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An investigation of an outbreak of *Salmonella* Typhimurium infections linked to cantaloupe – United States, 2022

Sharon Seelman Federman[a,*], **Erin Jenkins**[a], **Cullen Wilson**[b], **Arturo DeLaGarza**[c], **Colin Schwensohn**[d], **Benjamin Schneider**[d], **Johnson Nsubuga**[a], **Robert Literman**[a], **Allison Wellman**[a], **Brooke M. Whitney**[a], **Rebecca L. Bell**[a], **Kerri Harris-Garner**[a], **Crystal McKenna**[a], **Darcy Brillhart**[e], **Merri Cross**[f], **Kurt Rueber**[f], **Thao Schlichte**[f], **Kemi Oni**[g], **Jennifer Adams**[h], **Alvin J. Crosby**[a], **Michael C. Bazaco**[a], **Laura Gieraltowski**[d], **Kurt Nolte**[a], **Stelios Viazis**[a]

[a]Center for Food Safety and Applied Nutrition, Food and Drug Administration, College Park, MD, USA

[b]Office of Regulatory Affairs, Food and Drug Administration, Portland, ME, USA

[c]Office of Regulatory Affairs, Food and Drug Administration, Brownsville, TX, USA

[d]Centers for Disease Control and Prevention, Atlanta, GA, USA

[e]Office of Regulatory Affairs, Food and Drug Administration, Atlanta, GA, USA

[f]Iowa Department of Inspections, Appeals, and Licensing, Des Moines, IA, USA

[g]Iowa Department of Health and Human Services, Des Moines, IA, USA

[h]Association of Public Health Laboratories, Silver Spring, MD, USA

Abstract

[*]Corresponding author. Sharon.Seelman@fda.hhs.gov (S. Seelman Federman).

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

CRediT authorship contribution statement

Sharon Seelman Federman: Writing – review & editing, Writing – original draft, Visualization, Validation, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Erin Jenkins:** Writing – review & editing, Writing – original draft, Visualization, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Cullen Wilson:** Writing – review & editing, Writing – original draft, Investigation. **Arturo DeLaGarza:** Writing – review & editing, Writing – original draft, Investigation. **Colin Schwensohn:** Writing – review & editing, Writing – original draft, Visualization, Validation, Methodology, Investigation, Data curation. **Benjamin Schneider:** Writing – review & editing, Writing – original draft, Visualization, Investigation. **Johnson Nsubuga:** Writing – review & editing, Writing – original draft, Investigation. **Robert Literman:** Writing – review & editing, Writing – original draft, Visualization, Investigation, Conceptualization. **Allison Wellman:** Writing – review & editing, Writing – original draft, Investigation, Conceptualization. **Brooke M. Whitney:** Writing – review & editing, Writing – original draft, Investigation. **Rebecca L. Bell:** Writing – review & editing, Writing – original draft. **Kerri Harris-Garner:** Writing – review & editing, Investigation. **Crystal McKenna:** Writing – review & editing, Investigation, Conceptualization. **Darcy Brillhart:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Formal analysis, Data curation. **Merri Cross:** Writing – review & editing, Investigation. **Kurt Rueber:** Writing – review & editing, Writing – original draft, Investigation. **Thao Schlichte:** Writing – review & editing, Investigation. **Kemi Oni:** Writing – review & editing, Investigation. **Jennifer Adams:** Writing – review & editing, Investigation. **Alvin J. Crosby:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Investigation. **Michael C. Bazaco:** Writing – review & editing, Writing – original draft, Visualization, Formal analysis, Data curation, Conceptualization. **Laura Gieraltowski:** Writing – review & editing, Writing – original draft, Visualization, Investigation. **Kurt Nolte:** Writing – review & editing, Writing – original draft, Investigation. **Stelios Viazis:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Conceptualization.

In 2022, the Food and Drug Administration (FDA), the Centers for Disease Control and Prevention (CDC), and state health and regulatory partners investigated an outbreak of *Salmonella enterica* serovar Typhimurium infections linked to cantaloupes from southwest Indiana, resulting in 87 ill persons and 32 hospitalizations reported in 11 states. Epidemiologic and traceback evidence confirmed cantaloupe as the vehicle for these infections. Based on records collected by FDA, traceback of cantaloupe exposures for 14 ill people converged on a packing house in southwest Indiana, which supplied cantaloupe to eight of the 11 points of service where ill people purchased cantaloupe. *Salmonella* isolates were recovered from environmental samples collected by FDA from three growers and a packing house in southwest Indiana. Whole genome sequencing analyses of these isolates found that isolates collected from one grower matched the *Salmonella* Typhimurium outbreak strain, and samples collected from the other two growers and the packing house matched a 2020 *Salmonella* Newport outbreak strain. State and federal public health and agricultural partners identified potential conditions and practices that could have possibly resulted in the contamination of cantaloupe, including the presence of *Salmonella* spp. in on-farm, post-harvest, and off-farm environments. This is the third outbreak of salmonellosis confirmed to be linked to melons, sourced from southwest Indiana in the last decade. The 2012, 2020, and 2022 outbreaks of reoccurring and persisting strains of *Salmonella* illustrate the need for additional efforts to determine the source and extent of environmental contamination in the melon growing region of southwest Indiana and for outreach and education to help promote practices to reduce contamination of melons.

Keywords

Outbreak investigation; Contamination; Foodborne illness outbreaks; Traceback

1. Introduction

In the United States, *Salmonella* infections have been increasingly linked to melons (U.S. Centers for Disease Control and Prevention, 2002; Walsh, Bennett, Mahovic, & Gould, 2014). The United States is one of the world's leading consumers of melons and approximately 60% of melon consumption in the United States is produced domestically USDA ERS, 2021 As of 2020, the state of Indiana ranked sixth in total volume of cantaloupe grown domestically (Guan et al., 2020a; Guan et al., 2020b).

In 2022, the U.S. Food and Drug Administration (FDA), the Centers for Disease Control and Prevention (CDC), state, local health and regulatory partners investigated an outbreak of *Salmonella enterica* serovar Typhimurium infections linked to cantaloupe from southwest Indiana, resulting in 87 illnesses and 32 hospitalizations across 11 states. Preliminary findings from this investigation have been previously reported elsewhere (Schwensohn, 2024; U.S. Food and Drug Administration, 2023). Melons from this region of Indiana have been linked to recurring outbreaks of salmonellosis. In 2012, the FDA, CDC, and state health and regulatory partners investigated an outbreak of *Salmonella* Typhimurium and *Salmonella* Newport infections linked to cantaloupe grown in southwest Indiana (U.S. Food and Drug Administration, 2013b). In 2020, there was an investigation of an outbreak of *Salmonella* Newport infections linked to melons from southwest Indiana (Jenkins et al.,

2023). Here, we report the details of this 2022 investigation with a focus on the traceback analysis that determined the source of the contaminated cantaloupes and the laboratory findings that helped support public health actions.

2. MATERIALS and METHODS

2.1. Outbreak detection and epidemiologic investigation

For this outbreak, a case-patient was defined as an ill person with illness onset date from July 7, 2022 to September 11, 2022, and a laboratory-confirmed infection with *Salmonella* Typhimurium that is genetically related to the outbreak strain within a 0 to 10 allele difference by core genome multilocus sequence typing (cgMLST). Local and state public health partners interviewed case-patients using routine enteric disease questionnaires and/or a focused questionnaire specifically developed to collect details about melon exposures (i.e., purchase dates and locations, melon types and varieties) due to the history of this *Salmonella* strain. Food exposures reported by ill people were compared using a standard binomial model with responses from healthy people previously interviewed as part of the 2018–2019 FoodNet Population Survey (U.S. Centers for Disease Control and Prevention, 2022).

2.2. Traceback investigation

A traceback investigation was initiated for cantaloupe and watermelon as per standard FDA traceback practices to determine convergence within the supply chain (Council to Improve Foodborne Outbreak Response, 2014; Irvin et al., 2021).

2.3. Farm inspections

Based on the convergence noted in the cantaloupe traceback investigation, the FDA and state partners visited Packing House R and Growers V, W, and X located in southwest Indiana that supplied product to this packing house to collect records, product, and environmental samples, as described by Jenkins et al. (2003), and conducted detailed interviews with key farm representatives.

2.4. Laboratory investigation

Clinical isolates.—Clinical samples from ill people were cultured for *Salmonella*, serotyped, and subtyped by whole genome sequencing (WGS) at state public health laboratories using standard methods (Hassan et al., 2019; Hassan et al., 2017).

FDA and State samples.—State and FDA laboratories used the FDA *Bacteriological Analytical Manual* method to isolate *Salmonella* spp. (Andrews, Jacobson, Ge, Zhang, & Hammack, 2021) from environmental and water samples (Mull & Hill, 2009), using grab and dead-end ultrafiltration (DEUF) methods (Mull & Hill, 2012), cantaloupe and watermelon product samples collected by investigators at various points of distribution, including points of service (POS), distribution centers, packing houses, farms and public access sites (McClure et al., 2023).

After whole genome sequencing (WGS), single nucleotide polymorphisms (SNPs) were identified using the reference-based CFSAN SNP Pipeline Davis et al., 2015and

phylogenetic analyses of these data was performed using GARLI (Zwickl, 2006) to characterize the isolates and compare them to clinical isolates as well as historical environmental and product sample isolates (Andrews et al., 2021; Crowe et al., 2017). Based on the pairwise SNP distance among samples along with the statistical robustness of the phylogenetic inference, isolate comparisons can result in one of three possible designations (Pightling et al., 2018). Isolates that form a well-supported phylogenetic group with limited SNP differences are called a 'match' indicating a high probability of a recent common source, while isolates that cluster into separate, well-supported clades with larger SNP distances are designated as 'not a match'. When SNP distances are intermediate and/or tree topology is largely unresolved, unless there is a compelling reason to consider the isolates as a single diverse strain (e.g., isolates fall into the same SNP cluster at the NCBI Pathogen Database), these relationships are designated as 'inconclusive'.

3. Results

3.1. Epidemiologic investigation

A total of 87 illnesses were reported to CDC from 11 states (Fig. 1) (Schwensohn, 2024). Of 72 ill people with information available, 32 were hospitalized and no deaths were reported. *Salmonella* Typhimurium isolates were highly genetically related by cgMLST, within 0–10 allele differences. Illness onset dates, which are self-reported, ranged from July 7 to September 11, 2022 (Fig. 2). Ill people ranged in age from less than one to 93 years (median 65) and 58 of the 87 (67%) were female. Overall, 47 ill people were interviewed with the melon focused questionnaire and provided information on melon consumption in the seven days prior to illness onset. Among these 47 ill people, 42 (89%) consumed any melons, 36 (77%) consumed cantaloupe and 23 (49%) consumed watermelon. A total of 17 people reported consuming both types of melons, while 19 reported only cantaloupe and six reported only watermelon. Only cantaloupe consumption was reported significantly more frequently by ill people when compared to healthy people in the FoodNet Population Survey (77% vs. 29%, $P < 0.0005$) (U.S. Centers for Disease Control and Prevention, 2022). Cantaloupes were purchased at farm stands (n = 18), farmers' markets (n = 6), retail locations (n = 10), and the location was unknown for two purchases.

3.2. Traceback investigation

FDA, Iowa Department of Inspections, Appeals, and Licensing (DIAL), and Indiana Department of Health (IDOH) conducted a traceback for cantaloupe and watermelon, which included farmer's markets, roadside stands, and retail locations in Iowa and Indiana (Fig. 3).

Cantaloupe traceback was conducted on 14 purchases from 11 roadside stands, farmers markets or retail locations between late June 2022 through early August 2022. Traceback information was collected from 16 firms throughout the supply chain for these 11 roadside or retail operations. Of the 11 POS, eight were roadside stands or stands located within a larger farmers market. At least one of these POS operated roadside stands at multiple locations. Operators of roadside stands also sold product at larger farmers markets. State partners determined the hours of operation of the stands and farmers markets, to attempt to collect traceback records available. There was no convergence to a single cantaloupe

shipment or lot. Broker Q/Packing House R was a common source of cantaloupe purchased for eight of the 11 POS. Broker Q/Packing House R received product solely from three farms located in southwest Indiana during the timeframe of interest.

Traceback analysis was also conducted for watermelon purchased by seven ill people; only one of these ill people reported purchasing only whole fresh watermelon and the other six ill people also reported purchasing cantaloupes. The ill person that reported only watermelon consumption, purchased their watermelon from a retail location that may have been supplied by a farm (Supplier K) that also sold cantaloupe from Broker Q/Packing House R. Broker Q/Packing House R did not supply any watermelon to any retail locations during our timeframe of interest. The collected traceback information led to at least 24 different farms in Missouri, Kentucky, Iowa, Indiana, Georgia, and Mexico. Of these seven purchases of whole fresh watermelon from six different POS, no convergence to a distributor or harvest source was identified. Records were not collected from firms that did not supply multiple points in the supply chain.

3.3. Inspectional findings

Investigators were unable to observe the practices used to grow and manage cantaloupes produced by Growers X, V, and W and packed by Packing House R because operations had completed for the season approximately one week prior to the initiation of inspections. Information was collected through detailed interviews with key farm representatives, review of records and observations of fields, buildings, and equipment. A summary of these finding appears in Table 1.

3.3.1. Packing house R—Cantaloupes were transported from field to packing house via bulk trailers. Packing House R cleaned and removed physical debris from equipment surfaces that were subsequently rinsed. According to Packing House R protocols, visibly clean surfaces were swabbed by Packing House R employees with adenosine triphosphate (ATP) tests to determine cleaning efficacy, and a cleaning product (intended to assist in produce washing) was applied to surfaces with no rinse. An overhead spray system containing sodium chlorite was used to wash cantaloupes with brush rollers, after which they were graded and hand-packed into single-use corrugated boxes. Boxed cantaloupes were held at ambient temperatures in Packing House R and generally shipped the same day or within 48 h of packing. Packing House R maintained traceability documents of grower level information. Shipment occurred in temperature-controlled transport trailers.

3.4. Farm inspections

All fields were in the same general area in southwest Indiana, with nearby agricultural industry including three turkey feeding operations 1–6 miles from the growing locations. As noted in Table 1, two growers had verbal agreements that the leased land would not have biological soil amendments of animal origin (BSAAO) applied during the non-cantaloupe growing season. Grower V reported one of their leased fields did have BSAAO; untreated turkey manure was applied every two to two and a half years when cantaloupe was not being grown and under different management. This manure was provided by a third-party supplier

who also transported and managed broadcast applications to fields, however, specific details about the manure and its application were not available.

Observations of the area surrounding Grower W included a drainage ditch at the southeast border of the field in question. Grower W reported that flooding did not impact ground preparation and spring planting of cantaloupe nor the growth and harvest of the crop. Investigators did not detect sources or routes of potential water runoff from adjacent fields.

All three growers used their own dedicated wells for drip irrigation of the plants in the fields. Although well water was not available for sampling by the FDA during the time of the investigation, each grower reported different approaches to water sampling, as outlined in Table 1, but none tested for *Salmonella* spp. One of the growers, Grower W, reported cantaloupe transplanting occurred on May 1st and continued through the first week of June using a water wheel transplanter to manually transplant cantaloupe seedlings through plastic mulch into soil. Grower X indicated they prepared the cantaloupe field for planting in fall 2021 by a deep ripping operation followed by field cultivation and planting bed establishment during spring 2022.

Growers X, W, and V used contracted harvesters to harvest cantaloupe melons multiple times during the growing season, based on fruit maturity. Harvested melons were transported in open bulk trailers to Packing House R. Standardized transport equipment cleaning and sanitizing procedures were utilized (U.S. Food and Drug Administration, 2023).

3.5. Laboratory investigation

Table 2 outlines the FDA samples analyzed as part of this outbreak investigation. FDA collected two cantaloupes, and one watermelon sample during a records and sample collection assignment at Distributor N that were negative for *Salmonella* spp.

FDA, accompanied by IDOH officials, collected a total of 15 environmental samples at the farms investigated as well as from adjacent public land. Seven environmental samples yielded *Salmonella* isolates of various serotypes. A drag swab sample collected from Grower W yielded an isolate of *Salmonella* Typhimurium. A drag swab sample collected from Grower V, swabs collected from Packing House R packing line, and a drag swab sample collected from Grower X yielded isolates of *Salmonella* Newport. FDA investigators also collected three samples, one soil and two DEUF, which recovered multiple serovars of *Salmonella*, at public access sites along two water drainage conduits in the general vicinity of the farming and packing operations to assess potential human pathogen, presence, movement, and persistence in the environment.

IDOH collected a total of 30 watermelon and cantaloupe samples from Packing House R, POS G Farm Stand retail bin, POS F Farm Stand retail bin, and two additional growers not included in the FDA traceback investigation, all located in Indiana. DIAL collected a total of 54 melon samples, including Athena cantaloupe, and other types of cantaloupe, honeydew melons, musk melon, and watermelons from roadside produce stands, growing locations, a national retail chain, a local, independent supermarket, and farmers markets in Iowa. All samples were negative for *Salmonella* spp.

3.6. Whole genome sequencing analysis

The relationships between the isolates collected from farming operations during this investigation and isolates from the National Center for Biotechnology Information (NCBI) Pathogen Detection database are shown in Fig. 4. A general spatial distribution of farm investigation locations is shown in Fig. 5.

Based on genetic similarity, isolates collected from Grower W (FDA sample #1148254) were all classified into a single *Salmonella* Typhimurium grouping in the NCBI Pathogen Detection database (Fig. 4). WGS analysis using the CFSAN SNP Pipeline revealed these isolates represent a single strain matching the present outbreak strain, including 100 clinical isolates collected in 2022 and 103 clinical isolates collected between 2011 and 2021 indicating that this strain is pathogenic (Fig. 4). The isolates collected from Grower W also match (1) one 2013 isolate sampled from a cantaloupe grown by Grower W (FDA sample #789136), (2) two 2020 isolates from a southwest Indiana soil subsample from the same region (FDA sample #1131058) (Jenkins et al., 2023), (3) three 2016 isolates collected in Indiana during third party sampling of ground turkey products, and (4) one 2022 isolate collected from an Indiana turkey cecum (Food Safety and Inspection Service (FSIS) sample #12218280) (Fig. 4). Isolates from this strain varied by 0–26 SNPs (Mean SNP Distance: 9.5 SNPs).

Based on genetic similarity, isolates collected from Grower X (FDA sample #1172990), Grower V (FDA sample #1148694), and Packing House R (FDA sample #1154912) were classified into a single *S*. Newport grouping in the NCBI Pathogen Detection database (Fig. 4). WGS analysis using the FDA CFSAN SNP Pipeline revealed these isolates represent a single strain matching the 2020 *S*.. Newport outbreak linked to melons grown in the same region of southwest Indiana (Jenkins et al., 2023), including 87 clinical isolates collected in 2020, 30 clinical isolates collected between 2012 and 2019, and 26 clinical isolates collected in 2021 and 2022 indicating that this strain is also pathogenic (Fig. 4). These isolates also match six isolates collected as part of a 2016 investigation of Missouri turkey operations (FDA sample #911752, #911762; Fig. 4). Isolates from this strain varied by 0–25 SNPs (Mean SNP Distance: 10.6 SNPs).

A soil sample (FDA sample #1148696) collected at a drainage ditch embankment location resulted in the recovery of 18 *Salmonella* Newport isolates, none of which matched any isolates in the NCBI Pathogen database. Drainage water samples resulted in the recovery of multiple *Salmonella* serovars, including *Salmonella* Hartford, *Salmonella* Agbeni, *S*. I 4:b:, *Salmonella* Paratyphi B var. L (+) tartrate+, *Salmonella* Anatum, and *Salmonella* Berta. One water sample (FDA sample #1200081) resulted in the recovery of four *Salmonella* isolates that matched a 2020 Indiana human clinical isolate (SNP Distance Range: 0–8 SNPs; Mean SNP Distance: 2.67 SNPs). Two water samples collected from water drainage systems 4.5 miles apart resulted in 18 and 15 isolates (FDA sample #1200081; FDA sample #1200082, respectively), and several isolates matched each other (0 SNPs). These matching isolates fell into a SNP cluster containing 10 poultry-derived isolates recovered from Indiana in 2016, but these isolates were designated as ‘not a match’ based on SNP distance (0–41 SNPs). None of the isolates recovered from water drainage corridors clustered with isolates recovered from Growers V, W, and X, or the Packing House R.

3.7. Investigational outcomes

Growers V, W, X and Packing House R provided FDA with corrective actions they planned to take in response to observations noted during the inspection. Public communications were not issued at the time of the outbreak investigation since implicated cantaloupes were no longer available to consumers because any product that had entered commerce was past its shelf-life.

4. Discussion

4.1. Impact and significance

We present an outbreak investigation linking cases of salmonellosis to the consumption of cantaloupes grown in southwest Indiana. This was the third outbreak of salmonellosis investigated by the FDA confirmed to be linked to whole cantaloupe, or watermelons grown in this region (Jenkins et al., 2023; U.S. Food and Drug Administration, 2013b). In 2012 there was an outbreak of *S.* Typhimurium and *S.* Newport infections linked to cantaloupe and in 2020 there was an outbreak of *S.* Newport infections linked to melons grown in southwest Indiana. The 2012 outbreak strain was isolated from cantaloupe grown at a farm in southwest Indiana identified through the traceback investigation confirming cantaloupe was the vehicle and the farm was the source of the outbreak. In 2020 the outbreak was linked by traceback and epidemiology to a different farm in southwest Indiana however none of FDA's samples yielded the 2020 outbreak strain and it was not possible to delineate whether the outbreak vehicle was cantaloupe, watermelon, or both. In the 2022 outbreak, the traceback investigation for cantaloupe converged on a single packing house, which sourced cantaloupe from three different growers. The traceback investigation of watermelons did not result in convergence of a common firm. A common limitation for all three on-farm investigations was that they were conducted after growing, harvesting, and post-harvest activities had ceased, thus limiting direct observations of these processes. All three outbreaks are linked to melons from southwest Indiana, but they were traced to melons grown on different farms.

4.2. Epidemiologic and traceback challenges

Many of the challenges that investigators encountered during the traceback investigation were similar to those encountered in past produce-associated outbreaks (Irvin et al., 2021; McClure et al., 2023; Whitney et al., 2021). Several cases reported consuming watermelon in addition to cantaloupe during the seven days prior to illness onset. In addition, depending on storage method, whole melons may have a longer shelf-life than other produce so not knowing how consumers stored the melons made it challenging to determine a suspected purchase, with multiple exposures. One of the most notable challenges was collecting information from roadside stands. There were significant delays in traceback record collection that posed a challenge to investigators. With many cases reporting purchasing products from roadside stands, state partners were only able to obtain information during limited or irregular hours of operations for the stands. The name of the roadside stand was often not the name on bulk shipments or customer list from the supplier. Many times, the suppliers' traceability records were associated with a name of an individual instead of the name of the roadside stand from where the consumer reported purchasing the melons. There

were discrepancies in record keeping at the farm stand level, as receipts were not saved from purchases by the consumers or at the farm stand level and credit card purchase information was not available. Typically, in an investigation, electronic purchase information provides a defined timeline and description of product (Irvin et al., 2021). If available, many documents in this traceback were handwritten, with very limited information, or without information to assist with narrowing shipments further back in the supply chain. With the farm stands keeping a low inventory, product was comingled with other shipments. In several cases, ill people could not remember the exact address of the roadside stand or vendor they purchased melons from but rather reported purchasing from a stand in a town or on a road, where multiple stands were located, and thus investigators could not trace that purchase. Several ill people reported purchasing melons from a large farmers market where several vendors were selling melons, but without the name of the vendor, investigators were unable to trace these purchases. In addition, auction houses supplied melons early in the season to some of the locations in the traceback. For these auction houses, if the receipt with vendor number information was not available, the records for the transaction, including supplier name, were unavailable.

Diligence in record collection and analysis overcame enough of these challenges that FDA and state partners were able to gather and analyze sufficient useful data from each of the POS selected and identify a supply chain convergence regarding the source of the cantaloupe. However, record collection was time consuming. The food industry at large could benefit from improved traceability by digitization, interoperability, and standardization of traceability records. This would expedite traceback investigations and help to remove contaminated product from the marketplace more quickly, thus preventing further illnesses. This is not only important for growers, but also critical for shippers, manufacturers, and retailers as well, which would lead to improved overall traceability throughout the supply chain. Information and support for enhanced traceability at all levels in the supply chain can be found in the FDA Traceability Rule and New Era Initiatives (U.S. Food and Drug Administration, 2021a, 2021b, 2022).

4.3. Investigational findings

In the present investigation, several *Salmonella* strains were recovered, and isolates sampled from the farms and facilities clustered into two groupings. WGS analysis revealed that isolates from Grower W matched the present *Salmonella* Typhimurium outbreak strain (Fig. 4), indicating that these are the type of *Salmonella* capable of causing salmonellosis in humans, and are therefore of public health concern. In addition to clinical matches, the isolates from Grower W also matched environmental isolates, all recovered from Indiana, including a 2013 isolate sampled from a cantaloupe grown by Grower W and two isolates recovered from Indiana soil drag swabs collected as part of a 2020 investigation related to melons grown in southwest Indiana (Jenkins et al., 2023). Together, these findings suggest that this strain has been present in the region for the better part of a decade. The isolates also matched four isolates linked to Indiana turkey operations, including three 2016 isolates collected by a third-party lab and a 2022 isolate collected by FSIS from the digestive tract of an Indiana turkey. The geographic clustering of these related isolates suggests that these strains are endemic to southwest Indiana. As a result, CDC has designated the two strains

of *S*. Newport and *S*. Typhimurium as reoccurring, emerging, and persisting (REP) enteric bacterial strains (U.S. Centers for Disease Control and Prevention, 2023).

The second cluster is a grouping of *Salmonella* Newport isolates that includes the isolates recovered from Growers X, V, and Packing House R (Fig. 4), and these isolates fall into a much larger NCBI SNP cluster, which at the time of this writing contains 3423 isolates (3304 clinical isolates; Accessed September 29, 2023). Based on geographic metadata, the tree includes isolates from a wide geographic area of the United States. WGS analysis revealed that isolates from this investigation match clinical isolates associated with a 2020 *S*. Newport outbreak linked to melons grown in the same region of Indiana (Jenkins et al., 2023), as well as isolates associated with a 2016 investigation into turkey operations in Missouri.

In addition to uncovering the vehicle of the outbreak, this investigation also identified the presence of multiple strains of *Salmonella* at farms and in the environment. Some of these strains have been found in the region repeatedly over the course of years, while others are associated with historical multistate outbreaks. These strains are considered widespread in the environment in this region, and therefore it is important to understand how they become outbreak strains. Research into agricultural practices in the area that minimize the contamination of cantaloupe from soil that is contaminated will be helpful to produce growers in the region. Beyond contamination, it may be important to understand how conditions and practices during packing, transportation, and retail as well as conditions at roadside stands and practices that damage fruit, may impact the survival and proliferation of *Salmonella*.

While the investigation did not identify a specific source or route that resulted in the microbial contamination of cantaloupes linked to this outbreak, certain conditions and practices were identified that could have resulted in contamination, including the presence of *Salmonella* spp. in on-farm, post-harvest, and off-farm environments. The farms investigated were not under consistent management or control by cantaloupe growers since they were leased out to various subcontractors and, as a result, it was not possible to fully determine and evaluate a complete profile of land use hazards. This suggested that the cantaloupe farms did not routinely monitor for potential food safety hazards that may have been introduced into the fields outside of cantaloupe growing seasons, including the applications of untreated turkey manure to land later used to grow cantaloupe. WGS analysis showed that *Salmonella* isolates collected from all farms and the associated packing house were genetically related both to multistate outbreaks of salmonellosis associated with melons as well as poultry-related isolates. Poultry manure is a known reservoir for *Salmonella* spp. Proper application of manure that has been treated with a validated process to reduce pathogens can significantly reduce the potential for the integration of *Salmonella* or other human pathogens into soils (Bardsley et al., 2021; Murphy et al., 2022; U.S. Food and Drug Administration, 2020). It is possible that the outputs from poultry operations, such as untreated poultry manure, or manure that has not been adequately processed (e.g. composted to completion), may have played a significant role contributing to cantaloupe contamination (U.S. Food and Drug Administration, 2023). Additionally, during post-harvest melon operations, Packing House R applied an antimicrobial chemical in a single-pass wash water

system while cantaloupe fruit passed over a series of rotating brush rollers. *Salmonella* Newport was recovered from one brush roller during the inspection of Packing House R, which supports the hypothesis that cleaning procedures practiced by the firm were not adequate to limit cross-contamination at the post-harvest level. Despite conducting cleaning and sanitizing procedures after the last run of cantaloupe for the season, *Salmonella* Newport persisted on a brush roller more than one week later. Investigators determined that the brush rollers and other food contact surfaces of the packing line were not being effectively cleaned and sanitized. The chemical that Packing House R management reported to be applied to these surfaces did not have an EPA-approved label as a food contact surface sanitizer, but instead was labeled for cleaning fruits and vegetables. Use of the fruits and vegetables cleaner in this manner was also inconsistent with their written sanitation Standard Operating Procedures (SOPs). While packing line cleaning practices followed SOPs, they involved surface application of a foam cleaner that appeared to be ineffective in cleaning between brush roller bristles. The presence of *Salmonella* Newport on a brush roller following cleaning and sanitizing protocols suggests that cross-contamination of fruit was a possible outcome of the cantaloupe washing process. Brush rollers can be difficult to clean and sanitize effectively due to their dense composition, numerous bristles, and high surface area (Nyarko et al., 2018; Ruiz-Llacsahuanga, Hamilton, Zaches, Hanrahan, & Critzer, 2021). Additional research is needed to identify best practices for reduction of cross-contamination during cantaloupe washing, and effective cleaning and sanitizing procedures of brush rollers.

4.4. Potential foodborne pathogen reservoirs

During this investigation, the recovery of multiple *Salmonella* serovars within the immediate growing and non-growing environments suggests that these pathogens may have originated from a diverse assortment of reservoirs within the growing region. Southwestern Indiana grows melons and vegetable crops interspersed amongst grain, oilseed, dry bean, and dry pea crops (C. Mayen, 2005; United States Department of Agriculture, 1998). Additionally, the region is known to have a robust poultry industry, with the state ranking first in the United States for duck production, second in table chicken egg production, and fourth in turkey production (Jenkins et al., 2023; C. D. Mayen & McNamara, 2006; Wickenhauser, Brennan, Erasmus, Karcher, & Karcher, 2021). A 2012 outbreak investigation linked to cantaloupe from the same region in southwest Indiana led to an environmental assessment that recovered the outbreak strain, in addition to other *Salmonella* spp. Isolates, from environmental samples collected at the packing house and cantaloupe and environmental (mostly soil) samples collected from the field (U.S. Food and Drug Administration, 2013a). Similarly in this investigation, matching *Salmonella* Newport isolates were recovered from Grower V and X as well as the cantaloupe post-harvest Packing House R, demonstrating the highly complex environmental survival, proliferation, and transport mechanisms which can challenge food safety mitigation practices. Additionally, *Salmonella* Typhimurium isolates recovered from Grower W were a match by WGS analysis to environmental samples collected as part of a 2020 outbreak investigation in the same region (Jenkins et al., 2023), providing evidence that common contamination sources and resident *Salmonella* serovars could be actively present within this growing environment.

It has been well established that fecal matter from domesticated animals and wildlife can contaminate produce with *Salmonella* spp. (Hanning, Nutt, & Ricke, 2009), with similar findings reported in other past outbreak investigations from produce-growing regions in the United States where animal operations significantly overlap with produce growing operations (Angelo et al., 2015; Bottichio et al., 2020; Gu et al., 2018). In addition to isolates related to two separate multi-state outbreaks, the isolates collected from the growers and Packing House R were also genetically related to isolates associated with investigations of regional poultry operations, suggesting that the proximity between the poultry farms and agricultural fields in this region and the potential transportation of poultry litter to farmland around the region, may have contributed to the repeated outbreaks. The exact movement of pathogens through the environment is unknown, but water movement from weather events could have potentially played a role. For example, widespread precipitation during spring 2022 prompted the Indiana Department of Environmental Management, Confined Feeding Operations Program to aid confined animal feeding operations and concentrated animal feeding operations in appropriate guidance for storage or land application of manure. Media outlets reported heavy rains between July 23, 2022, and July 29, 2022, which resulted in power outages, road and bridge damage, road closures, and flooding in the growing area National Weather Service, 2022 To determine the potential impact and significance of the proximity, focused and longitudinal regional studies are required to determine the magnitude and mechanisms underlying any potential increased risk. Additionally, research into the potential for pathogenic growth during packing, shipping, storage, and under retail conditions could be helpful to determine practical prevention strategies for the industry at large. Growers in the area should assess risks that may be posed by adjacent and nearby land use, including applications of biological soil amendments, especially as it relates to the presence of livestock, including poultry, and the interface between farmland, and other agricultural areas. Additional tools such as pre-harvest and/or post-harvest risk assessments may help inform specific prevention measures to consider. A more thorough list of recommendations and requirements applicable to firms, such as growers of melons and similar produce, can be found in the associated 2023 Outbreak Investigation Report released by FDA (U.S. Food and Drug Administration, 2023). Melon growers that are subject to the Produce Safety Rule must comply, as appropriate (U.S. Food and Drug Administration, 2020).

5. Conclusions

Several factors, which potentially contributed to the contamination of cantaloupe melons grown in the southwest Indiana region were noted in this investigation. The traceback investigation played an important role in identifying Growers V, W, and X that provided cantaloupes to Packing House R, leading to a thorough on-farm investigation and the collection of environmental and product samples. WGS analysis revealed that isolates recovered from Grower W were a match to the outbreak strain of *Salmonella* Typhimurium. Additionally, several other samples collected in farming and packing operations, and at off-farm locations were positive for *Salmonella*, with isolates primarily consisting of *Salmonella* Newport, along with other *Salmonella* serovars, with some matching historical multistate outbreaks, confirming the accuracy of the traceback investigation. The investigation did

not result in the identification of a specific microbial source or route at the identified growers or packinghouses that resulted in the contamination of cantaloupes associated with this outbreak. However, state, and federal public health and agricultural partners identified conditions and practices that could result in contamination, including the presence of *Salmonella* spp. in on-farm, post-harvest, and off-farm environments. Additional resources and initiatives are necessary to help identify sources and routes of contamination of melons in the region as well as research aimed at identifying agricultural practices that can help prevent contamination. These strains are widespread in the region, and it is important to understand how they become outbreak strains.

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Disclaimer

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention and the US Food and Drug Administration.

Data availability

Data will be made available on request.

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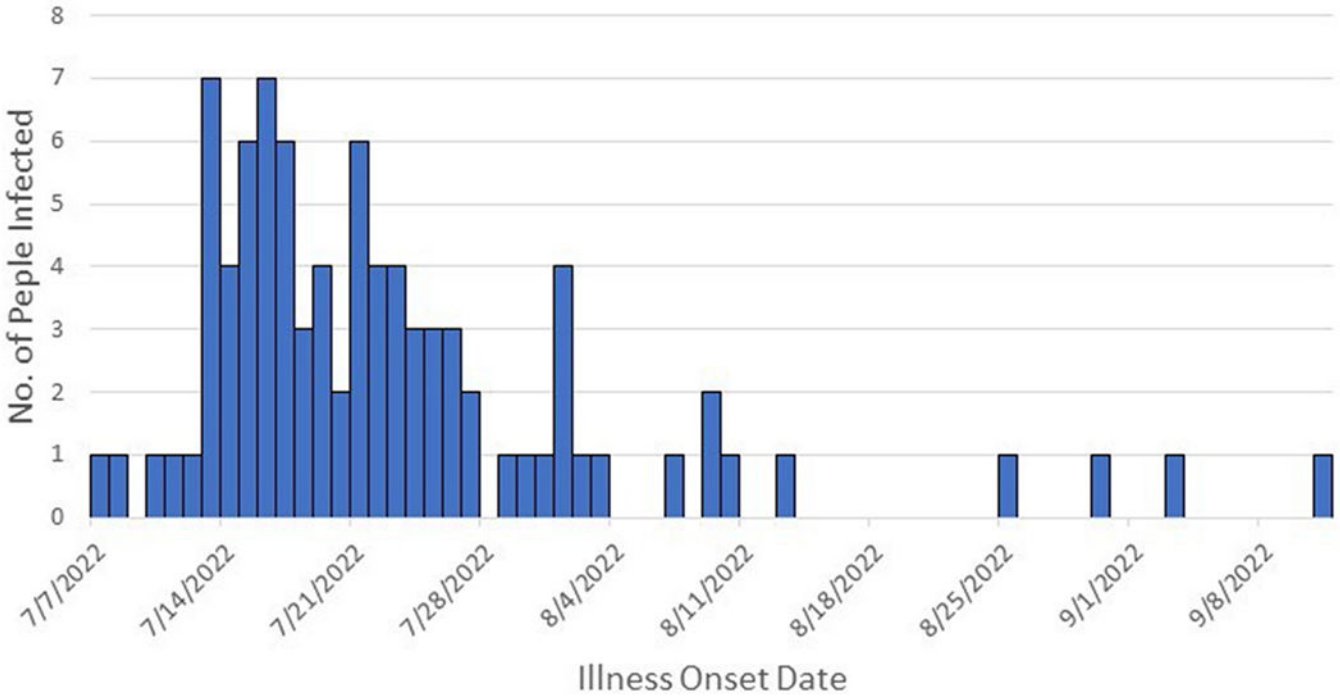

Fig. 1.

People infected with the outbreak strain of *Salmonella* Typhimurium, by date of illness onset, July 7 to September 11, 2022, 2022 (n = 87).

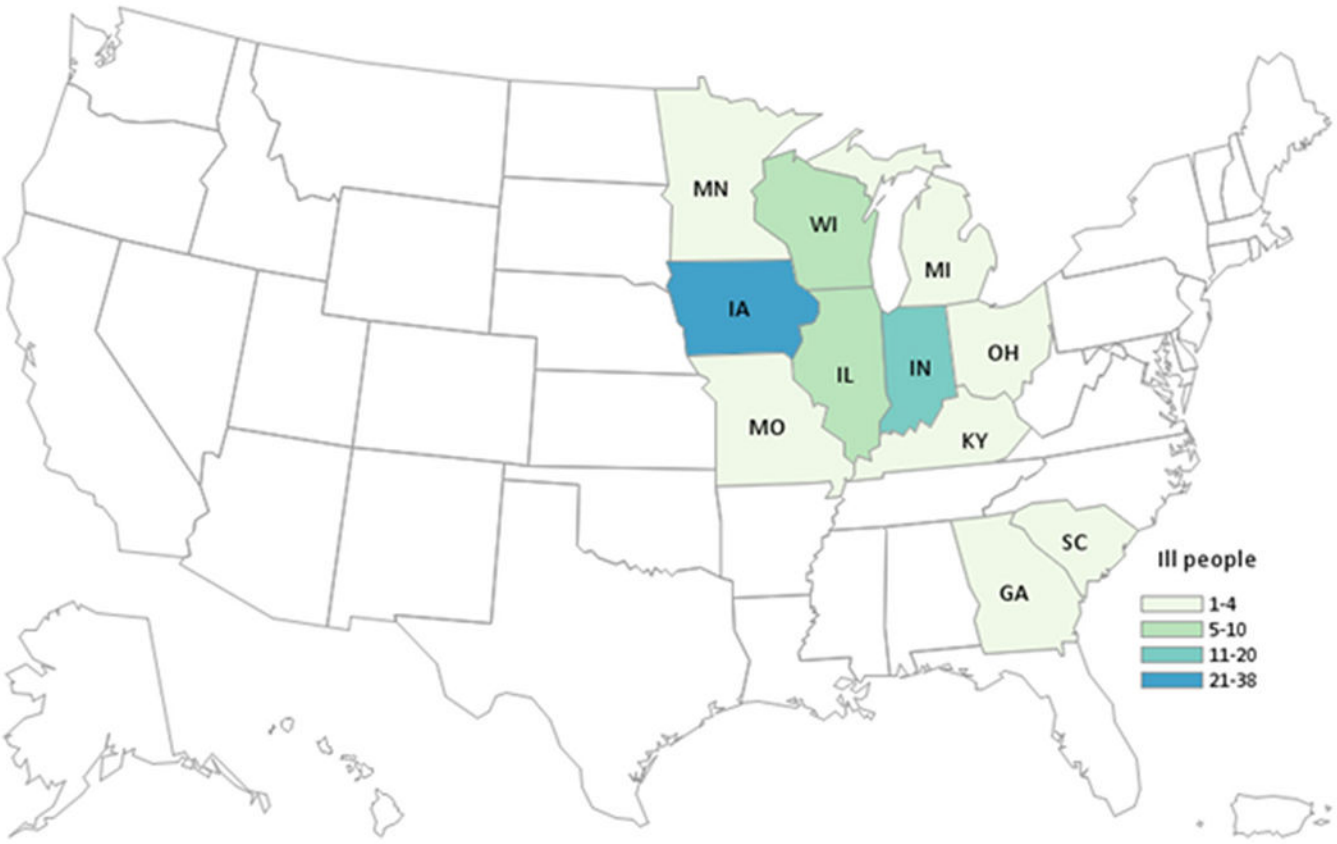

Fig. 2.

People infected with the outbreak strain of *Salmonella* Typhimurium, by state of residence (n = 87).

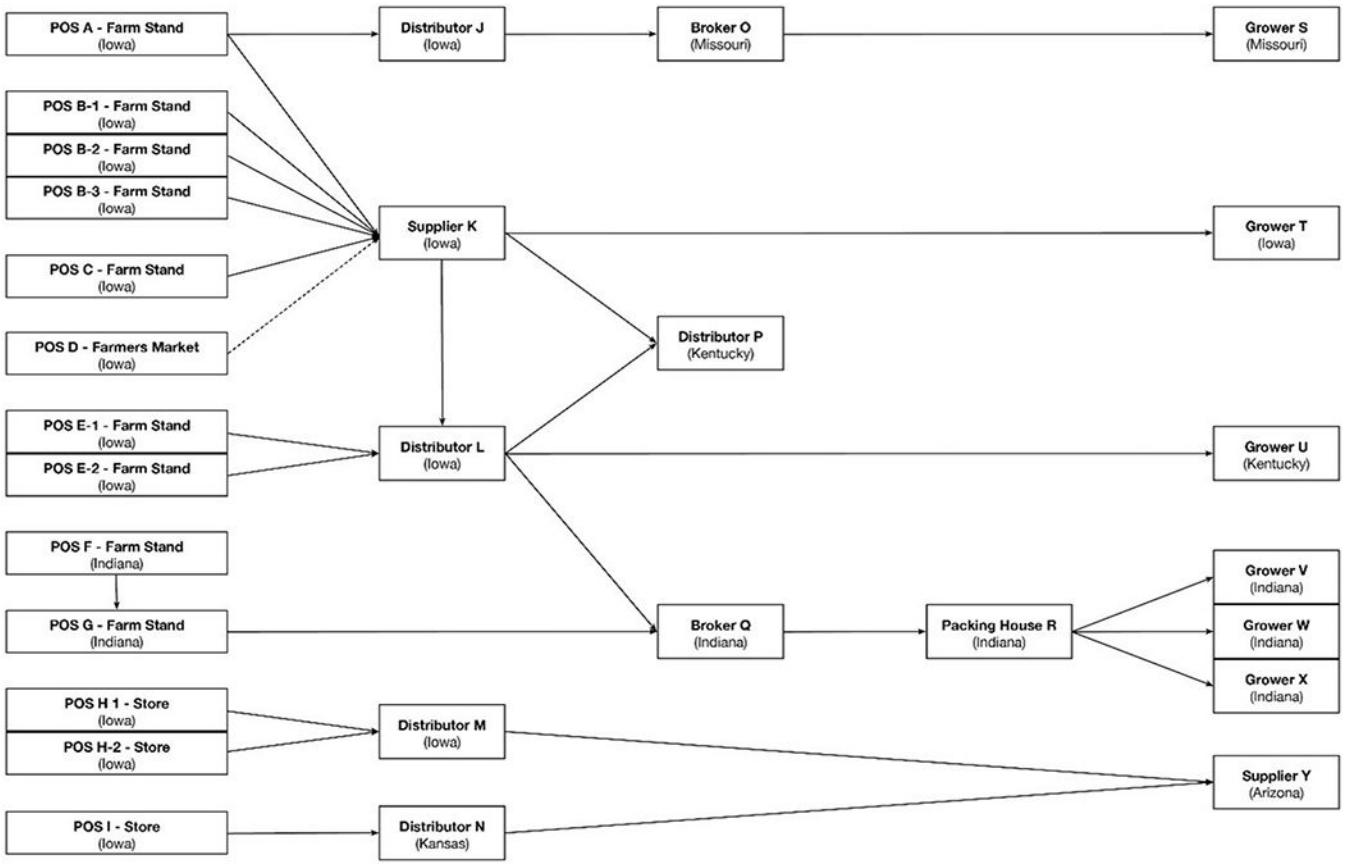

Fig. 3.

Traceback diagram of cantaloupe for multistate outbreak of *Salmonella* Typhimurium infections in the United States, 2022. Purchases of implicated products are traced from the point of service, through the distribution chain, to distributors. Product originates from growers that are denoted on the right side of the diagram.

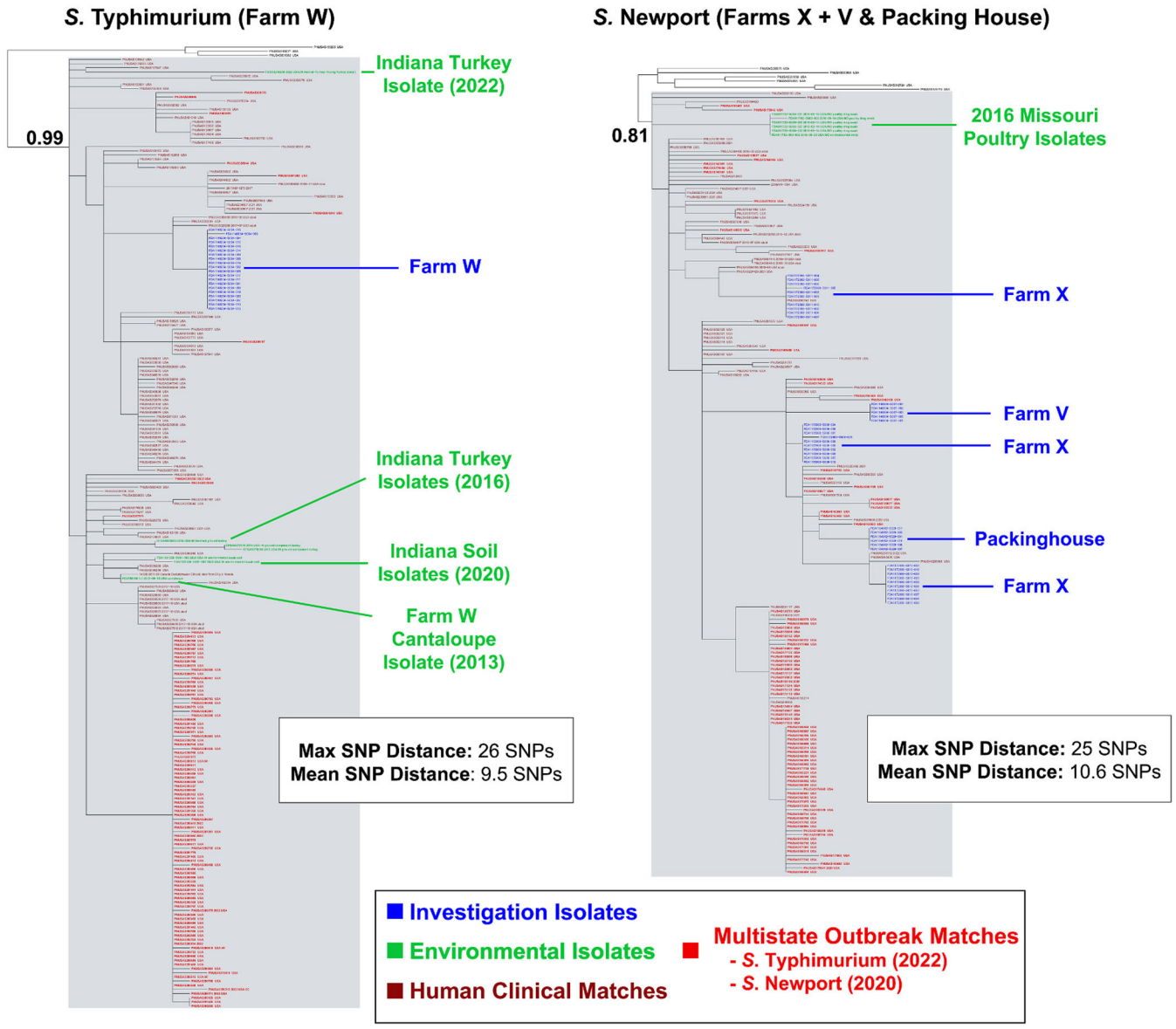

Fig. 4.

Relationships between *Salmonella* isolates collected as part of this investigation (blue) and isolates from the public NCBI Pathogen database. Isolates designated as a 'match' to the investigation isolates are outlined in the gray boxes. Matching human clinical cases are noted with dark red text, and clinical cases occurring during multistate outbreak years (*S.* Typhimurium: 2022; *S.* Newport: 2020) are noted in bright red. Environmental samples (e.g., isolates derived from facilities, goods, or natural areas collected independently from this investigation) found to match the investigation isolates are noted with green text. Isolates from Grower W match the focal *Salmonella* Typhimurium multistate outbreak, along with isolates collected from Indiana soil from 2020, a 2013 cantaloupe sample grown by Grower W, 2016isolates sampled from Indiana ground turkey, and a 2022 isolate from the digestive tract of an Indiana turkey. Like the *Salmonella* Typhimurium grouping, isolates

from Grower X, Grower V and Packing House R also match a multistate outbreak (2020 *S.* Newport), as well as isolates derived from a 2016 poultry investigation in Missouri.

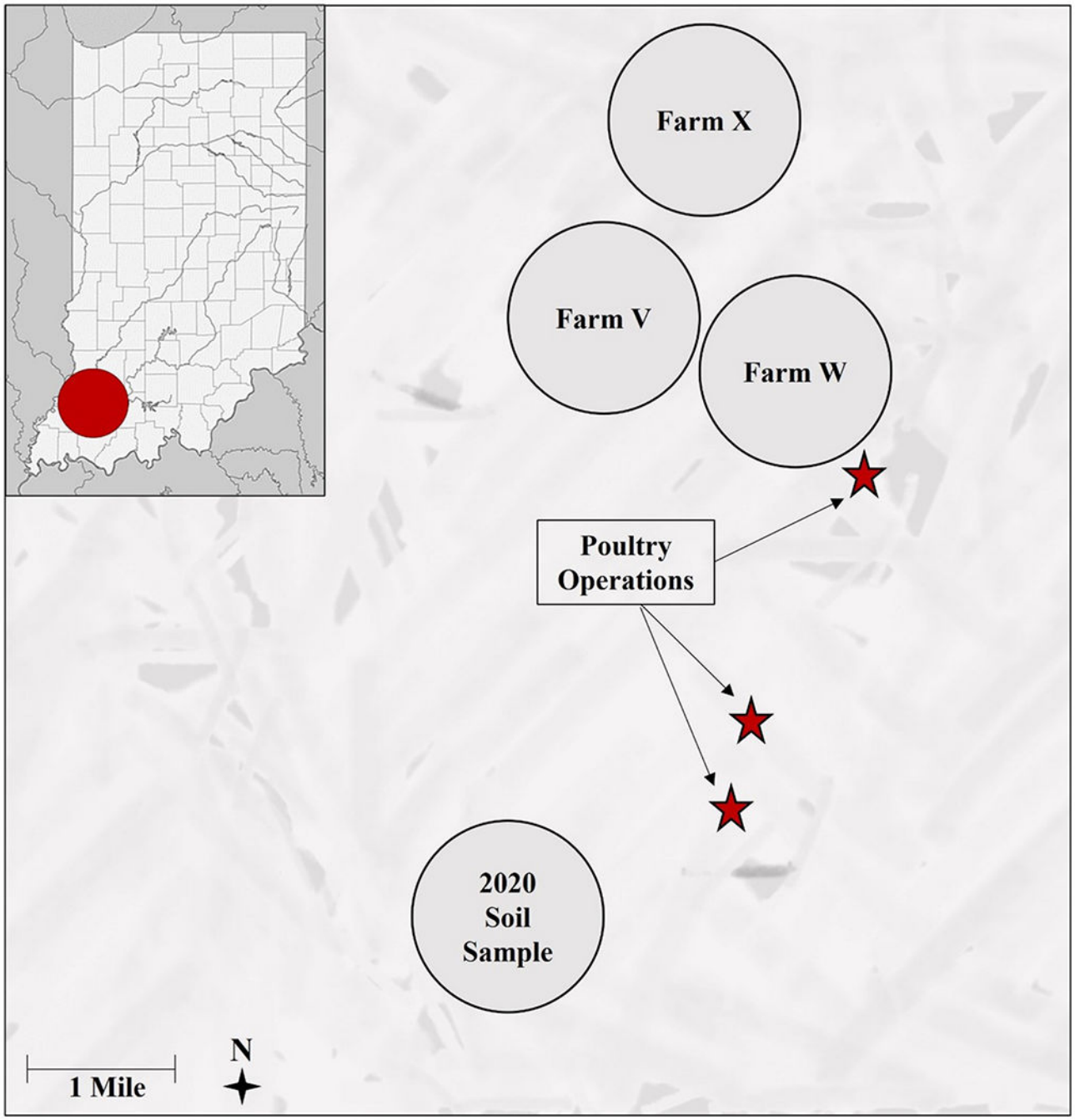

Fig. 5.

A spatial distribution of investigated cantaloupe farm locations in southwest Indiana during for-cause inspections in 2022 (Growers V, W, and X). The location of a 2020, for-cause cantaloupe inspection resulted in the recovery of a *Salmonella* Typhimurium isolate from a soil subsample that matched isolates recovered in 2022 at Grower W. Red stars indicate the relative proximities of poultry operations within the region.

Table 1

Summary of findings during FDA's farm investigations of Growers X, W, and V during the outbreak investigation of *Salmonella* Typhimurium infections in 2022.

Grower	Acres (est.)	Biological soil amendments of animal origin (BSAAO)	Wildlife activity	Water testing	Closest Turkey Feeding Operation	Crop rotation when not planted with cantaloupe
X	45	No BSAAO known to be used during the production of the cantaloupe. Verbal agreements were used between the lessor and lessee to determine the use of BSAAO during non-cantaloupe cropping years. The grower used chemical fertilizer and did not apply insecticides, fungicides, or herbicides.	Indications of wild animal activity, such as animal tracks, during the time of the investigation	An analytical record from May 2022 indicated that water used to grow cantaloupes did not yield generic *E. coli* or generic coliforms.	6 miles	The land is subleased to other farmers to grow non-produce crops (e.g. field corn or wheat). At the time of inspection, crops grown on adjacent land and near the field of interest consisted of field corn, soybeans, and alfalfa.
W	60	BSAAO were not used during the growing and harvesting of the cantaloupe crop nor in the production of rotation crops grown on the same field. Verbal agreements were in place with owners of adjacent farmland not to use BSAAO.	Operation visually monitored for animal activity in growing areas. No mammalian activity reported during the investigation. Field border lined with trees and small shrubs.	The well was tested for generic *E. coli* four times during the crop growth cycle (May–July). *E. coli* was not detected.	1 mile	Crops cultivated during the time of inspection on lands adjacent to the field of interest included field corn and soybeans.
V	140	Applications of untreated turkey manure were conducted within a two to two and a half-year cycle, during non-cantaloupe growing seasons when the field of interest was under the control of different management.	Operation visually monitored for animal activity in the growing areas. No mammalian activity reported during the investigation.	Well water was tested two to three times during the growing season. Tests did not yield generic *E. coli* or generic coliforms.	2 miles	Specific crop rotation cycles or growing practices used by other land lessees was unknown.

Table 2

Summary of laboratory results of the FDA product and environmental samples collected during the outbreak investigation of *Salmonella* Typhimurium infections in 2022. ND: Not detected; DEUF: Dead-End ultrafiltration.

Sample Type	Sample Details	Firm	Result	WGS ID	FDA Sample #
Food (Produce)	10 cantaloupes in bulk form	Distributor N	ND		1,186,812
Food (Produce)	10 whole cantaloupes	Distributor N	ND		1,199,108
Food (Produce)	10 whole seedless watermelons	Distributor N	ND		1,199,110
Complex Environmental	12 drag swabs collected	Grower W	FDA1148254-S004-001 to −020 *Salmonella* Typhimurium	SRR21578182; SRR21578183; SRR21578184; SRR21581298; SRR21581301; SRR21581707; SRR21582766; SRR21582774;SRR21628407; SRR21628718; SRR21639401; SRR21639451; SRR21639452; SRR21639453; SRR21639461; SRR21639466; SRR21639469; SRR21639470; SRR21639473; SRR21639474	1,148,254
Complex Environmental	5 soil subs (4 corners & middle)	Grower V	ND		1,148,693
Complex Environmental	12 drag swabs	Grower V	FDA1148694-S007-001 to −005 *Salmonella* Newport	SRR21578177; SRR21581347; SRR21639471; SRR21639472; SRR21639477	1,148,694
Environmental Swabs	55 environmental swabs collected from their packing line equipment. Subs consist of zones 1–4.	Packing House R	FDA1154912-S029-001, −003, −007, −008, −017, −019 *Salmonella* Newport	SRR21508686; SRR21508687; SRR21536775; SRR21536781; SRR21536809; SRR21640538	1,154,912
Complex Environmental	6 soil subs (4 corners & 2 middle)	Grower X	ND		1,172,989
Complex Environmental	12 Drag swabs	Grower X	FDA1172990-S006-001 to −010 *Salmonella* Newport FDA1172990-S010-001 to −010 *Salmonella* Newport FDA1172990-S011-001 to −010 *Salmonella* Newport	SRR21578179; SRR21581294; SRR21581297; SRR21581345; SRR21581348; SRR21581349; SRR21581352; SRR21581353; SRR21581354; SRR21581357; SRR21582775; SRR21582770; SRR21628723; SRR21628738; SRR21639393; SRR21639395; SRR21639396; SRR21639397; SRR21639398; SRR21639463; SRR21639464; SRR21639465; SRR21639467; SRR21639468; SRR21639475; SRR21639476; SRR21639478; SRR21639479; SRR21904452; SRR21904453	1,172,990
Complex Environmental	5 subs of soil sediment	Grower W	ND		1,199,862
Complex Environmental	1 Sub (soil)	Public Land Sample	ND		1,148,695
Complex Environmental	2 Subs (soil)	Public Land Sample	FDA1148696-S001-001 to −003, and −006 to −020 *Salmonella* Newport	SRR21578176; SRR21578181; SRR21581299; SRR21581300; SRR21581356; SRR21582764; SRR21582765; SRR21578175; SRR21628405; SRR21628406; SRR21628408; SRR21628721;	1,148,696

Sample Type	Sample Details	Firm	Result	WGS ID	FDA Sample #
				SRR21639392; SRR21639394; SRR21639399; SRR21639400; SRR21639460; SRR21639462	
Environmental Swabs	20 Subs (Environmental Swabs)	Packing House R	ND		1,154,913
Environmental Swabs	33 Subs (Environmental Swabs)	Packing House R	ND		1,160,813
Water Filtration	1 Sub (DEUF)	Public Land Sample	ND		1,172,991
Water Filtration	1 Sub (DEUF)	Public Land Sample	ND		1,172,992
Water Filtration	DEUF filter	Public Land Sample	FDA1200081-S001-001, −002, −005, −010 *Salmonella* Agbeni FDA1200081-S001-003, −004, −007, −009, −011 to −013, −016 to −020 *Salmonella* Hartford FDA1200081-S001-006 *Salmonella* I 4:b: FDA1200081-S001-008 *Salmonella* Paratyphi B var. L (+) tartrate+	SRR21598470; SRR21598484; SRR21598485; SRR21598493; SRR21598494; SRR21598495; SRR21598496; SRR21598497; SRR21598499; SRR21598500; SRR21598503; SRR21598504; SRR21599001; SRR21598466; SRR21598489; SRR21598491; SRR21598492; SRR21598498	1,200,081
Water Filtration	DEUF filter	Public Land Sample	FDA1200082-S001-001 *Salmonella* Paratyphi B var. L (+) tartrate+ FDA1200082-S001-004, −005, and −007 to −010 *Salmonella* I 4:b: FDA1200082-S001-006 *Salmonella* Hartford FDA1200082-S001-011, −017, −019, −020 *Salmonella* Anatum FDA1200082-S001-012, −016, −018 *Salmonella* Berta	SRR21598482; SRR21598483; SRR21598487; SRR21598490; SRR21598501; SRR21598505; SRR21599002; SRR21977165; SRR21977171	1,200,082

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