.

Common Human Salmonella Patterns

The 20 most common human Salmonella XbaI patterns are shown in Fig. 1 and described in Table 2. These patterns represent 39% of the human Salmonella isolates (4,722/11,967) from Pennsylvania described in this paper. Six serotypes-Berta, Enteritidis, Heidelberg, Newport, Thompson, and Typhimurium (including variant 5–)–and one antigenic formula (I,4,[5],12:i:-) were represented among these 20 patterns. Each XbaI pattern is shown with all associated BlnI patterns that occurred at least three times in the dataset. One to seven different BlnI patterns were associated with a particular XbaI pattern.

Sixteen (80%) of the 20 most common human Salmonella patterns shown in Fig. 1 were also found among the 2,083 food animal Salmonella isolates (Table 2). A total of 4,235 (35%) of the 11,967 human Salmonella isolates shared these 16 PFGE patterns with 273 (13%) of the 2,083 food animal Salmonella isolates. All six serotypes and the antigenic formula identified in the 20 most common human Salmonella patterns were also represented among the shared common patterns.

The most frequently observed shared common pattern from human Salmonella isolates was Enteritidis pattern JEGX01.0004 (JEGX01.0003ARS), which accounted for 16% of all human Salmonella. Among food animal Salmonella, this pattern was the second most common pattern, accounting for 5% of all food animal Salmonella isolates. Serotype Kentucky pattern JGPX01.0027 (JGPX01.0220 ARS) was the most common PFGE pattern in food animal Salmonella, occurring in 13% of food animal isolates.

### Table 1. Food Animal Sources of Salmonella Recovered at Federally Inspected Slaughter and Processing Facilities in the Northeastern U.S.1 with Human Isolates Shown for Reference.

| Year | Total No. (%) Positive for Salmonella |
|------|-------------------------------------|
| 2005 | 1,175 (12.4) |
| 2006 | 1,072 (11.9) |
| 2007 | 1,052 (12.0) |
| 2008 | 1,013 (11.3) |
| 2009 | 949 (10.9) |
| 2010 | 924 (11.4) |
| 2011 | 1,071 (11.6) |
| TOTAL | 6,861 (13.2) |

1From Pennsylvania, also described in this paper.

**Correlation of Antimicrobial Resistance with Invasiveness**

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| Serotype   | PFGE-Xba-pattern | PFGE-Bln-pattern |
|------------|------------------|------------------|
| Berta      | JAXX01.0001      | JAXA26.0004      |
| Enteritidis| JEGX01.0002      | JEGA26.0010      |
| Enteritidis| JEGX01.0004      | JEGA26.0002      |
| Enteritidis| JEGX01.0006      | JEGA26.0004      |
| Enteritidis| JEGX01.0009      | JEGA26.0016      |
| Enteritidis| JEGX01.0009      | JEGA26.0017      |
| Enteritidis| JEGX01.0009      | JEGA26.0036      |
| Enteritidis| JEGX01.0021      | JEGA26.0002      |
| Enteritidis| JEGX01.0021      | JEGA26.0005      |
| Enteritidis| JEGX01.0034      | JEGA26.0002      |
| Heidelberg | JF6X01.0022      | JF6A26.0001      |
| Heidelberg | JF6X01.0022      | JF6A26.0002      |
| Heidelberg | JF6X01.0022      | JF6A26.0013      |
| Newport    | JJPX01.0011      | JJPX26.0044      |
| Newport    | JJPX01.0011      | JJPX26.0194      |
| Newport    | JJPX01.0061      | JJPX26.0021      |
| Newport    | JJPX01.0061      | JJPX26.0062      |
| Thompson   | J6X01.0001       | J6A26.0012       |
| Thompson   | J6X01.0001       | J6A26.0024       |
| Thompson   | J6X01.0001       | J6A26.0026       |
| Typhimurium| JPPX01.0001      | JPPX26.0001      |
| Typhimurium| JPPX01.0001      | JPPX26.0063      |
| Typhimurium| JPPX01.0001      | JPPX26.0084      |
| Typhimurium| JPPX01.0003      | JPPX26.0003      |
| Typhimurium| JPPX01.0003      | JPPX26.0007      |
| Typhimurium| JPPX01.0003      | JPPX26.0042      |
| Typhimurium| JPPX01.0003      | JPPX26.0106      |
| Typhimurium| JPPX01.0003      | JPPX26.0248      |
| Typhimurium| JPPX01.0003      | JPPX26.0488      |
| Typhimurium| JPPX01.0018      | JPPX26.0156      |
| I 4,[5],12:i-| JPPX01.0026      | JPPX26.0033      |
| Typhimurium| JPPX01.0146      | JPPX26.0021      |
| Typhimurium| JPPX01.0146      | JPPX26.0172      |
| Typhimurium| JPPX01.0146      | JPPX26.0174      |
| Typhimurium| JPPX01.0146      | JPPX26.0291      |
| Typhimurium| JPPX01.0146      | JPPX26.0292      |
| Typhimurium| JPPX01.0146      | JPPX26.0297      |
| Typhimurium| JPPX01.0146      | JPPX26.0313      |
| Typhimurium| JPPX01.0302      | JPPX26.0183      |
| Typhimurium| JPPX01.0302      | JPPX26.0234      |
| Typhimurium| JPPX01.0604      | JPPX26.0174      |
| Typhimurium| JPPX01.0604      | JPPX26.0292      |
| I 4,[5],12:i-| JPPX01.0621      | JPPX26.0055      |
| I 4,[5],12:i-| JPPX01.0621      | JPPX26.0057      |
| I 4,[5],12:i-| JPPX01.1212      | JPPX26.0108      |
| I 4,[5],12:i-| JPPX01.1212      | JPPX26.0181      |
Salmonella isolates (data not shown). This pattern was rarely seen in BOL human Salmonella isolates (0.25%).

Of the 275 food animal Salmonella isolates with shared common patterns, 238 (87%) were recovered from chicken, 16 (6%) from cattle, 11 (4%) from turkey and 10 (4%) from swine (Table 2). Sixty seven percent (n = 186) of these 275 food animal Salmonella isolates belonged to serotype Enteritidis, and all but two isolates were recovered from chicken. The most common Enteritidis pattern in Salmonella from chickens was JEGX01.0004 (JEGX01.0003 ARS) (n = 105/184; 57%). Chicken was also the most common source of Heidelberg pattern JF6X01.0022 (JF6X01.0015 ARS), with 25 of 30 isolates (83%) recovered from chicken (Table 2).

In contrast to the strong association of S. Enteritidis and Heidelberg patterns with chicken, Typhimurium pattern JPXX01.0003 (JPXX01.0003 ARS) (n = 18) was observed in Salmonella recovered in comparable numbers from cattle (n = 6), chicken (n = 5), turkey (n = 4) and swine (n = 3). The second most common food animal Typhimurium pattern, JPXX01.0064 (JPXX01.0079 ARS) (n = 10) was primarily recovered from chicken (n = 7). The two isolates of pattern JPXX01.0018 (JPXX01.0002 ARS) were recovered from cattle and swine, respectively, and Typhimurium pattern JPXX01.0146 (JPXX01.0081 ARS) (n = 5) was recovered primarily from swine (n = 4). Berta pattern JAXX01.0001 (JAXX01.0003 ARS) (n = 3) was found exclusively in turkey.

All 16 shared common patterns were found in human Salmonella during each of the seven years of the study. Three of the 16 shared common patterns, Enteritidis patterns JEGX01.0004 (JEGX01.0005 ARS), JEGX01.0005 (JEGX01.0002 ARS) and JEGX01.0034 (JEGX01.0005 ARS), were also found in food animal Salmonella during each of the seven years of the study. Similarly, Heidelberg pattern JF6X01.0022 (JF6X01.0015 ARS) was recovered from food animals in each of five years, and Typhimurium pattern JPXX01.0003 (JPXX01.0003 ARS) in each of four years (data not shown).

Unshared PFGE Patterns
A total of 261 different patterns were identified among the 11,967 human Salmonella isolates in Pennsylvania, and 794 were identified among the 2,083 food animal Salmonella isolates (data not shown). Many of the identified human patterns were not shared by food animal Salmonella isolates, and many of the identified food animal Salmonella patterns were not shared by human Salmonella isolates. Of the 2,083 food animal Salmonella isolates, only 1,034 (50%) shared PFGE patterns with the human Salmonella patterns that had been assigned pattern names. Of the 11,967 human Salmonella isolates, only 5,266 (44%) had named patterns found among the 2,083 food animal Salmonella isolates recovered from northeastern slaughter and processing facilities.

Of the 20 most common human Salmonella patterns (Fig. 1 and Table 2), two Enteritidis patterns (JEGX01.0002 and JEGX01.0009) and two Typhimurium/I 4,5,[12]:- patterns (JPXX01.0026 and JPXX01.1212) were not observed among food animal Salmonella isolates. Pattern JEGX01.0002 was found to be associated with travel. Travel histories were available for 200 persons associated with Salmonella pattern JEGX01.0002; of these, 164 (82%) reported traveling outside the U.S., notably to the Dominican Republic (n = 71) and Mexico (n = 53).

Association of Invasiveness with PFGE Patterns
Isolation from blood was used as an indicator of invasiveness. A total of 646 Salmonella isolates from humans were recovered from blood, representing 5.4% of the 11,967 human Salmonella isolates tested (Table 2). Four patterns were found to be significantly associated with increased frequency of isolation from blood: Enteritidis JEGX01.0004 (JEGX01.0003 ARS) (OR = 1.30; p = 0.01), Enteritidis JEGX01.0005 (JEGX01.0002 ARS) (OR = 1.60; p = 0.01), Enteritidis JEGX01.0009 (JEGX01.0022 ARS) (OR = 2.06; p = 0.02) and Heidelberg JF6X01.0002 (JF6X01.0015 ARS) (OR = 2.10; p = 0.01). Five patterns were found to be significantly associated with decreased frequency of isolation from blood: Enteritidis JEGX01.0034 (JEGX01.0005 ARS) (OR = 0.10; p = 0.00), Newport patterns JPXX01.0011 (JPXX01.0204 ARS) (OR = 0.00; p = 0.05) and JPXX01.0061 (JPXX01.0069 ARS) (OR = 0.00; p = 0.02), and Typhimurium patterns JPXX01.0146 (JPXX01.0081 ARS) (OR = 0.06; p = 0.00) and JPXX01.0302 (JPXX01.0106 ARS) (OR = 0.36; p = 0.03).

Antimicrobial Susceptibility Associated with Shared Common Patterns
Of the 4,235 human Salmonella isolates with shared common patterns, 467 (11%) were tested for susceptibility to antimicrobial agents (Table 3). Of these 467, a total of 367 (79%) were pansusceptible, 100 (21%) were resistant to at least one class of antimicrobial agent, 75 (16%) were MDR, and 62 (13%) were resistant to five or more classes of antimicrobial agents. Of the 275 food animal Salmonella isolates, 226 (82%) were pansusceptible, 49 (18%) were resistant to at least one class of antimicrobial agents, 40 (14%) were MDR, and 16 (6%) were resistant to five or more classes of antimicrobial agents.

Multidrug resistance (resistance to ≥3 classes of antimicrobial agents) was associated with eight of the 16 shared common patterns in human Salmonella (Table 3). Five of these patterns were also associated with multidrug resistance in food animal Salmonella. Berta pattern JAXX01.0001 (JAXX01.0003 ARS), Heidelberg pattern JF6X01.0022 (JF6X01.0015 ARS), Typhimurium patterns JPXX01.0003 (JPXX01.0003 ARS) and JPXX01.0018 (JPXX01.0002 ARS), and I 4,[5],12:-- pattern JPXX01.0621 (TERX01.0001 ARS). The incidence of multidrug resistance in both human and food animal Salmonella isolates exceeded 90% for Typhimurium patterns JPXX01.0003 (JPXX01.0003 ARS) and JPXX01.0018 (JPXX01.0002 ARS) (Table 3), patterns that differ by two bands (Fig. 1). When these two patterns were considered together, a total of 58 (89%) of the 65 human and 15 (75%) of the 20 food animal Typhimurium isolates were resistant to the following five antimicrobial agents: ampicillin, chloramphenicol, streptomycin, sulfisoxazole, and tetracycline (the ACSSuT phenotype and resistance to five classes of antimicrobial agents). Two of the human Salmonella isolates exhibited resistance to amoxicillin/clavulanic acid and cefidifor in addition to the ACSSuT phenotype. The food animal Salmonella isolates exhibiting the ACSSuT phenotype were recovered from cattle (n = 3), chickens (n = 3), swine (n = 3) and turkeys (n = 3). An additional isolate recovered from a turkey exhibited the ACSSuT phenotype plus resistance to gentamicin, and three additional isolates (two from cattle; one from swine) lacked only the streptomycin resistance of this phenotype (ACSuT). One human isolate and three food animal isolates with patterns JPXX01.0003 (JPXX01.0003 ARS)
| Serotype         | PulseNet XbaI Pattern$^3$ | No. (% of All Human Salmonella)$^2$ | No. Linked to Outbreaks | No. from Blood | % from Blood within Blood$^2$ | Odds Ratio (95% CI); p | Corresponding VetNet Pattern$^4$ | No. (%) of Food Animal Salmonella | No. from Cattle | No. from Chicken | No. from Swine | No. from Turkey |
|-----------------|---------------------------|------------------------------------|------------------------|----------------|-----------------------------|----------------------------|-------------------------------|-------------------------------|----------------|----------------|---------------|----------------|
| Berta           | JAXX01.0001               | 49 (0.41)                          | 0                      | 5              | 10.20                       | 2.00 (0.70-4.75); 0.17     | JAXX01.0003 ARS                | 3 (0.14)                      | 0              | 0              | 0             | 3              |
| Enteritidis     | JEGX01.0002               | 235 (1.96)                         | 3                      | 14             | 5.96                        | 1.11 (0.62-1.87); 0.68     | JEGX01.0017 ARS                | 0                            | 0              | 0              | 0             | 0              |
| Enteritidis     | JEGX01.0004               | 1,968 (16.45)                      | 79                     | 130            | 6.61                        | 1.30 (1.06-1.58); 0.01      | JEGX01.0003 ARS                | 106 (5.09)                   | 1              | 105            | 0             | 0              |
| Enteritidis     | JEGX01.0005               | 426 (3.56)                         | 12                     | 35             | 8.22                        | 1.60 (1.11-2.26); 0.01      | JEGX01.0002 ARS                | 65 (3.12)                    | 1              | 64             | 0             | 0              |
| Enteritidis     | JEGX01.0009               | 144 (1.20)                         | 1                      | 15             | 10.42                       | 2.04 (1.63-4.68); 0.02      | JEGX01.0022 ARS                | 0                            | 0              | 0              | 0             | 0              |
| Enteritidis     | JEGX01.0021               | 331 (2.77)                         | 24                     | 21             | 6.34                        | 1.19 (0.74-1.84); 0.43      | JEGX01.0010 ARS, JEGX01.0052 ARS$^5$ | 1 (0.05)                     | 0              | 1              | 0             | 0              |
| Enteritidis     | JEGX01.0034               | 176 (1.47)                         | 11                     | 1              | 0.57                        | 1.00 (0.00-4.49); 0.00      | JEGX01.0005 ARS                | 14 (0.67)                    | 0              | 14             | 0             | 0              |
| Heidelberg      | JFX01.0002                | 151 (1.26)                         | 18                     | 16             | 10.60                       | 2.10 (1.21-3.48); 0.01      | JFX01.0015 ARS                 | 30 (1.44)                    | 3              | 25             | 0             | 2              |
| Newport         | JJPX01.0011               | 54 (0.45)                          | 0                      | 0              | 0                           | 0.00 (0.00-1.00); 0.05      | JJPX01.0024 ARS                | 1 (0.05)                     | 0              | 1              | 0             | 0              |
| Newport         | JJPX01.0061               | 72 (0.60)                          | 28                     | 0              | 0                           | 0.00 (0.00-0.74); 0.02      | JJPX01.0007 ARS                | 1 (0.05)                     | 0              | 0              | 1             | 0              |
| Thompson        | JPX01.0001                | 54 (0.45)                          | 0                      | 3              | 5.56                        | 1.03 (0.52-2.93); 0.90      | JPX01.0024 ARS                 | 1 (0.05)                     | 0              | 1              | 0             | 0              |
| Typhimurium     | JXX001.0001               | 53 (0.44)                          | 2                      | 3              | 5.66                        | 1.05 (0.26-3.02); 0.87      | JXX001.0021 ARS                | 1 (0.05)                     | 0              | 1              | 0             | 0              |
| Typhimurium     | JXX001.0003               | 113 (0.94)                         | 2                      | 9              | 7.96                        | 1.52 (0.72-2.93); 0.24      | JXX001.0003 ARS                | 18 (0.86)                    | 6              | 5              | 3             | 4              |
| Typhimurium     | JXX001.0018               | 81 (0.68)                          | 0                      | 2              | 2.47                        | 0.44 (0.07-1.51); 0.24      | JXX001.0002 ARS                | 2 (0.10)                     | 1              | 0              | 1             | 0              |
| Typhimurium     | JXX001.0046               | 278 (2.23)                         | 16                     | 1              | 0.36                        | 0.06 (0.00-0.31); 0.00      | JXX001.0001 ARS                | 5 (0.24)                     | 0              | 1              | 4             | 0              |
| Typhimurium     | JXX001.0032               | 149 (1.25)                         | 46                     | 3              | 2.01                        | 0.36 (0.09-0.99); 0.05      | JXX001.0016 ARS                | 2 (0.10)                     | 1              | 1              | 0             | 0              |
| Typhimurium     | JXX001.0064               | 61 (0.51)                          | 3                      | 1              | 1.64                        | 0.29 (0.01-1.49); 0.18      | JXX001.0079 ARS                | 10 (0.48)                    | 1              | 7              | 0             | 2              |
| Typhimurium; I 4,[5],12:i:- | JXX001.0026               | 61 (0.51)                          | 4                      | 1              | 1.64                        | 0.29 (0.01-1.49); 0.18      | JXX001.0038 ARS, TERRX001.0010 ARS | 0                           | 0              | 0              | 0             | 0              |
| I 4,[5],12:i:-  | JXX001.0062               | 219 (1.83)                         | 2                      | 8              | 3.65                        | 0.66 (0.30-1.28); 0.25      | TERRX001.0001 ARS              | 15 (0.72)                    | 2              | 12             | 0             | 1              |
| I 4,[5],12:i:-  | JXX001.1212               | 47 (0.39)                          | 0                      | 3              | 3.38                        | 1.20 (0.29-4.35); 0.72      | JXX001.0034 ARS, TERRX001.0008 ARS | 0                           | 0              | 0              | 0             | 0              |
| TOTAL           |                           | 4,722 (39.46)                      | 251                    | 271            | NA                          | TOTAL 275 (13.20)           | 16                          | 238             | 10             | 11            |                |

$^1$ Pattern names include a three-letter code that indicates serotype (e.g., JEG for serotype Enteritidis in the pattern names JEGX01.0004 and JEGA26.0002), followed by a three-character code for restriction enzyme (e.g., X01 for XbaI in JEGX01.0004 and JEGA26.0002), and a four-digit number for the unique strain designation (e.g., 0004 in JEGX01.0004) (Gerner-Smidt et al., 2006).

$^2$ Percentage of total number of human Salmonella isolates (11,967).

$^3$ Number of human Salmonella isolates recovered from blood for a particular pattern expressed as a percentage of the total number from all sources for that PFGE pattern; e.g., for Berta XbaI pattern JAXX01.0001, (5/49) = 10.20%.

$^4$ Statistical method for determining Odds Ratio is described in Materials and Methods.

$^5$ VetNet's pattern nomenclature conforms to PulseNet's nomenclature, with three exceptions: (1) PulseNet uses a single three-letter code (JPX) to designate both serotype Typhimurium and antigenic formula I 4,[5],12:i:- whereas VetNet uses two different codes, JPX for Typhimurium and TER for I 4,[5],12:i:-; (2) the four-digit strain designation codes are different in the two systems; and (3) "ARS" (for Agricultural Research Service of the USDA) is appended to VetNet pattern names.

$^6$ VetNet identified two different patterns within PulseNet pattern JEGX01.0021.

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# Table 3. Antimicrobial resistance associated with the 16 most common human *Salmonella* PFGE patterns shared by food animal *Salmonella*.

| Human *Salmonella* | Food Animal *Salmonella* |
|-------------------|--------------------------|
| **Serotype** | **PulseNet XbaI Pattern** | **No. Tested** | **No. (%)** | **No. (%)** | **No. (%)** | **No. (%)** | **No. (%)** | **No. (%)** | **No. (%)** | **No. (%)** | **No. (%)** | **No. (%)** |
| Berta | JAXX01.0001 | 16 | 9 (56.3) | 2 (12.5) | 5 (31.3) | 1 (6.3) | 1 (2.5) | 1 (2.5) | 1 (2.5) | 1 (2.5) | 1 (2.5) | 1 (2.5) |
| Enteritidis | JEGX01.0004 | 114 | 108 (94.7) | 5 (4.4) | 1 (0.9) | 0 (0.0) | 1 (0.9) | 1 (0.9) | 1 (0.9) | 1 (0.9) | 1 (0.9) | 1 (0.9) |
| Enteritidis | JEGX01.0005 | 25 | 25 (100.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Enteritidis | JEGX01.0021 | 33 | 27 (81.8) | 6 (7.3) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Enteritidis | JEGX01.0034 | 22 | 21 (95.5) | 1 (4.5) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Heidelberg | JF6X01.0015 | 14 | 13 (92.9) | 0 (0.0) | 1 (7.1) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Newport | JJPX01.0011 | 9 | 9 (100.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Newport | JJPX01.0061 | 13 | 13 (100.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Thompson | JPPX01.0001 | 8 | 8 (100.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Typhimurium | JPPX01.0001 | 13 | 10 (76.9) | 1 (7.7) | 2 (15.4) | 1 (7.7) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Typhimurium | JPPX01.0003 | 38 | 2 (2.6) | 3 (13.3) | 19 (56.6) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Typhimurium | JPPX01.0018 | 27 | 21 (77.8) | 2 (7.4) | 5 (18.5) | 1 (3.7) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Typhimurium | JPPX01.0046 | 24 | 23 (95.8) | 1 (4.2) | 8 (20.8) | 1 (2.1) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Typhimurium | JPPX01.0032 | 22 | 20 (90.9) | 1 (4.5) | 1 (4.5) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| Typhimurium | JPPX01.0043 | 13 | 13 (100.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |
| TOTAL | 467 | 367 (78.6) | 25 (5.4) | 75 (16.1) | 162 (13.3) | 3 (5) | 0 (0.0) | 0 (0.0) | 3 (100.0) | 0 (0.0) | 0 (0.0) | 0 (0.0) |

1 Typhimurium includes var. 05.9.
2 Resistant to at least three classes of antimicrobial agents.
3 Abbreviations: nalidixic acid (Nal); ceftriaxone (Axo).
4 VetNet identified two different patterns within PulseNet pattern JEGX01.0021.
5 Based on 467 isolates tested for antimicrobial susceptibility.
6 Based on 275 isolates tested for antimicrobial susceptibility.
7 Antimicrobial classes (antimicrobial agents in parentheses; resistance breakpoints in brackets): aminoglycosides (amikacin [≥64 mg/mL], gentamicin [≥16 mg/mL], kanamycin [≥64 mg/mL] and streptomycin [≥64 mg/mL]), ß-lactam/ß-lactamase inhibitor combinations (amoxicillin/clavulanic acid [≥32/16 mg/mL], cephems (cefoxitin [≥32 mg/mL], ceftiofur [≥8 mg/mL] and ceftriaxone [≥4 mg/mL]), penicillins (ampicillin [≥32 mg/mL]), quinolones (ciprofloxacin [≥4 mg/mL] and nalidixic acid [≥32 mg/mL]), folate pathway inhibitors (sulfadiazine [≥512 mg/mL], trimethoprim/sulfamethoxazole [≥8/16 mg/mL], phenicols (chloramphenicol [≥32 mg/mL]), and tetracyclines (tetracycline [≥16 mg/mL]).

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and JPXX01.0018 (JPXX01.0002 ARS) were resistant only to streptomycin and sulfisoxazole. Collectively Typhimurium patterns JPXX01.0003 (JPXX01.0003 ARS) and JPXX01.0018 (JPXX01.0002 ARS) were associated with resistance to five or more classes of antimicrobial agents in 60 (92%) of the 65 human Salmonella and 16 (80%) of the 20 food animal Salmonella.

Of the 15 food animal Salmonella isolates exhibiting I4,[5],12:i- pattern JPXX01.00621 (TERX01.0001 ARS), seven were resistant to amoxicillin/clavulanic acid, ampicillin, cefoxitin, ceftriaxone and cefixime. Of the 76 susceptibility-tested human Salmonella isolates exhibiting pattern JPXX01.00621 (TERX01.0001 ARS), only one exhibited the exact resistance pattern. A second human Salmonella isolate exhibited a closely related resistance profile: the isolate was intermediate instead of resistant to ceftriaxone. The resistance patterns of the additional MDR food animal Salmonella isolates and human Salmonella isolate with pattern JPXX01.00621 (TERX01.0001 ARS) did not match.

Although we did not find resistance to the fluoroquinolone ciprofloxacin in any human or food animal Salmonella isolate, three human Salmonella isolates, Berta pattern JAXX01.0001, Enteritidis pattern JEGX01.0004 (JEGX01.0003 ARS) and Typhimurium pattern JPXX01.00302 (JPXX01.0106 ARS), were resistant to nalidixic acid (Nal), an indicator of decreasing susceptibility to quinolones [14].

Invasiveness and Antimicrobial Resistance to Antimicrobial Agents

Of the 467 human Salmonella isolates tested for antimicrobial susceptibility, 367 were pansusceptible, and 100 were resistant to one or more antimicrobial agents (Table 3). Twelve (3.2%) of the 367 pansusceptible isolates and 10 (10%) of the 100 isolates resistant to one or more antimicrobial agents were recovered from blood. This difference was found to be significant (p = 0.0129). Included among the 10 resistant blood isolates were four Typhimurium pattern JPXX01.0003 (JPXX01.0003 ARS) isolates, two Enteritidis pattern JEGX01.0021 (JEGX01.0010 ARS and JEGX01.0002 ARS), one each of Typhimurium patterns JPXX01.0018 (JPXX01.0002 ARS and JEGX01.0146 (JPXX01.0081 ARS), one Berta pattern JAXX01.0001 (JAXX01.0003 ARS), and one nalidixic acid-resistant Enteritidis pattern JEGX01.0004 (JEGX01.0003 ARS).

Discussion

We compared clinical isolates of Salmonella recovered from ill humans received as part of routine operations in Pennsylvania during 2005-2011 with Salmonella isolates collected during the same period from food animals at federally inspected slaughter and processing facilities in the northeastern U.S. We also correlated PFGE patterns of Salmonella from humans with animal sources, invasiveness, and antimicrobial susceptibility profiles. Our analysis was based on the most common human Salmonella PFGE patterns identified during this period, regardless of serotype. This approach differs from many studies because of its focus on PFGE patterns rather than serotypes and on PFGE patterns that are frequently observed with sporadic disease, rather than solely on patterns linked to outbreaks. However, it is important to note that outbreak isolates were a portion of the overall number of isolates in this study. This is the first study to compare the PFGE patterns of human Salmonella isolates recovered during routine surveillance with food animal Salmonella isolates recovered at federally inspected slaughter and processing facilities. We found that subtyping Salmonella isolates by PFGE revealed differences within serotypes in terms of antimicrobial susceptibility patterns and, for human Salmonella, differences in food animal sources and invasiveness that were not evident from serotyping alone.

We found that most (16) but not all of the 20 most common PFGE patterns identified in human Salmonella in Pennsylvania were also found in Salmonella recovered from food animals in the United Kingdom [32]. Data collected in the coming years will provide critical information regarding the potential reduction of salmonellosis caused by serotypes Enteritidis [23-25] and Heidelberg [26], and our PFGE results support these associations. Enteritidis pattern JEGX01.0004 (JEGX01.0003 ARS) was the most common human Salmonella pattern in Pennsylvania, accounting for 1,968 (16%) of the 11,967 human Salmonella isolates and 130 (20%) of the 646 invasive salmonellosis cases. The presence of Salmonella Enteritidis pattern JEGX01.0004 (JEGX01.0003) in chickens during every year of this study suggests the potential for a significant impact on public health and requires further investigation to determine what attributes sustain the persistence of this strain and what measures could reduce its incidence. This further supports our assertion that consideration of strain diversity (i.e., PFGE pattern diversity) is a critical factor for developing control measures.

The frequent occurrence of human salmonellosis associated with pattern JEGX01.0004 (JEGX01.0003 ARS) makes case investigations difficult unless there is a strong epidemiological connection linking the cases. Lacking such a connection, salmonellosis cases associated with this pattern are generally given less scrutiny by epidemiologists, in spite of the fact that the number of cases associated with this pattern in Pennsylvania (n = 1,968) is much greater than the number of identified outbreak-associated isolates for all patterns combined (n = 251) (Table 2). S. Enteritidis pattern JEGX01.0004 (JEGX01.0003 ARS) was associated with a national outbreak involving approximately 1,939 illnesses [27] and recalls of more than 500 million shell eggs [28]. New regulations governing egg safety in the U.S. [29] may help to reduce the incidence of salmonellosis associated with pattern JEGX01.0004 (JEGX01.0003 ARS). However, since our study has demonstrated seven years of this pattern’s high level of persistence in poultry meat, it is reasonable to conclude that Salmonella Enteritidis pattern JEGX01.0004 (JEGX01.0003 ARS) is persistent and endemic in poultry. Efforts focused on reducing Salmonella in broiler flocks have met with very encouraging results in Denmark [30,31] and the United Kingdom [32]. Data collected in the coming years will provide critical information regarding the potential reduction of Salmonella Enteritidis pattern JEGX01.0004 (JEGX01.0003 ARS) in the United States.

Eleven of the 16 shared PFGE patterns were associated with susceptibility to all antimicrobial agents tested or resistance to...
fewer than three classes of antimicrobial agents in food animal Salmonella (Table 3). This is encouraging from an antimicrobial resistance perspective, indicating that not all PFGE subtypes and serotypes acquire the same degree or type of resistance. Multidrug resistance was associated with Berta pattern JAXX01.0001 (JAXX01.0003 ARS), Heidelberg pattern JF6X01.0022 (JF6X01.0015 ARS), Typhimurium patterns JPPX01.0003 (JPPX01.0003 ARS) and JPPX01.0018 (JPPX01.0002 ARS), and I 4,[5],12:i- pattern JPXX01.0621 (TERX01.0001 ARS) in both human and food animal Salmonella. The high degree of correspondence between PFGE patterns and antimicrobial resistance profiles for Typhimurium patterns JPPX01.0003 (JPPX01.0003 ARS) and JPPX01.0018 (JPPX01.0002 ARS) in all four types of food animals contrasts sharply with the strong association of most other patterns with chicken (Table 2), although this may be confounded by differences in the number of animals of each type that were tested (Table 1). Monitoring the incidence of these patterns and their associated resistance phenotypes could aid in assessing the effect of efforts to reduce the use of antimicrobial agents for growth promotion and disease prevention in food animals on public health.

Differences in the percentage of blood isolates representing each pattern suggest that there may be differences in invasiveness among Salmonella having different patterns, even for patterns within a serotype. Further work is needed to determine why certain patterns were associated with increased or decreased invasiveness.

In our sample of 467 human Salmonella isolates that were tested for susceptibility to antimicrobial agents, we did not observe a direct correlation between resistance and invasiveness within specific PFGE patterns; however, we did find that the percentage of antimicrobial-resistant isolates that were recovered from blood (10%) was approximately three times the percentage found to be pansusceptible (3.2%; p = 0.0129). Further work is needed to confirm this correlation.

For some of the four unshared common patterns, sources other than food animals slaughtered or processed in northeastern U.S. facilities are likely. For example, we found that S. Enteritidis pattern JEGX01.0002 was associated with travel outside the U.S., especially to the Dominican Republic and Mexico. Another common human Salmonella pattern that was not noted in food animal Salmonella isolates, Enteritidis pattern JEGX01.0009, has been associated with imported food: Salmonella with this pattern has been recovered from shrimp imported from Bangladesh and pompano from Taiwan (PulseNet national PulseNet Salmonella database was searched on 2012-06-11 and included data uploaded between 2008-06-12 and 2012-06-11).

In some cases, the absence of common human Salmonella PFGE patterns in food animal Salmonella may have resulted from an insufficient number of animals. From 2005 through 2011, the number of food animals tested for Salmonella in northeastern slaughter and processing facilities declined by more than half—from 13,834 in 2005 to 6,381 in 2011. Although Typhimurium pattern JPPX01.1212 and I 4,[5],12:i- pattern JPPX01.0026 were not observed in our sample of food animal Salmonella, they have repeatedly been observed in Salmonella recovered from chicken (PulseNet data; searches of the PulseNet national Salmonella database were conducted on 2012-06-11 and included data uploaded between 2008-06-12 and 2012-06-11). The absence of these patterns in Salmonella recovered from food animals in the northeast may simply reflect the limited amount of testing during the study period. Alternatively, the food responsible for illness may have come from outside the northeastern U.S., as some of the patterns have been observed in food animals from other areas in the U.S. (data not shown).

**Limitations**

This study has several limitations. The first is the absence of data for testing food animal Salmonella isolates with a second enzyme (BlnI). Testing human Salmonella isolates with BlnI has helped to discriminate within most PFGE patterns produced with XbaI. Beginning in 2011, VetNet specimens have been tested with BlnI, so this information will be available for future studies. A second limitation is the reduced number of samples collected by FSIS for Salmonella testing at federally inspected slaughter and processing plants in the northeast in recent years. A third limitation is the fact that only 11% of the human Salmonella isolates with the 16 common shared PFGE patterns were tested for susceptibility to antimicrobial agents. Finally, we recognize that not all food slaughtered and processed in a particular geographic region is consumed in the same region and that different regions of the U.S. vary in their poultry production concentrations.

**Conclusions**

This work shows that 16 of the 20 most common PFGE patterns found in human Salmonella in Pennsylvania were also found in Salmonella recovered from food animals sampled at federally inspected slaughter and processing facilities in the northeastern U.S. Multidrug resistance was correlated with five PFGE patterns shared by food animal and human Salmonella: Berta pattern JAXX01.0001 (JAXX01.0003 ARS), Heidelberg pattern JF6X01.0022 (JF6X01.0015 ARS), Typhimurium patterns JPPX01.0003 (JPPX01.0003 ARS) and JPPX01.0018 (JPPX01.0002 ARS), and I 4,[5],12:i- pattern JPXX01.0621 (TERX01.0001 ARS). The most common human pattern, S. Enteritidis patterns JEGX01.0004 (JEGX01.0003 ARS), accounting for 16% of all human Salmonella, was also common in Salmonella recovered from food animals, especially chicken. Our findings suggest an association between the most prevalent forms of human salmonellosis and contaminated meat and poultry. They also show a persistence of Enteritidis pattern JEGX01.0004 (JEGX01.0003 ARS), the association of differences in invasiveness with different PFGE patterns, and the tendency for some but not all PFGE subtypes within a serotype to acquire multidrug resistance.

Comparing the PFGE fingerprint patterns and antimicrobial susceptibility profiles of Salmonella from humans with those from food animals inspected in slaughter and processing facilities located in a specific geographic region provides information that may assist in source attribution and outbreak investigations.

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Conceived and designed the experiments: CHS PJF-C. Performed the experiments: CHS DT KJ. Analyzed the data: CHS PJF-C SO NMM. Wrote the paper: CHS PJF-C DT KJ SO NMM.