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# Multidrug-Resistant *Salmonella* I 4,[5],12:i:– and *Salmonella* Infantis Infections Linked to Whole Roasted Pigs from a Single Slaughter and Processing Facility

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## Abstract

We describe two outbreaks of multidrug-resistant (MDR) *Salmonella* I 4,[5],12:i:– infection, occurring in 2015 to 2016, linked to pork products, including whole roaster pigs sold raw from a single Washington slaughter and processing facility (establishment A). Food histories from 80 ill persons were compared with food histories reported in the FoodNet 2006 to 2007 survey of healthy persons from all 10 U.S. FoodNet sites who reported these exposures in the week before interview. Antimicrobial susceptibility testing and whole genome sequencing were conducted on

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selected clinical, food, and environmental isolates. During 2015, a total of 192 ill persons were identified from five states; among ill persons with available information, 30 (17%) of 180 were hospitalized, and none died. More ill persons than healthy survey respondents consumed pork (74 versus 43%, $P < 0.001$). Seventeen (23%) of 73 ill persons for which a response was available reported attending an event where whole roaster pig was served in the 7 days before illness onset. All 25 clinical isolates tested from the 2015 outbreak and a subsequent 2016 smaller outbreak ($n = 15$) linked to establishment A demonstrated MDR. Whole genome sequencing of clinical, environmental, and food isolates ($n = 69$) collected in both investigations revealed one clade of highly related isolates, supporting epidemiologic and traceback data that establishment A as the source of both outbreaks. These investigations highlight that whole roaster pigs, an uncommon food vehicle for MDR *Salmonella* I 4,[5],12:i:– outbreaks, will need further attention from food safety researchers and educators for developing science-based consumer guidelines, specifically with a focus on the preparation process.

### Keywords

Food safety; Multidrug resistant; Pig; Pork; *Salmonella* I 4,[5],12:i:–; Swine

Nontyphoidal *Salmonella* (NTS) is the leading bacterial cause of foodborne illness in the United States, with an estimated one million illnesses, 20,000 hospitalizations, and 400 deaths annually (19). Since 2010, U.S. laboratories have identified an increasing number of *Salmonella* I 4,[5],12:i:– infections, and in 2015, this serotype was the fifth most reported laboratory-confirmed NTS serotype from human isolates (9). The prevalence of multidrug resistance (MDR), defined as resistance to one or more drugs in three or more antimicrobial classes, has increased in clinical *Salmonella* I 4,[5],12:i:– isolates during 2010 to 2015 (8). MDR NTS infections in humans are associated with an increased risk for hospitalization, bloodstream infection, and treatment failure (3, 35).

Globally, *Salmonella* I 4,[5],12:i:– human infections have been linked predominately to consumption of contaminated beef, poultry, and pork products (12, 14,22). In particular, swine has been identified as a principal *Salmonella* I 4,[5],12:i:– reservoir and source of foodborne outbreaks in Europe and, more recently, in the United States (11, 17, 20).

From June to July 2015, Public Health—Seattle & King County (PHSKC) and the Washington State Department of Health (WADOH) detected an outbreak of 61 *Salmonella* serotype I 4,[5],12:i:– infections in Washington through notifiable disease surveillance. The number of these infections was a marked increase above Washington's baseline. During 2010 to 2014, a total of 3,620 NTS cases were reported in Washington, with an average annual incidence of 10.6 cases per 100,000 persons. Serotype I 4,[5],12:i:– accounted for 4.3% of Washington NTS isolates where serotype data were available (37). PHSKC and WADOH worked with the Centers for Disease Control and Prevention (CDC) and the U.S. Department of Agriculture, Food Safety and Inspection Service (FSIS) to determine the scope and the source of the outbreak and to identify control measures to prevent further illness.

This report describes the investigation of two outbreaks of gastrointestinal illness caused by MDR *Salmonella* I 4,[5],12:i:– linked to pork products in 2015 to 2016. The pork products were predominately whole roaster pigs from a single processing facility in Washington that was inspected by FSIS.

## MATERIALS AND METHODS

### Epidemiologic investigation.

A confirmed case was initially defined as gastrointestinal illness with symptom onset on or after 25 April 2015 and isolation of *Salmonella* I 4,[5],12:i:– with pulsed-field gel electrophoresis (PFGE) *XbaI* pattern JPXX01.1314 in a Washington resident. Cases were identified through notifiable disease surveillance. WADOH Public Health Laboratories performed PFGE analysis on clinical isolates of *Salmonella* I 4,[5], 12:i:– and submitted results to PulseNet USA, the national molecular subtyping network for foodborne disease surveillance, coordinated by CDC. CDC also conducted whole genome sequencing (WGS) analysis on selected bacterial isolates from ill persons. As the investigation progressed, four additional PFGE *XbaI* patterns (JPXX01.2311, JPXX01.2429, JPXX01.3161, and JPXX01.3336) were added to the case definition because they were closely related to PFGE *XbaI* pattern JPXX01.1314. During April 2015, the five PFGE patterns were rare in Washington but common in other states. Because I 4,[5],12:i:– was a prevalent serotype of *Salmonella* in the United States, PulseNet used WGS for outbreak case finding among non-Washington residents. WGS provides increased precision in determination of the genetic relatedness of isolates compared with PFGE analysis alone (5, 23). Therefore, a case among non-Washington residents had to first meet the confirmed case definition and yield an isolate of *Salmonella* I 4,[5],12:i:– that was closely related genetically by high-quality single-nucleotide polymorphism (SNP) analysis to the isolates from Washington residents. Clinical isolates from other states differed by 0 to 7 high-quality SNPs from the Washington isolates. On 16 September 2015, the case definition was expanded to include persons with a culture-confirmed *Salmonella* Infantis infection with PFGE *XbaI* pattern JFXX01.0046 and an epidemiologic link to a confirmed outbreak case, based on information obtained later in the investigation.

From April 2015 to July 2015, public health investigators interviewed case patients or a proxy (e.g., a parent or spouse) with a standardized NTS questionnaire regarding clinical illness, food consumption the week before illness onset, and travel history. A supplemental questionnaire was developed that focused on pork, beef, and livestock exposure to better characterize these exposures. Attempts were made to interview all persons who met the case definition with both questionnaires, including those previously interviewed with only the standardized NTS questionnaire.

Questionnaire data were analyzed using SAS version 9.3 (SAS Institute Inc., Cary, NC). The proportion of outbreak-associated cases reporting pork or beef consumption or exposure to livestock in the 7 days before illness onset was compared with the proportion of healthy persons from all 10 U.S. FoodNet sites who reported these exposures in the week before interview, as described in the CDC Foodborne Diseases Active Surveillance Network (FoodNet) Population Survey Atlas of Exposures, 2006 to 2007 (7). A binomial probability distribution was used to generate *P* values to determine whether consumption of specific foods was reported by ill persons more frequently than by healthy adults in the FoodNet Population Survey (7). Calculating binomial probability distribution is useful in identifying potential common exposures during an outbreak investigation (18).

### Environmental and traceback investigations.

WADOH, PHSKC, and FSIS conducted environmental and traceback investigations of possible livestock exposures and of restaurants, markets, and common events where ill persons purchased or consumed food. Investigations included a comprehensive review of meat sources, evaluation of safe food handling practices, and collection of food and environmental samples for microbiological testing. On 31 July 2015, WADOH visited a Washington slaughter and processing establishment (establishment A), based on the meat source traceback investigation, which indicated a common pork supplier. Ten pooled environmental samples were collected from different areas of establishment A, including the lairage (pens holding swine before slaughter), bleeding station drains, carcass evisceration area and drains, equipment, and the processing room where the finished pork products were stored before sale. A swab sample was also collected from one swine carcass. During 10 to 14 August 2015, FSIS collected 16 environmental, 14 swine carcass, and 8 swine cecal samples from establishment A.

### Laboratory investigations.

WADOH Public Health Laboratories tested clinical, food, and environmental samples collected during the investigation. WADOH Public Health Laboratories used a Bio-Plex instrument (Bio-Rad, Hercules, CA) to conduct confirmatory testing and molecular serotyping of *Salmonella* isolates from patients' clinical samples and traditional culture-based and biochemical identification methods based on the U.S. Food and Drug Administration's *Bacteriological Analytical Manual* protocols for food and environmental samples (2). FSIS further characterized *Salmonella* confirmed positive isolates from samples collected from the implicated establishment, including PFGE and serotype analyses.

Additionally, WADOH, PHSKC, and FSIS performed WGS on a subset of 59 isolates from the 2015 outbreak investigation, with the combined sequence data analyzed by CDC (Table 1). The analysis was generated with Lyve-SET version 1.1.4f, using 2013k-0676 as a reference with no phage masking. Reads were cleaned with CG Pipeline (options: -no-singletons); SNPs were called with Varscan, and Lyve-SET was run with the following options: minimum coverage, 20; min alternative fraction, 0.95; and allowed flanking, 5 bp (15).

The CDC National Antimicrobial Resistance Monitoring System (NARMS) reference laboratory performed antimicrobial susceptibility testing on selected clinical isolates by broth microdilution (Sensititre, Cleveland, OH) to determine MICs for the following 15 antimicrobial agents: ampicillin, amoxicillin–clavulanic acid, azithromycin, cefoxitin, ceftiofur, ceftriaxone, chloramphenicol, ciprofloxacin, gentamicin, kanamycin, nalidixic acid, streptomycin, sulfisoxazole, tetracycline, and trimethoprim-sulfamethoxazole (8). Resistance was defined by the Clinical and Laboratory Standards Institute (CLSI) interpretive standards, when available (10). For streptomycin, where no CLSI interpretive criteria for human isolates exist, resistance was defined as ≥64 mg/L. Testing was performed according to manufacturer instructions and using the following quality control strains: *Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 29213, *Enterococcus faecalis* ATCC 29212, and *Pseudomonas aeruginosa* ATCC 27853. FSIS performed antimicrobial susceptibility testing on establishment A *Salmonella* isolates collected by FSIS during 10 to 14 August 2015. CDC reviewed this investigation for human subject protections and deemed it to be nonresearch.

## RESULTS

### Demographic and clinical characteristics.

A total of 192 confirmed cases from five states were identified: 1 from Alaska, 2 from California, 2 from Idaho, 3 from Oregon, and 184 from Washington. A total of 191 (99%) ill persons resided in or traveled to Washington during part of their incubation periods. Dates of illness onset ranged from 25 April 2015 to 6 October 2015 (Fig. 1). Median patient age was 35 years (range, <1 to 90 years), and 51% were female. Among 180 ill persons with available information, 30 (17%) were hospitalized, and no deaths were reported. Among 80 ill persons with supplemental questionnaire data available, 59 (74%) reported eating pork during the 7 days before illness onset, compared with 43% who reported eating pork in the FoodNet Population Survey, a statistically significant difference ($P < 0.001$) (Table 2). Commonly reported pork products included bacon (9 of 59, 15%), pork chops (8 of 59, 14%), and barbecue pork (7 of 59, 12%), and 19 (32%) reported eating more than one type of pork product. Of 73 ill persons for which a response was available, 17 (23%) reported attending a pig roast in the 7 days before illness onset.

### Environmental and traceback investigations.

Traceback of the sources of pork products was completed for 36 (61%) of 59 ill persons interviewed with the supplemental questionnaire; of these, 35 consumed pork sourced from one Washington slaughter and processing facility (establishment A). Establishment A’s main product was freshly slaughtered, raw roaster pigs that typically weighed <220 lb (100 kg); these are commonly prepared and roasted whole. Establishment A distributed raw, whole roaster pigs and other pork products to Washington, Oregon, and Alaska during the outbreak period, primarily sourcing from six farms (five in Montana and one in Washington). Of the 21 ill persons interviewed with the supplemental questionnaire who did not report consuming pork, 13 (62%) reported eating at one of two restaurants (restaurants A and B) or shopping at a market (market A), where pork from establishment A was served or sold. PHSKC inspections of these venues identified high potential for cross-contamination of raw pork with other meats and produce, including inadequate employee hand washing and insufficient cleaning and sanitizing of food contact surfaces and utensils used to prepare raw meat.

We identified 18 pig roast events where establishment A whole roaster pigs were served during June to August 2015. Roaster pig preparation and cooking details at three outbreak-linked pig roast events had several commonalities. Cooking and preparation of roaster pigs at the three events were completed outdoors using a slow, whole-carcass cooking process (range, 5 to 18 h); the meat was cut into smaller pieces to be served with side dishes that were prepared concurrently. All three cooks reported taking adequate precautions to prevent cross-contamination (i.e., hand washing and using diluted bleach or soap and hot water on food preparation surfaces and equipment). The three cooks reported cooking the roaster pigs to a minimum internal temperature of 62.8°C (145°F), confirmed by a food thermometer placed in the thickest parts (e.g., shoulder or hindquarters) of the whole pig during the cooking process.

### Laboratory investigations.

Outbreak PFGE patterns were identified in multiple environmental isolates from market A, restaurants A and B, and one leftover roasted pork sample from a pig roast event. Outbreak strains of *Salmonella* I 4,[5],12:i:– were isolated from 8 of 10 pooled environmental samples, collected by WADOH on 31 July 2015, from different areas and equipment involved in the slaughter process in establishment A. Sample sources included the lairage, bleeding station drains, knives and hooks used for trimming and evisceration, the carcass-splitting hacksaw, and the evisceration tables, floor, and nearby drains. *Salmonella* was not isolated from the two pooled environmental samples in the processing room and the one swine carcass swab. Of the FSIS samples collected during 10 to 14 August 2015 at establishment A, *Salmonella* was isolated from 14 of 14 carcass swabs and 8 of 8 swine cecal samples. Environmental samples were collected by FSIS during operations and after sanitation but prior to the start of production each day (preoperational). *Salmonella* was isolated from 2 of 8 preoperational and 6 of 8 operational samples; 20 (67%) of the 30 *Salmonella* isolates were *Salmonella* I 4,[5],12:i:– or *Salmonella* Infantis with PFGE patterns indistinguishable from the outbreak clinical isolates. Based on isolation of *Salmonella* Infantis with PFGE JFXX01.0046 during FSIS establishment A carcass and environmental sampling, it was added to the case definition for the outbreak investigation.

### WGS analysis.

Fifty-nine isolates, which included all five *Salmonella* I 4,[5],12:i:– PFGE outbreak patterns, underwent WGS. Fifty-four (92%) of the 2015 isolates (35 clinical, 13 environmental, and 11 food) were categorized in one clade (clade 1) with SNP differences ranging from 0 to 7 among isolates (Fig. 2). All 35 (100%) sequenced clinical isolates were collected from ill persons who consumed pork during the incubation periods. We were able to document exposure to establishment A pork products for 30 (86%) ill persons. The remaining five clinical isolates ranged from 6 to 57 SNP differences from clade 1. The sequenced clinical isolates included two ill persons who reported live swine exposure in addition to consuming pork. For these five cases, we were unable to complete a traceback of the source of the pork consumed and the live swine.

### Antimicrobial susceptibility testing.

Twenty-one clinical *Salmonella* I 4,[5],12:i:– isolates were submitted to NARMS. Seventeen (95%) of 18 isolates with PFGE pattern JPXX01.1314 displayed a resistance pattern that included ampicillin (A), streptomycin (S), sulfisoxazole (Su), and tetracycline (T) (ASSuT), with the remaining JPXX01.1314 isolate resistant to ampicillin, streptomycin, and sulfisoxazole (ASSu). Three PFGE pattern JPXX01.2429 isolates (100%) displayed an ASSuT resistance profile.

FSIS used NARMS antimicrobial susceptibility testing laboratory methods (8) to characterize 14 *Salmonella* I 4,[5],12:i:– isolates from establishment A (environmental, carcass swabs, and cecal) samples; 13 (93%) with PFGE pattern JPXX01.1314 displayed an ASSuT resistance profile. The remaining JPXX01.1314 isolate displayed an ASSu resistance profile. The *Salmonella* Infantis isolates collected from establishment A and characterized by FSIS were pansusceptible.

### Control measures.

On 31 July 2015, FSIS issued a public health alert regarding illnesses associated with whole pigs used for pig roasts (29). The alert informed consumers of the complexity of pig roasting and important food safety steps to prevent foodborne illnesses. On 12 August 2015, WADOH released a food safety technical sheet detailing safe handling and cooking practices for whole roaster pigs (38). On 13 August 2015, FSIS announced a voluntary recall by establishment A of 52,745 kg (116,282 lb) of whole roaster pig carcasses produced from 18 April to 27 July 2015 because of potential *Salmonella* I 4,[5],12:i:– contamination and illnesses linked to consumption of products produced by the establishment (28). FSIS determined that their sampling results collected at establishment A during 10 to 14 August 2015 demonstrated unsanitary conditions at establishment A. This may have contributed to cross-contamination of the raw pork products. On 27 August 2015, establishment A voluntarily recalled an additional 237,401 kg (523,380 lb) of pork products produced between 18 April and 26 August 2015 (27). The recall expansion coincided with establishment A voluntarily ceasing operations. Establishment A hired a private consulting group and worked with FSIS to improve slaughter management practices to control *Salmonella* and ensure compliance with FSIS guidelines (26). Improvements included implementation of recommended best practices for sanitation during scalding and singeing steps, antimicrobial intervention and verification sampling procedures for *Salmonella*, and proper chilling and refrigeration of whole roaster carcasses throughout slaughter and storage before sale.

### Second outbreak and subsequent investigation.

On 13 June 2016, establishment A resumed swine slaughter and processing after implementing corrective actions that were verified by FSIS to mitigate *Salmonella* contamination. In July 2016, PHSKC and WADOH worked with CDC and FSIS to investigate an additional 15 *Salmonella* I 4,[5],12:i:– infections linked to establishment A whole roaster pigs served at two separate pig roast events in Washington. PFGE patterns JPXX01.1314 and JPXX01.2429 were included in the investigation; 13 (93%) of 14 clinical isolates were JPXX01.1314. All 15 cases were among Washington residents, with illness onset dates ranging from 1 June to 10 August 2016 (Fig. 1). Median patient age was 26 years (range, 8 to 72 years), and 33% were female. Among 14 ill persons with available information, none were hospitalized and no deaths were reported. Thirteen (93%) of 14 ill persons reported consuming pork in the 7 days before illness. Of the 13, 8 (62%) reported attending a pig roast in the 7 days before illness onset. Of those 8, all (100%) consumed pork that traced back to establishment A. On 20 July 2016, FSIS issued a public health alert (32). The next day, establishment A conducted a voluntary recall of 5,288 kg (11,658 lb) of whole roaster pigs owing to potential *Salmonella* I 4,[5],12:i:– contamination and illnesses linked to consumption of its products (31). Establishment A ceased operations on 11 August 2016. On 25 and 26 August 2016, more than a week after the establishment ceased operations, FSIS collected and analyzed carcasses held in their chiller ($n$ = 20) and environmental samples ($n$ = 40) to determine whether there was evidence of the outbreak strain in the establishment. Four (20%) of the 20 carcasses and 1 (3%) of the 40 environmental samples were positive for *Salmonella* I 4,[5],12:i:– with PFGE patterns JPXX01.1314 and JPXX01.2311. FSIS characterized the five isolates using NARMS antimicrobial susceptibility testing laboratory methods, and all five isolates displayed an ASSuT resistance profile. The four clinical isolates submitted to NARMS were PFGE pattern JPXX01.1314 and displayed ASSuT. WGS analysis of 10 clinical isolates confirmed the close genetic association with the 2015 outbreak (Fig. 2). Concurrently, WGS analysis by FSIS of the establishment A carcass and environmental isolates demonstrated they were closely related to the clinical isolates from the 2015 and 2016 outbreaks (not included in Fig. 2). Establishment A voluntarily suspended operations, and FSIS rescinded its grant of inspection in response to the establishment's request. As of 19 October 2018, establishment A has not reopened.

## DISCUSSION

We describe the first reported *Salmonella* I 4,[5],12:i:– foodborne outbreak in the United States in which epidemiological, traceback, and laboratory evidence implicated pork processed at a single FSIS-inspected swine slaughter and processing establishment. The second outbreak of *Salmonella* I 4,[5],12:i:– infections, coinciding with establishment A reopening, highlights the challenges of reducing MDR *Salmonella* I 4,[5],12:i:– contamination during swine slaughter and processing. Additionally, this outbreak highlights commercially slaughtered, raw, whole roaster pigs as an uncommon *Salmonella* vehicle.

During 2016 to 2017, nationwide sampling by FSIS to estimate the prevalence of *Salmonella* at swine slaughter and processing facilities demonstrated that 12.2% of raw, intact pork cuts sampled were positive for *Salmonella* (34). Although *Salmonella* is not considered an adulterant in not-ready-to-eat meat products, when not-ready-to-eat poultry or meat products are associated with an illness outbreak and contain pathogens that are not considered adulterants, FSIS likely will consider the product linked to the illness outbreak to be adulterated (25). Additionally, following *Salmonella* outbreaks linked to raw poultry products, FSIS published guidelines in 2012 for commercial poultry slaughter and processing establishments to implement robust interventions that proactively minimize *Salmonella* contamination (25). Similarly, FSIS raw pork sampling data can inform development of pathogen reduction performance standards for verification of process controls in slaughter and processing establishments to decrease salmonellosis linked to intact pork cuts.

Our investigation demonstrated the ability of WGS to determine the genetic relatedness among *Salmonella* I 4,[5],12:i:– isolates of multiple, closely related PFGE patterns from different specimen types collected at different times and link them to a common outbreak source. Sixty-three isolates collected from human, food, and environmental sources during 2015 to 2016 represented five *Salmonella* I 4,[5],12:i:– PFGE patterns that were categorized into one clade of closely related isolates that included environmental and pork isolates collected at establishment A. WGS provided increased subtype discrimination beyond serotype and PFGE analysis to provide concordance with our epidemiological and traceback investigations. WGS further supported the decisions for establishment A to recall its products in 2015 and 2016.

Furthermore, WGS allowed us to exclude cases during the outbreak investigation. The primary outbreak PFGE pattern JPXX01.1314 was the fifth most commonly isolated NTS PFGE pattern in the United States before the 2015 outbreak but was uncommon in Washington (9, 37). WGS of clinical isolates provided increased confidence to exclude suspect, non-Washington residents, especially early in the outbreak when the epidemiologic and traceback investigations were ongoing.

In response to the outbreaks, WADOH, FSIS, and the U.S. National Pork Board released new guidelines for cooking whole roaster pigs, based on general food safety practices when preparing pork products (16, 30, 38). Food safety experts agree that adequate cooking and minimizing cross-contamination are the most crucial consumer food-handling behaviors to prevent illnesses caused by NTS (13). However, preventing cross-contamination when preparing a large pig carcass can pose additional challenges compared with smaller cuts of pork. A previous quantitative microbiological risk assessment model for *Salmonella* indicated that pork products requiring knives and cutting boards for preparation increased the risk for cross-contamination to side dishes (21). Although roaster pigs generally do not require knives and cutting boards when raw, the details of roaster pig preparation and cooking at three outbreak-linked pig roast events indicated that knives were used to cut supposed cooked roaster pigs into smaller pieces while side dishes were prepared concurrently. Because cooking whole roaster pigs is a particularly slow process, bacteria exposed to nonlethal temperatures can produce heat-shock proteins that improve survivability to lethal temperatures (6, 36, 40). A comprehensive assessment of best practices is needed for preparation and cooking of whole roaster pigs.

The primary antimicrobial resistance pattern (ASSuT) in both outbreaks did not show evidence of resistance to fluoroquinolones, an antimicrobial class commonly used to treat invasive NTS infections. However, evidence reveals that a small percentage of ASSuT-resistant *Salmonella* I 4,[5],12:i:– circulating in the U.S. swine population have plasmid-mediated quinolone resistance genes that might be transferred horizontally to other bacteria (11, 24). Studies suggest that different types of livestock environments (e.g., porcine versus avian or bovine) have specific selective pressures that play a key role in the spread of distinct NTS antimicrobial resistance genes (1). FSIS swine cecal sampling for *Salmonella* at federally inspected slaughter and processing facilities in 2014 indicated that *Salmonella* I 4,[5],12:i:– had one of the highest proportions of MDR isolates among all *Salmonella* serotypes (33). All of the *Salmonella* I 4,[5],12:i:– samples recovered from swine were MDR and had the typical ASSuT resistance profile (33). This is concurrent with a notable increase of MDR *Salmonella* I 4,[5],12:i:– infections as an important serotype associated with pork and pork products in the United States (20). Besides control of *Salmonella* in pig production, additional research is needed to better understand the occurrence of MDR *Salmonella* I 4,[5],12:i:– infections (8).

Our investigation could not determine the relative importance of specific points in the pork production process that contributed to this outbreak. The ecology of *Salmonella* I 4,[5],12:i:– during pork production might differ from other *Salmonella* serotypes commonly linked to pork products. In a recent 12-month longitudinal study of multiple swine herds in Australia where multiple NTS serotypes were detected, *Salmonella* I 4,[5],12:i:– isolates displayed persistently higher rates of bacterial shedding compared with other NTS serotypes (39). This might increase the bacterial load introduced into the slaughter facility with potential to establish as residential flora. Implementing interventions at the slaughter level can reduce or prevent *Salmonella* contamination of pork carcasses but might be insufficient if high levels of *Salmonella* are present (4). Further research is needed to identify factors associated with the worldwide increase of MDR *Salmonella* I 4,[5],12:i:– associated with pork processing.

Our findings are subject to two main limitations. First, the strict case definition for non-Washington residents might have resulted in underestimating the actual number of ill persons outside of Washington. Second, we were unable to assess practices or conduct environmental or animal testing at establishment A's source farms because farms were reluctant to participate, and unclear jurisdictional authority of state agriculture agencies did not require farms to comply with our request. Consequently, we could not determine whether the prevalence of *Salmonella* I 4,[5],12:i:– at source farms or preharvest factors (i.e., farm animal husbandry, transport, and holding) might have contributed to a higher level of *Salmonella* contamination on swine carcasses before pork processing.

This report highlights the need for increased collaboration among federal partners, pork industry, state and local public health, and agricultural partners to better understand the epidemiology and ecology of MDR *Salmonella* I 4,[5],12:i:– in the entire pork production chain, from on-farm to slaughter and processing. Additionally, food safety researchers and educators should consider developing science-based consumer guidelines specifically for preparing and cooking whole roaster pigs.

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## HIGHLIGHTS

- Multidrug-resistant *Salmonella* I 4,[5],12:i:– is increasingly associated with pigs.
- We describe two multidrug-resistant outbreaks linked to whole roaster pigs.
- Whole pig preparation can be difficult compared with smaller pork cuts.
- Best practices are needed for preparing and cooking whole roaster pigs.

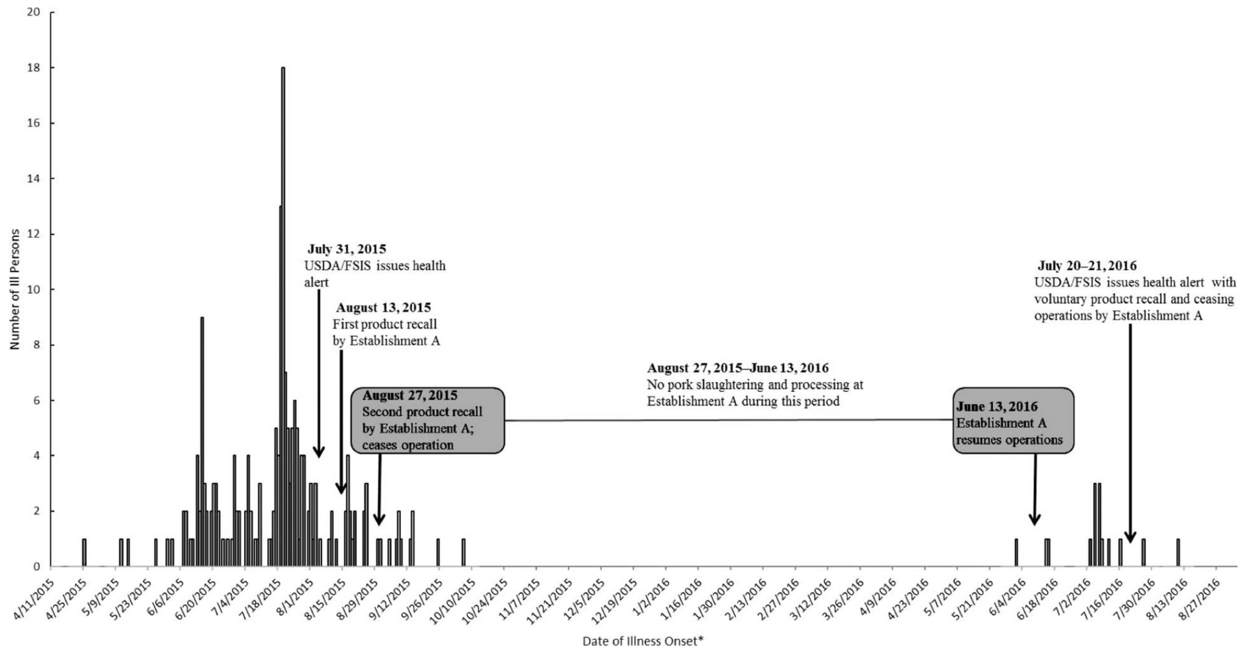


**FIGURE 1.**

*Infections with outbreak strains of* Salmonella *I 4,[5],12:i:– or* Salmonella *Infantis by date of illness onset. Multiple states, 25 April 2015 to 12 August 2016. ** n *= 192 for 2015 outbreak*; n *= 15 for 2016 outbreak. When unknown, illness onset dates were estimated by this formula: isolation date of outbreak strains of* Salmonella *I 4,[5],12:i:– or* Salmonella *Infantis minus 3 days*.

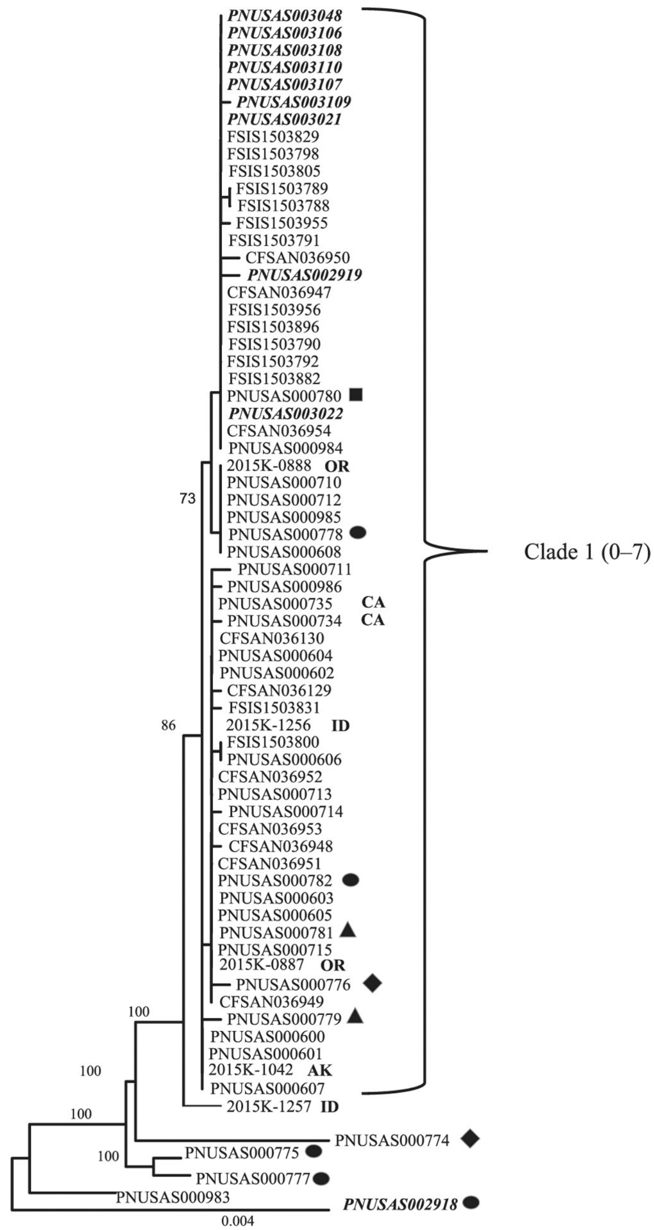


**FIGURE 2.**

*Phylogenetic tree of single nucleotide polymorphisms (SNPs) analyses of clinical, food, and environmental* Salmonella *I 4,[5],12:i:– isolates from the 2015 and 2016 (bold and italicized) outbreak investigations (*n *= 69). AK, Alaska; OR, Oregon; CA, California; ID, Idaho. All isolates are of Washington origin with pulsed-field gel electrophoresis (PFGE) pattern JPXX01.1314, unless noted. PFGE patterns are indicated by different shapes: JPXX01.2311 (▲), JPXX01.2429 (●), JPXX01.3161 (♦), JPXX01.3336 (■). Sixty-three isolates were within the main clade (clade 1) with 0 to 7 SNPs among isolates.*

## TABLE 1.

Overview of 69 *Salmonella* I 4,[5],12:i:– isolates selected for WGS and analysis, collected during two outbreaks[a]

| WGS ID | SRA ID | Collection date (mo/day/yr) | Source state[b] | Source | PFGE *Xba*I pattern |
|---|---|---|---|---|---|
| 2015K-0887 | SRR2975854 | 6/25/2015 | OR | Stool | JPXX01.1314 |
| 2015K-0888 | SRR2975855 | 7/8/2015 | OR | Stool | JPXX01.1314 |
| 2015K-1042 | SRR2585450 | 7/30/2015 | AK | Stool | JPXX01.1314 |
| 2015K-1256 | SRR2913358 | 7/20/2015 | ID | Stool | JPXX01.1314 |
| 2015K-1257 | SRR2913538 | 7/28/2015 | ID | Stool | JPXX01.1314 |
| FSIS1503788 | SRR2421550 | 8/10/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503789 | SRR2546335 | 8/10/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503790 | SRR2546344 | 8/11/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503791 | SRR2546347 | 8/12/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503792 | SRR2546348 | 8/11/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503798 | SRR2420877 | 8/10/2015 | WA | Environmental | JPXX01.1314 |
| FSIS1503800 | SRR2421549 | 8/11/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503805 | SRR2420882 | 8/11/2015 | WA | Environmental | JPXX01.1314 |
| FSIS1503829 | SRR2421534 | 8/13/2015 | WA | Environmental | JPXX01.1314 |
| FSIS1503831 | SRR2420879 | 8/14/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503882 | SRR2354274 | 8/13/2015 | WA | Environmental | JPXX01.1314 |
| FSIS1503896 | SRR2353812 | 8/14/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503955 | SRR2637904 | 8/12/2015 | WA | Pork | JPXX01.1314 |
| FSIS1503956 | SRR2637921 | 8/13/2015 | WA | Pork | JPXX01.1314 |
| PNUSAS000600 | SRR2183036 | 6/10/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000601 | SRR2183037 | 6/17/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000602 | SRR2183038 | 6/16/2015 | WA | Unknown (human) | JPXX01.1314 |
| PNUSAS000603 | SRR2191980 | 6/16/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000604 | SRR2183039 | 6/17/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000605 | SRR2191982 | 6/23/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000606 | SRR2192102 | 6/21/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000607 | SRR2192120 | 7/7/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000608 | SRR2192246 | 7/5/2015 | WA | Unknown (human) | JPXX01.1314 |

| WGS ID | SRA ID | Collection date (mo/day/yr) | Source state[b] | Source | PFGE *Xba*I pattern |
|---|---|---|---|---|---|
| PNUSAS000710 | SRR2192245 | 7/6/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000711 | SRR2194004 | 7/16/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000712 | SRR2194002 | 7/10/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000713 | SRR2194003 | 7/9/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000714 | SRR2191983 | 7/5/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000715 | SRR2194005 | 7/22/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000734 | SRR2194006 | 7/24/2015 | CA | Stool | JPXX01.1314 |
| PNUSAS000735 | SRR2194007 | 7/23/2015 | CA | Stool | JPXX01.1314 |
| PNUSAS000774 | SRR2243429 | 5/13/2015 | WA | Stool | JPXX01.3161 |
| PNUSAS000775 | SRR2243431 | 6/12/2015 | WA | Stool | JPXX01.2429 |
| PNUSAS000776 | SRR2243435 | 6/15/2015 | WA | Stool | JPXX01.3161 |
| PNUSAS000777 | SRR2243437 | 6/23/2015 | WA | Stool | JPXX01.2429 |
| PNUSAS000778 | SRR2243438 | 7/1/2015 | WA | Stool | JPXX01.2429 |
| PNUSAS000779 | SRR2243457 | 7/8/2015 | WA | Stool | JPXX01.2311 |
| PNUSAS000780 | SRR2243462 | 7/15/2015 | WA | Unknown (human) | JPXX01.3336 |
| PNUSAS000781 | SRR2243463 | 7/21/2015 | WA | Stool | JPXX01.2311 |
| PNUSAS000782 | SRR2243466 | 7/31/2015 | WA | Stool | JPXX01.2429 |
| PNUSAS000983 | SRR2976014 | 9/10/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000984 | SRR2976015 | 9/12/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000985 | SRR2976016 | 9/14/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS000986 | SRR2732606 | 9/15/2015 | WA | Stool | JPXX01.1314 |
| PNUSAS002918 | SRR3930408 | 6/17/2016 | WA | Stool | JPXX01.2429 |
| PNUSAS002919 | SRR3930409 | 6/18/2016 | WA | Urine | JPXX01.1314 |
| PNUSAS003021 | SRR3996868 | 7/10/2016 | WA | Stool | JPXX01.1314 |
| PNUSAS003022 | SRR3996869 | 7/8/2016 | WA | Stool | JPXX01.1314 |
| PNUSAS003048 | SRR3996867 | 7/6/2016 | WA | Stool | JPXX01.1314 |
| PNUSAS003106 | SRR3996870 | 7/11/2016 | WA | Stool | JPXX01.1314 |
| PNUSAS003107 | SRR3996871 | 7/11/2016 | WA | Stool | JPXX01.1314 |
| PNUSAS003108 | SRR3996875 | 7/15/2016 | WA | Stool | JPXX01.1314 |
| PNUSAS003109 | SRR3996874 | 7/10/2016 | WA | Stool | JPXX01.1314 |
| PNUSAS003110 | SRR3996873 | 7/11/2016 | WA | Stool | JPXX01.1314 |

| WGS ID | SRA ID | Collection date (mo/day/yr) | Source state[b] | Source | PFGE *Xba*I pattern |
|---|---|---|---|---|---|
| CFSAN036947 | SRR2669935 | 8/3/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036948 | SRR2669965 | 8/3/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036129 | SRR2669933 | 6/24/2015 | WA | Meat | JPXX01.1314 |
| CFSAN036130 | SRR2669934 | 6/24/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036949 | SRR2670129 | 8/3/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036950 | SRR2670130 | 8/3/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036951 | SRR2175317 | 8/3/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036952 | SRR2670132 | 8/3/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036953 | SRR2670133 | 8/3/2015 | WA | Environmental | JPXX01.1314 |
| CFSAN036954 | SRR2670134 | 8/3/2015 | WA | Environmental | JPXX01.1314 |

[a]WGS, whole genome sequencing; SRA, Sequence Read Archive. The outbreaks were in 2015 ($n = 59$) and 2016 ($n = 10$).

[b]OR, Oregon; AK, Alaska; ID, Idaho; WA, Washington State.

**TABLE 2.**

Frequency of selected food and livestock exposures in persons with outbreak-associated illness, interviewed with a supplemental questionnaire versus the 2006 to 2007 FoodNet population survey, as of 25 September 2015

| Exposure | Cases, *n/N* (%)[a] | FoodNet population survey (%)[b] | *P* value |
|---|---|---|---|
| Pork | 59/80 (73.8) | 43.2 | <0.001 |
| Pig roast attendance | 17/73 (23.3) | NA | |
| Ground beef | 18/80 (22.5) | 39.8 | <0.001 |
| Live pigs | 5/61 (8.2) | 0.9 | <0.001 |

[a] Consumption or exposure in the 7 days before illness onset.

[b] Foodborne Diseases Active Surveillance Network (FoodNet) Population Survey Atlas of Exposures, 2006 to 2007 (7). NA, not applicable.