

Shiga Toxin-Producing *E. coli* Infections Associated with Romaine Lettuce — United States, 2018

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Summary: This investigation identified romaine lettuce as the vehicle, but questions remain how to further enhance U.S. produce safety. This outbreak highlighted challenges in determining the route of contaminated lettuce, and difficulties in rapidly providing actionable guidance during leafy greens-associated outbreaks.

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Abstract:

Background: Produce-associated outbreaks of Shiga toxin-producing *Escherichia coli* (STEC) were first identified in 1991. In April 2018, New Jersey and Pennsylvania officials reported a cluster of STEC O157 infections associated with multiple locations of a restaurant chain. CDC queried PulseNet, the national laboratory network for foodborne disease surveillance, for additional cases and began a national investigation.

Methods: A case was defined as an infection between March 13 and August 22, 2018 with one of the 22 identified outbreak-associated *E. coli* O157:H7 or *E. coli* O61 pulsed-field gel electrophoresis pattern combinations, or with a strain STEC O157 that was closely related to the main outbreak strain by whole genome sequencing. We conducted epidemiologic and traceback investigations to identify illness sub-clusters and common sources. An FDA-led environmental assessment, which tested water, soil, manure, compost, and scat samples, was conducted to evaluate potential sources of STEC contamination.

Results: We identified 240 case-patients from 37 states; 104 were hospitalized, 28 developed hemolytic uremic syndrome, and five died. Of 179 people who were interviewed, 152 (85%) reported consuming romaine lettuce in the week before illness onset. Twenty sub-clusters were identified. Product traceback from sub-cluster restaurants identified numerous romaine lettuce distributors and growers; all lettuce originated from the Yuma growing region. Water samples collected from an irrigation canal in the region yielded the outbreak strain of STEC O157.

Conclusion: We report on the largest multistate leafy green-linked STEC O157 outbreak in several decades. The investigation highlights the complexities associated with investigating outbreaks involving widespread environmental contamination.

INTRODUCTION

Produce-associated outbreaks of Shiga toxin-producing *Escherichia coli* (STEC) were first identified in 1991 and produce remains a common outbreak vehicle today [1,2]. STEC are estimated to cause more than 265,000 infections in the United States annually, with 3,600 hospitalizations and 30 deaths [5]. Most outbreaks of STEC infections are caused by STEC O157; 7% of STEC O157 outbreaks were leafy greens-associated during 2003–2012 [6,7].

In 2006, spinach was implicated as the outbreak vehicle in a large, multistate outbreak of *E. coli* O157:H7 (STEC O157) [3]. This outbreak resulted in enhanced industry guidance to improve the safety of leafy green vegetables and was one of several factors driving implementation of the Food Safety Modernization Act (FSMA) in 2007 [3,4].

Symptoms of STEC infection typically begin 2-5 days after infection and include severe diarrhea, often bloody, and abdominal pain. STEC O157 patients might also develop hemolytic uremic syndrome (HUS). Most cases of HUS in the United States result from an STEC O157 infection [8].

In April 2018, local, state, and federal officials began investigating a large multistate outbreak of STEC O157 infections, which was ultimately linked to romaine lettuce from the Yuma growing region. We describe the epidemiologic, laboratory, and traceback investigations that identified romaine lettuce as the source of this outbreak, and the public health implications of the investigation.

METHODS

Outbreak Detection

In April 2018, the New Jersey Department of Health and the Pennsylvania Department of Health notified the Centers for Disease Control and Prevention (CDC) of two STEC infection clusters. Before becoming ill, people in both clusters reported eating salads at a national restaurant chain. Pulsed-field gel electrophoresis (PFGE) showed that the STEC O157 isolated from ill people in both states had the same, rare PFGE pattern combination.

Case Identification

Cases were identified in PulseNet, the national molecular subtyping network for foodborne disease surveillance [9]. Cases were included in this outbreak that were related by PFGE or whole genome sequencing (WGS). Cases were defined as infection with *E. coli* O157:H7 or *E. coli* O61 with one of the 22 outbreak PFGE pattern combinations, (as one case-patient was co-infected with both STEC O157 and STEC O61, and two additional case-patients shared the same rare STEC O61 PFGE pattern (Table 1)), and with illness onset occurring between March 13, 2018, to August 22, 2018. The isolates from these ill people were also found to be highly related (0-40 single-nucleotide polymorphisms (SNPs)) to each other by WGS and were subsequently included in the outbreak. Public health scientists at federal and state laboratories performed WGS on clinical and non-clinical isolates, using standard methods. The Lyve-SET pipeline was used to perform high-quality SNP analysis using standard setting for *E. coli* and TW14359 as a reference with phages masked [10].

Hypothesis Generation

Based on initial reports of food exposures, CDC developed a focused questionnaire, which asked case-patients detailed questions about leafy greens consumption, where their household purchased groceries, restaurants visited, and specific menu items consumed in the week before illness onset. The proportion of case-patients reporting exposure to specific foods was compared to the proportion of healthy people reporting consumption of that food item in the 2006-2007 Foodborne Disease Active Surveillance Network (FoodNet) Population Survey [11]. This survey contains data on food consumption frequencies in healthy persons in the days prior to interview. A binomial probability distribution was used to identify food exposures that were reported by a significantly higher proportion of case-patients than healthy people.

Sub-Cluster Identification

We defined outbreak sub-clusters as two or more unrelated case-patients who reported eating at the same restaurant location, different locations of the same restaurant chain, the same institutional

setting, or shopping at the same grocery store in the week before becoming ill. These sub-clusters were used as starting points for traceback activities.

Product Traceback and Environmental Assessment

Locations, menus, meal items, meal dates, and invoices regarding restaurant and institutional sub-clusters were provided to CDC by state health departments. Individual shopper histories and receipts were also collected. These records were analyzed by the Food and Drug Administration (FDA) to identify distributors, processors, and farms that supplied produce to the sub-cluster locations.

An environmental assessment (EA) was initiated in June 2018 to help determine the source of STEC contamination. The EA was conducted to assist FDA in identifying factors that potentially contributed to the introduction and spread of the outbreak strain of STEC O157 that contaminated products associated with this outbreak. The EA was focused on, but not limited to: agricultural water, soil amendments, growing and harvesting practices, animal intrusion, adjacent land use, concentrated animal feeding and manure composting operations, and employee health and hygiene practices [12]. Water, soil, manure, compost, scat, and other environmental samples were collected, and analyzed for the outbreak strain of STEC O157 by culture; STEC isolates were genetically characterized by PFGE and WGS. The EA was completed with two subsequent trips and additional sampling.

Antimicrobial Susceptibility Testing

CDC's National Antimicrobial Resistance Monitoring System (NARMS) performed antimicrobial susceptibility testing (AST) among selected clinical isolates using standard methods [13]. Drug resistance was defined as resistance to ≥ 1 antimicrobial and multi-drug resistance was defined as resistance to ≥ 1 antimicrobial in ≥ 3 drug classes [14]. We used WGS to identify virulence genes, and predicted resistance based on identification of known resistance genes.

RESULTS

Case Identification

We identified 240 case-patients from 37 states; 238 case-patients were infected with STEC O157, one case-patient was co-infected with STEC O157 and STEC O61, and two case-patients were infected with only STEC O61. Case-patients were 1–93 years (median 26 years), and 66% (158/239) were female. One hundred four case-patients were hospitalized, 28 developed HUS, and five died (Figures 1 and 2). All outbreak isolates were related genetically by WGS (0–40 SNP differences). We identified two distinct sub-clades that included the majority of outbreak isolates, which had isolates with 0–19 SNP differences (Figure 3; clades A and B).

Hypothesis Generation

Among 179 case-patients who completed the focused questionnaire, 85% reported consuming romaine lettuce in the week prior to illness onset, compared to 47% in the FoodNet Population Survey ($p < 0.001$).

Twenty illness sub-clusters, encompassing >50% of case-patients, were identified. The first sub-clusters were identified at multiple locations of a national restaurant chain by officials in New Jersey. Further investigation identified case-patients who had eaten at locations of the chain in 14 states over the course of the outbreak. Among case-patients who ate at this chain, 90% reported consuming salads containing pre-chopped romaine lettuce.

Idaho officials identified additional sub-clusters at two Idaho restaurants. Case-patients also reported eating salads containing pre-chopped romaine prior to illness onset. Alaska identified a sub-cluster of case-patients at a correctional facility where only whole head romaine was served prior to illness onset, which was distinct from all other sub-clusters serving pre-chopped romaine.

Product Traceback and Environmental Assessment

Product traceback efforts by local health jurisdictions, state health departments, and FDA could not identify a single product lot, processor, or farm as the source of the entire outbreak. In total, 36 fields on 23 farms were identified during the traceback investigation (Figure 4). Only the Alaska correctional facility sub-cluster could be traced to a single farm. All of the romaine lettuce identified

was traced to farms in the Yuma growing region. FDA, CDC and state partners conducted an EA in the growing region, which consisted of farms in Imperial County, CA and Yuma County, AZ.

In June 2018, STEC O157 with PFGE patterns indistinguishable from clinical outbreak isolates and closely related genetically to clinical isolates in both main clades (Figure 3) were detected in irrigation water from the Yuma growing region. The outbreak strains were detected in three separate water samples from sites along a 3.5-mile section of the Wellton irrigation canal that runs adjacent to romaine lettuce farms identified during traceback and next to a concentrated animal feeding operation (CAFO) with approximately 105,000 cattle. No STEC O61 was identified from the environmental assessment or water samples collected. No romaine lettuce was available for sampling during this outbreak since harvesting had ended in this region by the time the environmental assessment began.

Antimicrobial Susceptibility Testing

WGS analysis of case-patient isolates (n = 184) and standard antibiotic resistance testing of case-patient isolates by CDC's NARMS laboratory (n = 13) identified antibiotic resistance to chloramphenicol, streptomycin, sulfisoxazole, tetracycline, and trimethoprim-sulfamethoxazole. Ampicillin and ceftriaxone resistance genes were also identified in isolates from four case-patients. These findings did not affect treatment guidance since antibiotics are generally not recommended for patients with STEC O157 infections.

Public Health Actions

On April 10, 2018, CDC and FDA issued public notices indicating that a multistate STEC O157 outbreak of an unknown source was under investigation. Although the investigation had not yet identified a responsible food vehicle by April 13, romaine lettuce from the Yuma growing region was the leading hypothesis due to identified sub-clusters and traceback efforts. Consequently, CDC and FDA advised consumers and retailers on this date not to eat, sell, or serve chopped romaine lettuce from the Yuma growing region. This warning was issued because contaminated lettuce was likely still available in consumers' homes, stores, and restaurants, as the last harvest of romaine lettuce from

Yuma shipped on April 16, 2018, and the product shelf life was 21 days. After the Alaska sub-cluster was identified, CDC recommended against consuming any romaine lettuce. The results from the environmental assessment, completed almost two months after romaine had been identified as the outbreak vehicle, solidified the messaging around romaine lettuce. In total, CDC and FDA issued 11 joint updates, resulting in over 1.5 million page views to both agencies' outbreak webpages.

DISCUSSION

Evidence collected during this investigation demonstrated that this large multistate outbreak was caused by contaminated romaine lettuce from the Yuma growing region. Epidemiologic data showed that a higher than expected proportion of case-patients consumed romaine lettuce prior to illness onset; traceback data showed that the romaine lettuce served at numerous illness sub-cluster locations was sourced from the Yuma growing region; and water testing identified the outbreak strain of STEC O157 in multiple locations of an irrigation canal that ran adjacent to several romaine fields identified during traceback.

This outbreak was the largest multistate STEC O157 outbreak in several decades, eclipsing in magnitude a 2006 outbreak linked to fresh spinach [3]. As there are an estimated 26 unreported illnesses for every STEC O157 case reported to PulseNet, the true size of this outbreak was likely much larger than the 240 illnesses reported through PulseNet, suggesting that thousands of people were actually sickened in this outbreak [5]. This outbreak was also much larger than any of the 28 multistate leafy green outbreaks reported from 1998–2016, which saw a mean size of 40 case-patients [15]. It is unclear why the size of the current outbreak exceeded that of previous similar outbreaks, but the volume of contaminated product may have played a role. This is supported by the fact that the outbreak strain was identified along multiple points of a 3.5-mile stretch of an irrigation canal and that traceback led to 36 romaine fields.

In addition to this outbreak being unusually large, case-patient clinical course was unusually severe. The proportion of case-patients developing HUS (12.7%) was twice as high as previous outbreaks of

STEC O157 (6.3%) [16]. There were five deaths in this outbreak (2.2%), which is almost four times higher than expected (0.6%) [16]. This could be explained by the strain's stx2a toxin subtype, which produces more virulent toxins than other types. Outbreaks with stx2 toxin are more likely to result in increased rates of HUS [16]. Communicating unusually severe outcomes associated with STEC infections during an outbreak to healthcare providers is important. Clinicians should be made aware of ongoing outbreaks, test patients exhibiting diarrhea, especially bloody, with low or absent fever. Clinicians should not administer antibiotics to these patients as it increases the risk of severe outcomes, even if testing indicates the bacteria may be susceptible to antibiotics. Increased vigilance amongst children less than five years of age, adults 65 years and older, and immunocompromised patients can reduce the likelihood of progression to severe illness. Creating clear and actionable messaging for consumers and retailers during this outbreak was challenging because a single source of contaminated romaine lettuce was never identified. Advice to consumers and retailers focused on avoiding romaine lettuce from a particular growing region, but leafy greens packaging rarely included growing region information, making it difficult to identify a specific product of concern. Many consumers and retailers may have simply avoided eating, selling, and serving any romaine lettuce during the outbreak because of this confusion. Several factors complicated the traceback investigation during this outbreak. Many case-patients reported frequent consumption of romaine lettuce prior to their illness onset. Since the majority of traceable information was provided through restaurant or institutional sub-clusters, the case-patients had limited knowledge of the provenance of their romaine, including brand or harvest location, and traceback relied heavily on information provided from suppliers. Many of the restaurants identified during the traceback investigation were part of regional or national chains, which handled produce in regional distribution centers before shipment to specific retail locations. Due to this practice, these restaurants could not identify their specific romaine sources. Traceback was further complicated by the fact that a single production lot of chopped romaine might have contained lettuce from multiple farms. Although the FSMA Produce Safety Rule established specific

recordkeeping requirements for farms, records specific to traceability of produce along the supply chain are not required [17]. During this outbreak, leafy greens were not classified as an FDA high-risk food, thus not subject to enhanced recordkeeping. Romaine served at the Alaskan correctional facility was the only product that was traced to a single farm due to the unique circumstance of being the only cluster that was associated with whole head romaine lettuce from a single distributor to Alaska. In response to this outbreak, shipment origin labeling was voluntarily added to romaine packages by produce packers in December 2018. Increased detail about the growing region and limiting product lots to a single farm could alleviate the burden of traceback and identify a source more quickly in the future.

The ultimate source of STEC O157 for this outbreak is unknown, but reasonable hypotheses exist that explain how romaine lettuce could have become contaminated. The STEC O157 outbreak strain was detected at multiple points in a Yuma growing region irrigation canal, and the contaminated canal water may have subsequently contacted romaine lettuce in several ways, including direct application to the crop through aerial or land-based spray chemicals diluted with canal water. However, how and when STEC was introduced into the irrigation canal is unknown, as well as why the majority of illnesses were associated with romaine when other types of lettuce were grown in the same area during the time of interest. A CAFO was located adjacent to the irrigation canal where the outbreak strain was found, but no obvious route for contamination from the facility was identified. Environmental contamination could have been caused by the adjacent CAFO, as cattle are a well-documented reservoir for pathogenic STEC [18-20]. More research into the ecology of pathogenic *E. coli* in concentrated animal settings may help determine if the proximity of CAFOs to lettuce fields and produce irrigation water is a concern for the produce industry. After the outbreak, several task forces were formed to address problems identified, including the Leafy Greens Food Safety Task Force (LG FSTF) and the Romaine Task Force (RTF). The LG FSTF recommended increasing the buffer zones between CAFOs and romaine farms. The RTF recommended traceability

improvements in addition to changes in agricultural water practices. Ongoing work from both of these task forces will be used in the future to help prevent additional outbreaks.

Conclusions

Although this outbreak investigation conclusively identified romaine lettuce as the responsible food vehicle, questions about how to further enhance U.S. produce safety remain. This outbreak highlighted challenges in quickly determining the source and route of outbreak pathogens contaminating leafy greens, and difficulties in rapidly providing actionable guidance to consumers and retailers during leafy greens-associated outbreaks. This STEC O157 outbreak strain was first identified in humans in 2015, and in environmental samples as part of a recreational swimming-associated outbreak in a Northern California lake in 2017. It is unclear how the contaminated water found in this previous outbreak might be linked to the contaminated Yuma growing region irrigation water identified during the current outbreak. This raises concern that longstanding environmental or zoonotic reservoirs exist for this STEC strain.

More research is needed to better understand STEC's ecology in regions that grow ready-to-eat foods, including the role of CAFOs and other domesticated and wild animal populations. Efforts to assure agricultural water is monitored appropriately will also require ongoing evaluation and research. Improved labeling and record-keeping may also improve the speed and accuracy of future traceback investigations, especially for produce-associated outbreaks. Enhanced collaboration between health and agriculture officials, food industries, and academia is needed to fully understand the etiology of this outbreak and, more importantly, how to prevent other, similar outbreaks.

Acknowledgements

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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 CDC.

Potential conflicts

The authors have no potential conflicts of interest or funding sources to be disclosed.

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Table 1. Breakdown of Pulsed-Field Gel Electrophoresis Patterns and Corresponding Counts

<u>PFGE Pattern Combination</u>	<u>Total Isolate Count</u>	<u>Non-human Samples</u>	<u>Percent of Total</u>
A	4	4	2.2
B	2	0	0.6
C	1	0	0.3
D	11	11	6.1
E	233	16	69.6
F	2	0	0.6
G	2	0	0.6
H	2	0	0.6
I	1	1	0.6
J	1	0	0.3
K	8	3	3.1
L	2	0	0.6
M	1	0	0.3
N	1	0	0.3
O	6	5	3.1
P	7	7	3.9
Q	4	4	2.2
R	3	0	0.8
S	1	1	0.6
T	4	4	2.2
U	1	1	0.6
V	2	2	1.1

Figure Legends

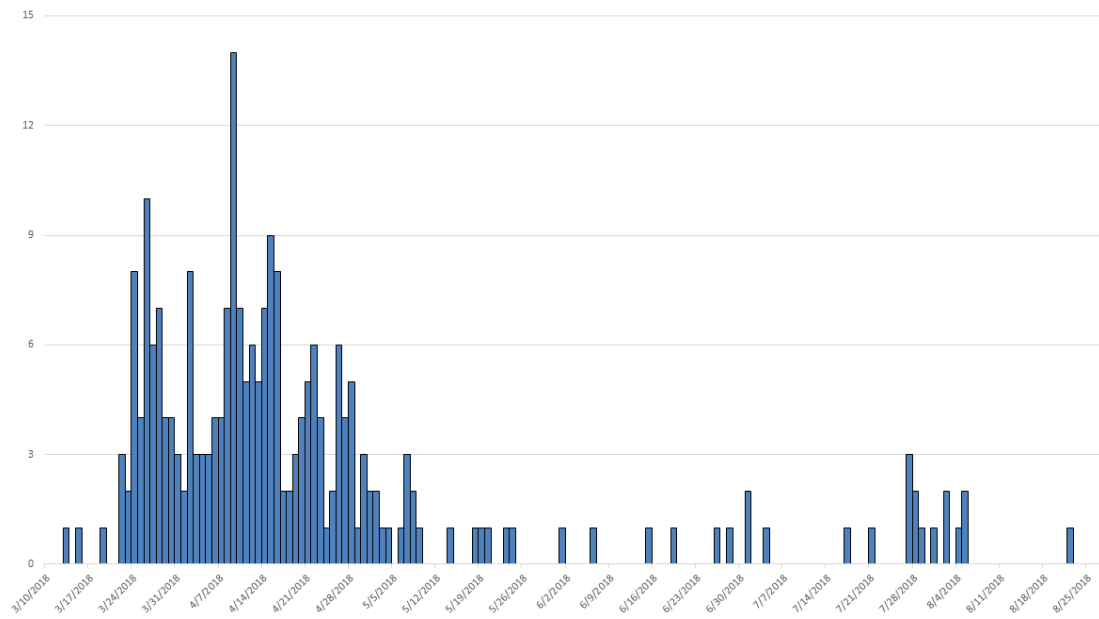
Figure 1. Number of Case-patients, According to Date of Illness Onset.

Figure 2. Number of Case-patients, According to State of Residence (n=240)

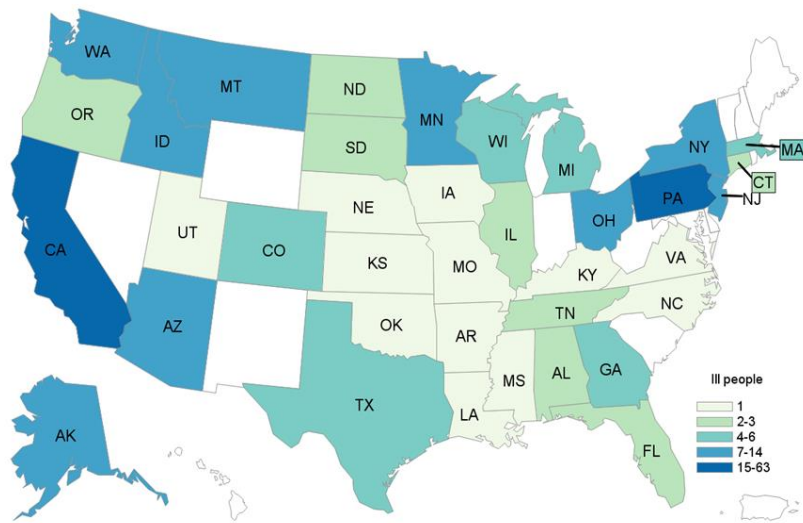
Figure 3. High quality SNP Phylogenetic Tree of Shiga Toxin–Producing *Escherichia coli* Serogroup O157 Isolates Involved in the Outbreak. Human and environmental isolates sequenced for this outbreak are shown below. Human isolates, denoted by blue bars, span the majority of the tree. Environmental isolates are shown in dark orange bars. Clades A and B contain the majority of isolates for this outbreak and differ by 8-18 SNPS. Environmental isolates fall into both clades A and B and are indistinguishable from human isolates.

Figure 4. US Food & Drug Administration Master Traceback Diagram. Purchases of implicated products are traced from the point of service, through the distribution chain, to shippers. Product originates at the farm, denoted on the right side of the diagram.

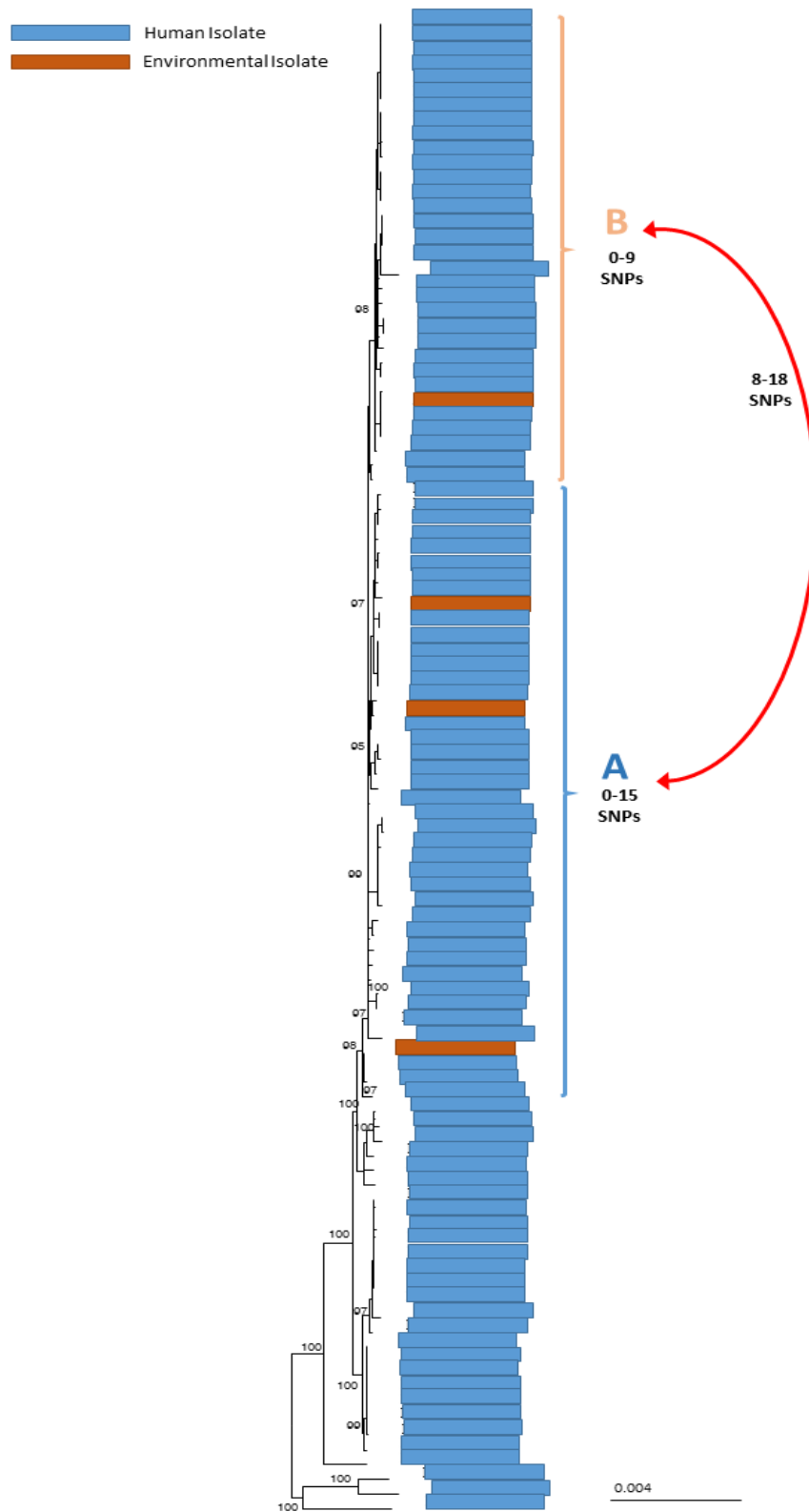
STEC O157 Figure 1



STEC O157 Figure 2

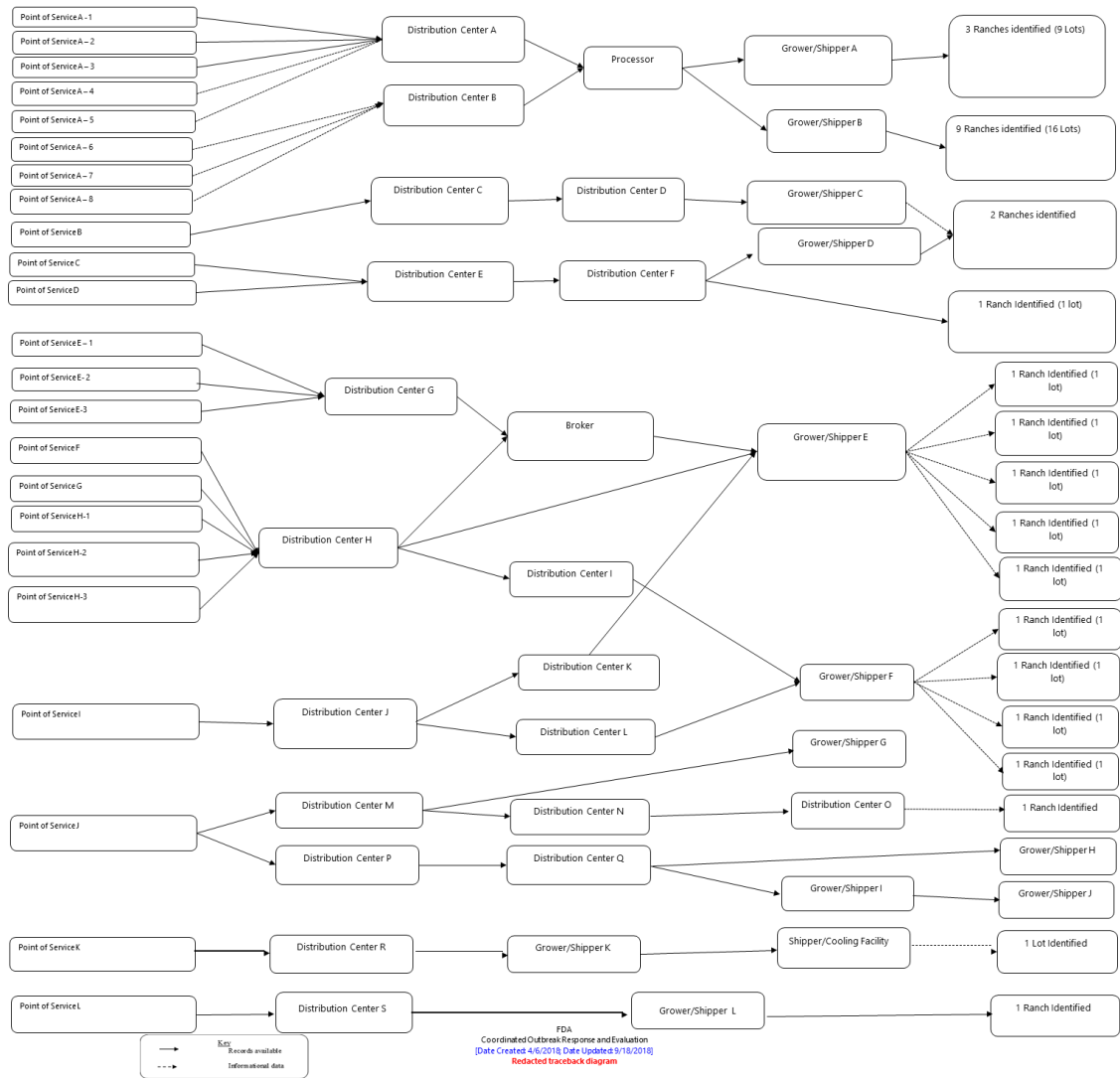


STEC O157 Figure 3



STEC O157 Figure 4

E. coli O157:H7 – Romaine
Multi-state Outbreak April 2018
 Master Redacted Traceback Diagram





Update: Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Romaine Lettuce, 2018

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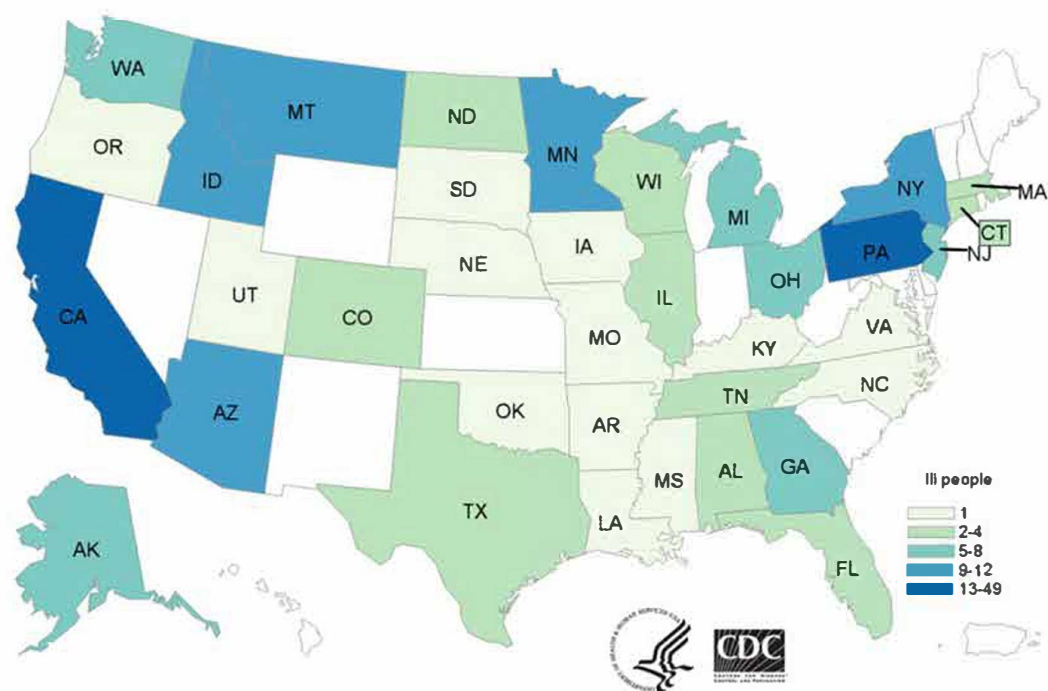
Leafy Green Food Safety Task Force Meeting - Yuma, AZ

July 31, 2018

***E. coli* O157 Infections Linked to Romaine Lettuce, 2018**

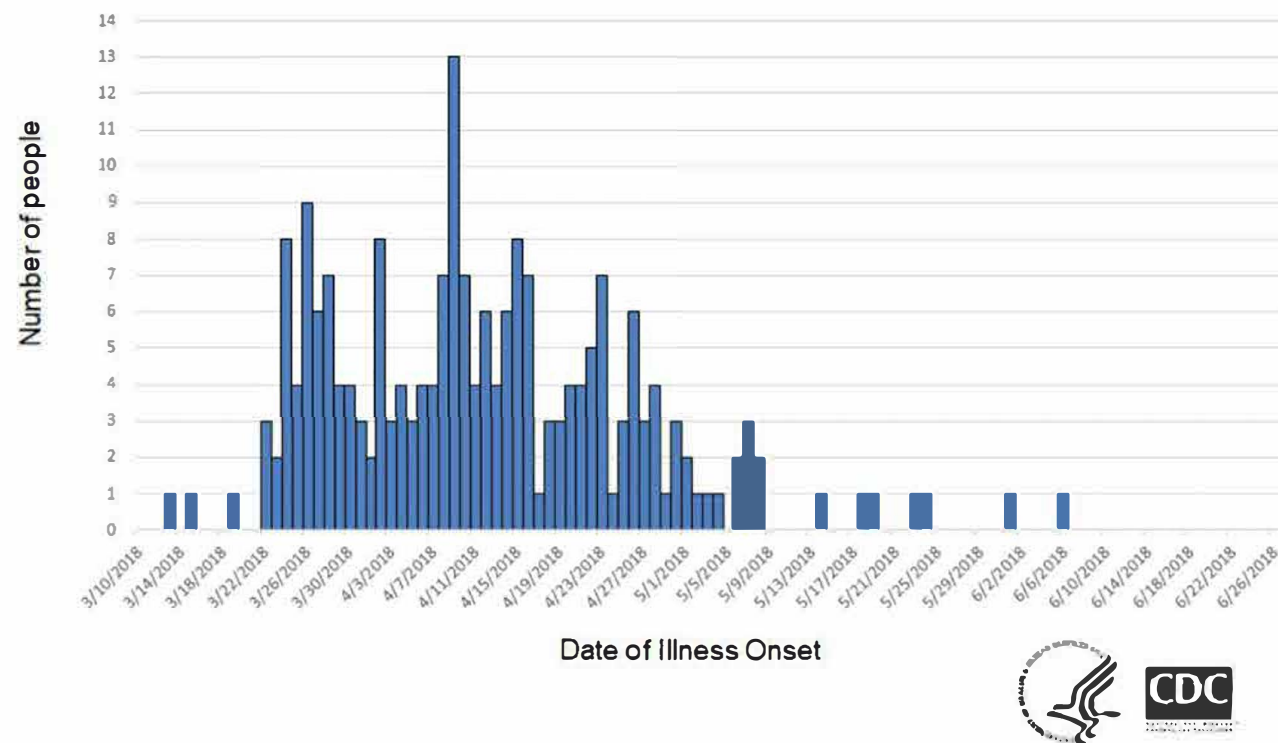
- **Total of 210 ill people in 36 states**
 - Illnesses started on dates from March 13, 2018 to June 6, 2018
 - 67% were female
 - Ages ranged from less than 1 to 97 years (median 67 yrs)
 - 96 (48%) were hospitalized, 27 developed HUS, 5 deaths
- **145/166 (87%) reporting eating romaine lettuce**
 - This percentage was significantly higher than results from a survey of healthy people, in which 46% reported eating romaine lettuce in the week before they were interviewed
- **WGS determine bacteria isolated from different ill people in this outbreak were closely related genetically and related to canal water samples taken from the Yuma growing region**
 - WGS also indicated the outbreak strain is resistant to multiple antibiotics
- **Final CDC web posting on June 28, 2018**
 - <https://www.cdc.gov/ecoli/2018/o157h7-04-18/index.html>

People infected with the outbreak strain of *E. coli* O157:H7, by state of residence, as of June 27, 2018 (n=210)



<https://www.cdc.gov/ecoli/2018/o157h7-04-18/map.html>

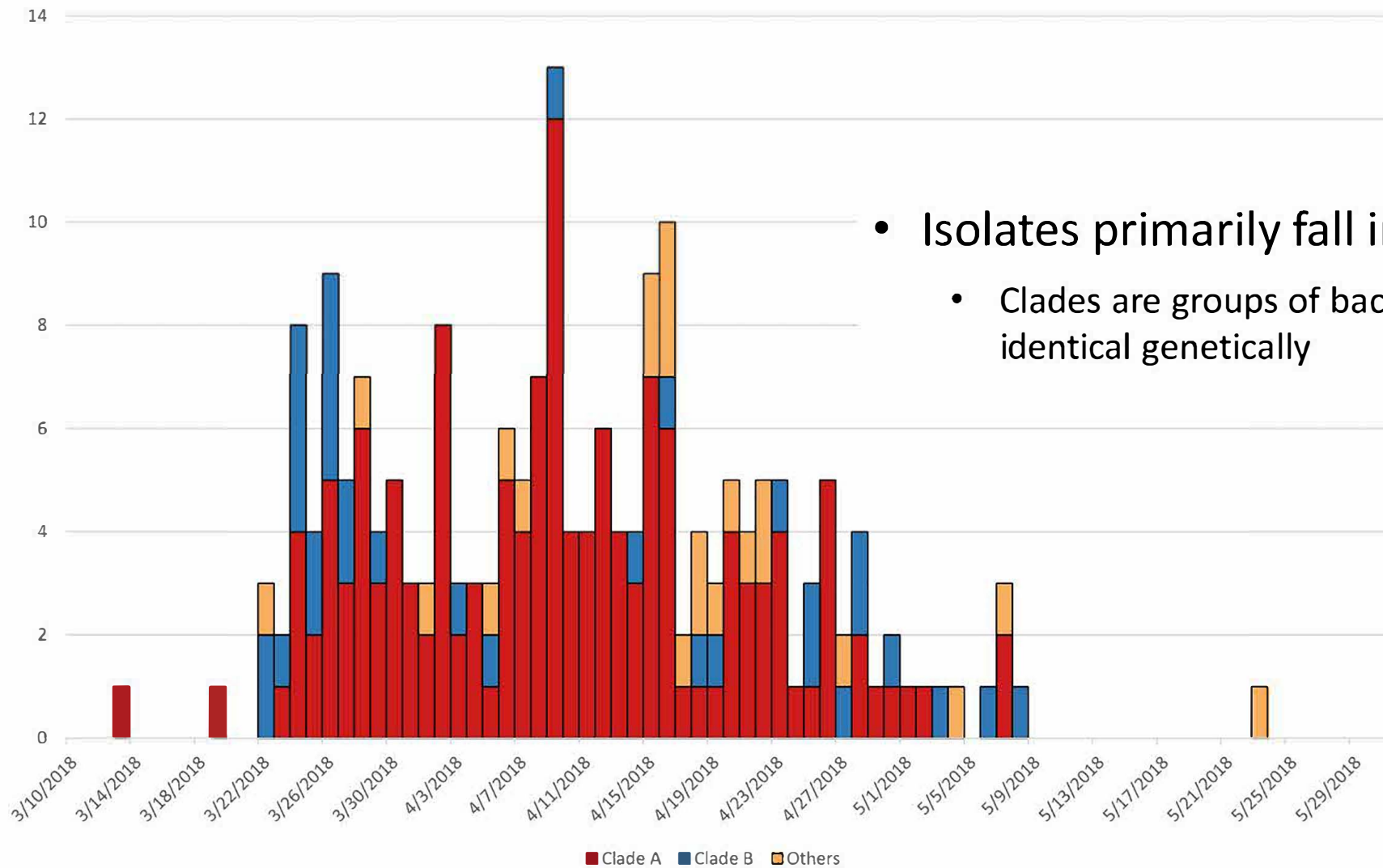
People infected with the outbreak strain of *E. coli* O157:H7, by date of illness onset*



*n=210 for whom information was reported as of June 27, 2018. Some illness onset dates have been estimated from other reported information.

<https://www.cdc.gov/ecoli/2018/o157h7-04-18/epi.html>

Epi Curve by WGS Clade: Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Romaine Lettuce

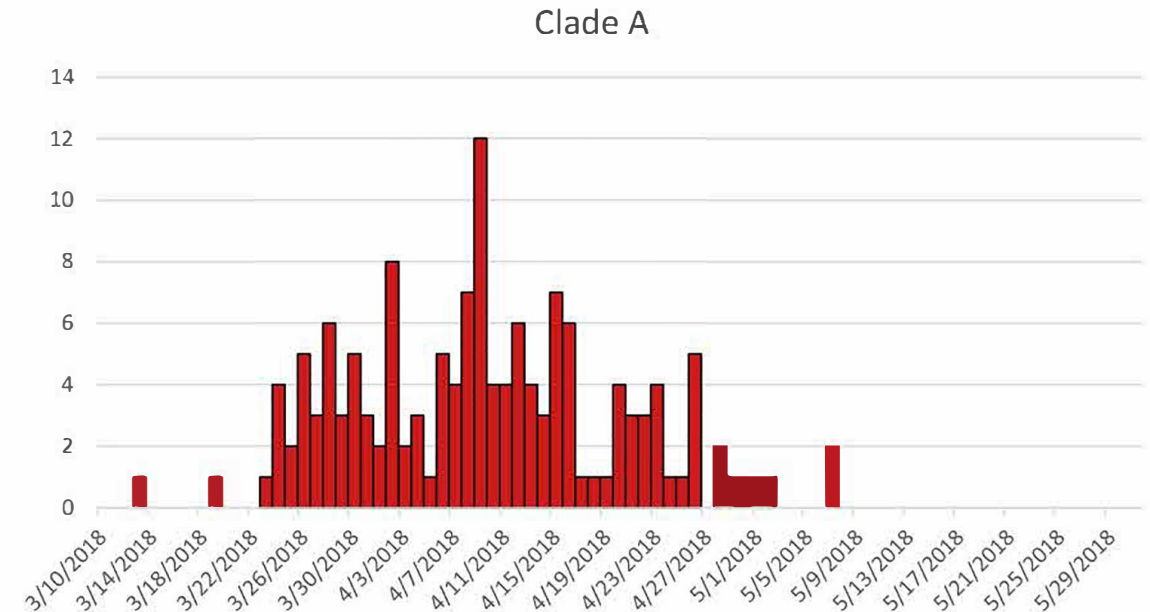


- Isolates primarily fall into 2 WGS clades
 - Clades are groups of bacteria that are nearly identical genetically

*** Data are preliminary and subject to change – As of 07/23/2018***

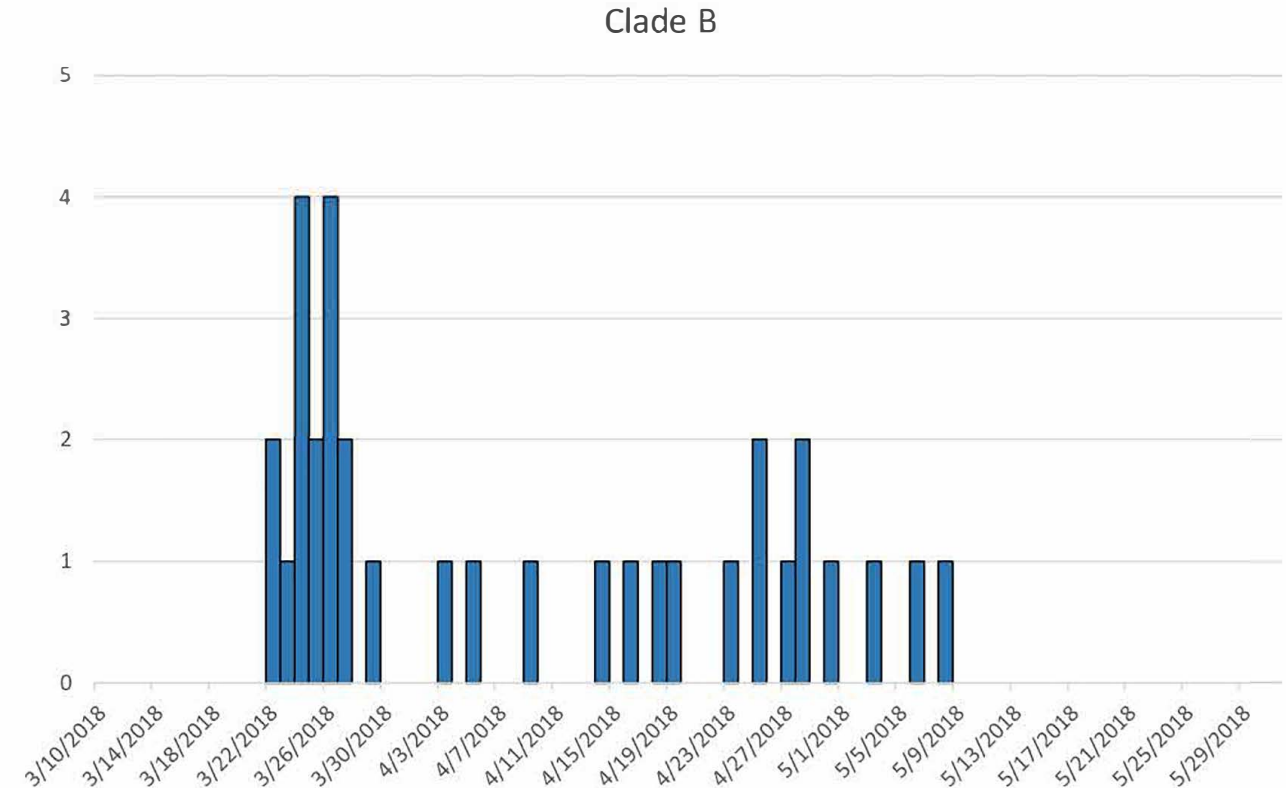
Clade A: Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Romaine Lettuce

- 179 isolates (0-13 SNPs)
- Reported onset dates: 3/13/2018 – 5/7/2018
- Encompasses 15 illness sub-clusters including the Alaska prison
- Historical Isolates:
 - Isolate from CO in 2017 outbreak, 4/11/2017 onset (Outbreak consisted of 9 cases with onsets from 4/5-5/8/2017, no vehicle identified, but a high proportion of leafy green eaters)
 - Isolates from CA in 2017 outbreak, 7/24/2017 onset (Lake Wildwood outbreak – Outbreak consisted of 11 cases with onsets from 7/24/2017 to 9/3/2017)
 - Isolate from ME in 2018 outbreak, 12/10/2017 onset (Outbreak consisted of 17 cases with onsets 11/6/2017 to 1/30/2018, no vehicle identified, but included a sub-cluster from a university that was suspected leafy greens. This isolate is not from that sub-cluster.)
 - Isolate from CO onset of 8/18/2017
 - Isolate from WA onset of 9/26/2017
 - Isolate from OH onset of 10/2/2017
 - Isolate from PA onset of 2/2/2018



Clade B: Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Romaine Lettuce

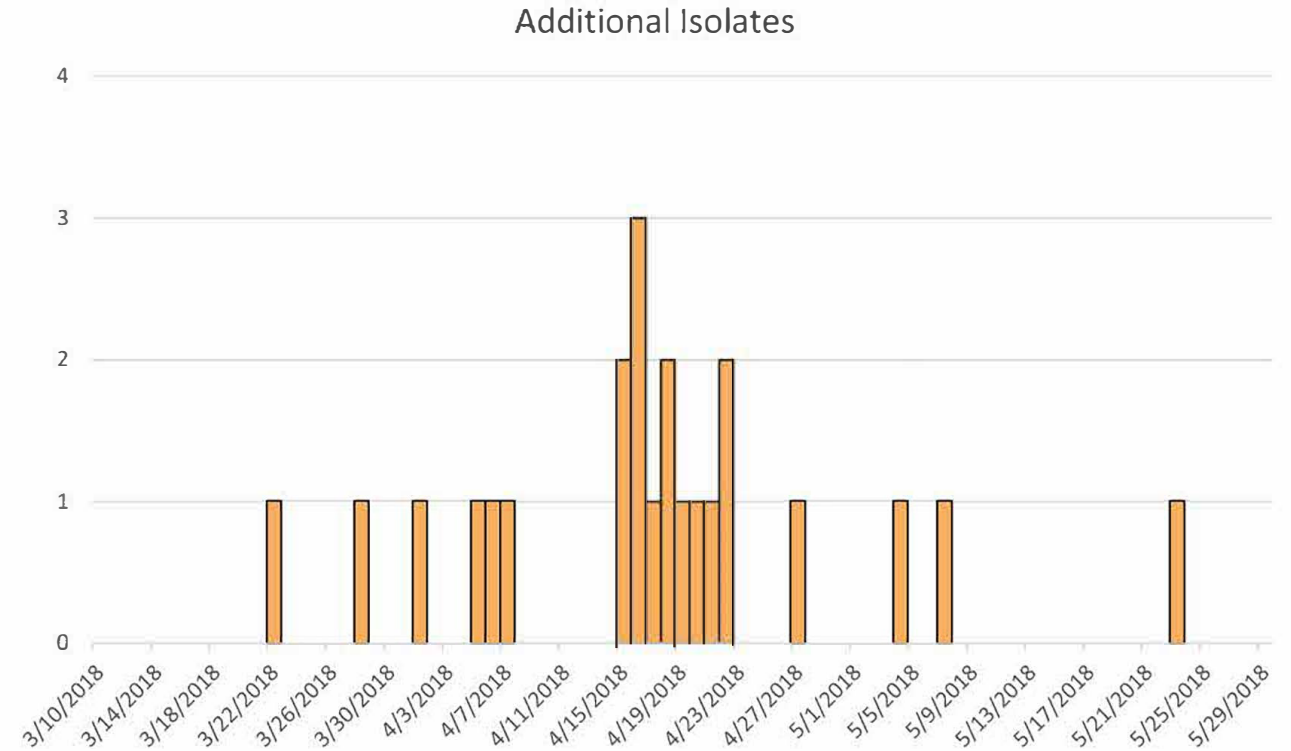
- 47 isolates (0-8 SNPs)
 - Differs from Clade A by 8-17 SNPs
- Reported onset dates: 3/22/2018 – 5/8/2018
- Encompasses 3 illness sub-clusters in the outbreak
- Historical isolate:
 - Isolate from WI in 2018 outbreak, 12/4/2017 onset (associated with a sub-cluster of cases at a university, leafy greens suspected, illness onset dates ranged from 12/1/2017 to 12/4/2017)



*** Data are preliminary and subject to change – As of 07/23/2018***

Additional Isolates: Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Romaine Lettuce

- 26 isolates
- Reported onset dates: 3/22/2018 – 5/23/2018
- Historical Isolates:
 - Isolate from WV: 9/18/2017 onset
 - Isolate from CO: 10/3/2017 onset
 - Isolate from CA: 12/19/2017 onset
 - Isolate from CA: 2/17/2018 onset



*** Data are preliminary and subject to change – As of 07/23/2018***



Multistate Outbreak of *E. coli* O157:H7 Infections Linked to Romaine Lettuce (Final Update)

- *E. coli* O157:H7 Infections Linked to Romaine Lettuce en Español
- Advice to Consumers, Restaurants, Retailers, and Clinicians
- Case Count Maps
- Epi Curves
- Signs & Symptoms
- Key Resources

Posted June 28, 2018 3:30 PM EST

This outbreak appears to be over. *E. coli* is an important cause of illness in the United States. More information about *E. coli*, and steps people can take to reduce their risk of infection, can be found on [the *E. coli* and Food Safety web page](#).

Highlights

- This outbreak appears to be over as of June 28, 2018.
- CDC, public health and regulatory officials in several states, and the U.S. Food and Drug Administration (<https://www.fda.gov/Food/RecallsOutbreaksEmergencies/Outbreaks/ucm604254.htm>) (FDA) investigated a multistate outbreak of *E. coli* O157:H7 infections.
 - 210 people infected with the outbreak strain were reported from 36 states.
 - 96 people were hospitalized, including 27 people who developed a type of kidney failure called hemolytic uremic syndrome.
 - 5 deaths were reported from Arkansas, California, Minnesota (2), and New York.
- Epidemiologic, laboratory, and traceback evidence indicated that romaine lettuce from the Yuma growing region was the likely source of this outbreak.
- CDC laboratory testing identified the outbreak strain of *E. coli* O157:H7 in canal water samples taken from the Yuma growing region. FDA is continuing to investigate the outbreak to learn more about how the *E. coli* bacteria could have entered the water and ways this water could have contaminated romaine lettuce.

- According to the FDA (<https://www.fda.gov/Food/RecallsOutbreaksEmergencies/Outbreaks/ucm604254.htm>) , the last shipments of romaine lettuce from the Yuma growing region were harvested on April 16, 2018, and the harvest season has ended. Contaminated lettuce that made people sick in this outbreak should no longer be available.
- The Public Health Agency of Canada (<https://www.canada.ca/en/public-health/services/public-health-notices/2018/public-health-notice-outbreak-e-coli-infections-linked-romaine-lettuce.html>) (PHAC) identified ill people in several Canadian provinces infected with the same DNA fingerprint of *E. coli* O157:H7. On June 22, 2018, PHAC reported that the outbreak in Canada appears to be over.
- Consumers should follow these steps to help keep fruits and vegetables safer to eat.
- Read more on general ways to prevent *E. coli* infection. Important steps to take are to cook meat thoroughly, and wash hands after using the restroom or changing diapers, before and after preparing or eating food, and after contact with animals.

Outbreak Summary

Introduction

CDC, public health and regulatory officials in several states, and the U.S. Food and Drug Administration

(<https://www.fda.gov/Food/RecallsOutbreaksEmergencies/Outbreaks/ucm604254.htm>) (FDA) investigated a multistate outbreak of *E. coli* O157:H7 infections.

Public health investigators used the PulseNet (<https://www.cdc.gov/pulsenet/index.html>) system to identify illnesses that were part of this outbreak. PulseNet is the national subtyping network of public health and food regulatory agency laboratories coordinated by CDC. DNA fingerprinting is performed on *E. coli* bacteria isolated from ill people by using techniques called pulsed-field gel electrophoresis (<https://www.cdc.gov/pulsenet/pathogens/pfge.html>) (PFGE) and whole genome sequencing (<https://www.cdc.gov/ncezid/dfwed/keyprograms/tracking-foodborne-illness-wgs.html>) (WGS). CDC PulseNet manages a national database of these DNA fingerprints to identify possible outbreaks. WGS gives a more detailed DNA fingerprint than PFGE. WGS performed on bacteria isolated from ill people in this outbreak showed that they were closely related genetically. This means that the ill people were more likely to share a common source of infection.

As of June 27, 2018, 210 people infected with the outbreak strain of *E. coli* O157:H7 were reported from 36 states. A list of the states and the number of cases in each can be found on the [Case Count Map page \(https://www.cdc.gov/ecoli/2018/o157h7-04-18/map.html\)](https://www.cdc.gov/ecoli/2018/o157h7-04-18/map.html). Illnesses started on dates ranging from [March 13, 2018 to June 6, 2018](#). Ill people ranged in age from 1 to 88 years, with a median age of 28. Sixty-seven percent of ill people were female. Of 201 people with information available, 96 (48%) were hospitalized, including 27 people who developed hemolytic uremic syndrome, a type of kidney failure. Five deaths were reported from Arkansas, California, Minnesota (2), and New York.

WGS analysis of isolates from 184 ill people identified antibiotic resistance to chloramphenicol, streptomycin, sulfisoxazole, tetracycline, and trimethoprim-sulfamethoxazole. [Standard antibiotic resistance testing \(https://www.cdc.gov/narms/resources/glossary.html\)](https://www.cdc.gov/narms/resources/glossary.html) of eight clinical isolates by [CDC's National Antimicrobial Resistance Monitoring System \(https://www.cdc.gov/narms/index.html\)](https://www.cdc.gov/narms/index.html) (NARMS) laboratory confirmed these findings. Isolates from four of those ill people also contained genes for resistance to ampicillin and ceftriaxone. These findings do not affect treatment guidance since antibiotics are not recommended for patients with *E. coli* O157 infections.

Investigation of the Outbreak

Epidemiologic, laboratory, and traceback

[\(https://www.cdc.gov/foodsafety/outbreaks/investigating-outbreaks/index.html\)](https://www.cdc.gov/foodsafety/outbreaks/investigating-outbreaks/index.html) evidence indicated that romaine lettuce from the Yuma growing region was the likely source of this outbreak.

In interviews, ill people answered questions about the foods they ate and other exposures they had before they became ill. Of the 166 people interviewed, 145 (87%) reported eating romaine lettuce in the week before their illness started. This percentage was significantly higher than results from a [survey](#) [PDF - 787 KB]

[\(https://www.cdc.gov/foodnet/surveys/FNExpAtl03022011.pdf\)](https://www.cdc.gov/foodnet/surveys/FNExpAtl03022011.pdf) of healthy people in which 46% reported eating romaine lettuce in the week before they were interviewed. Some people who became sick in this outbreak did not report eating romaine lettuce, but had close contact with someone else who got sick from eating romaine lettuce.

The FDA and state and local regulatory officials traced the romaine lettuce to many farms in the Yuma growing region. The FDA, along with CDC and state partners, started an environmental assessment in the Yuma growing region and collected samples of water, soil, and manure. CDC laboratory testing identified the outbreak strain of *E. coli* O157:H7 in water samples taken from a canal in the Yuma growing region. WGS showed that the *E. coli* O157:H7 found in the canal water is closely related genetically to the *E. coli* O157:H7 from ill people.

Laboratory testing for other environmental samples is continuing. FDA is continuing to investigate to learn more about how the *E. coli* bacteria could have entered the water and ways this water could have contaminated romaine lettuce in the region.

According to the FDA, the last shipments of romaine lettuce from the Yuma growing region were harvested on April 16, 2018, and the harvest season there has ended. Contaminated lettuce that made people sick in this outbreak should no longer be available.

As of June 28, 2018, this outbreak appears to be over.

Previous Outbreak Announcements

> June 1, 2018

> May 16, 2018

> May 9, 2018

> May 2, 2018

> April 27, 2018

> April 25, 2018

> April 20, 2018

> April 18, 2018

> April 13, 2018

> Initial Announcement

At A Glance

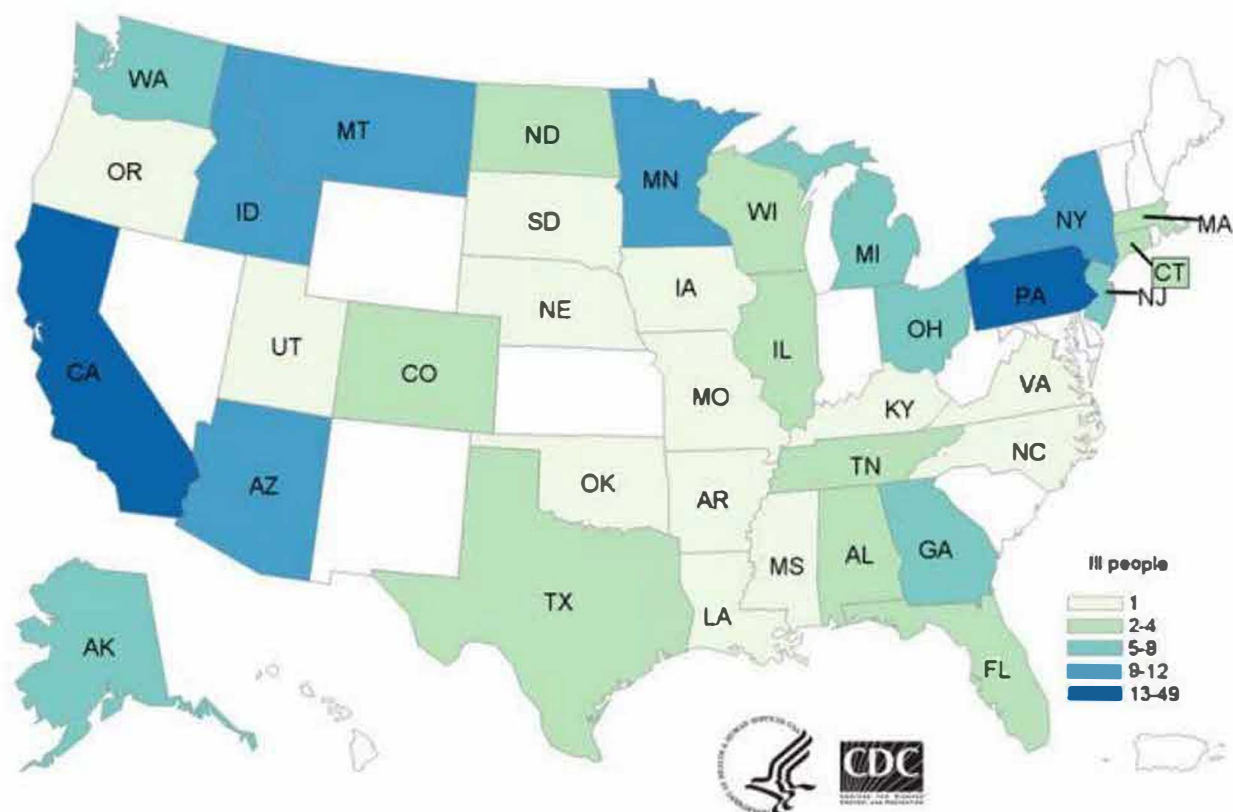
- Case Count: 210
- States: 36
- Deaths: 5
- Hospitalizations: 96

- Recall: No

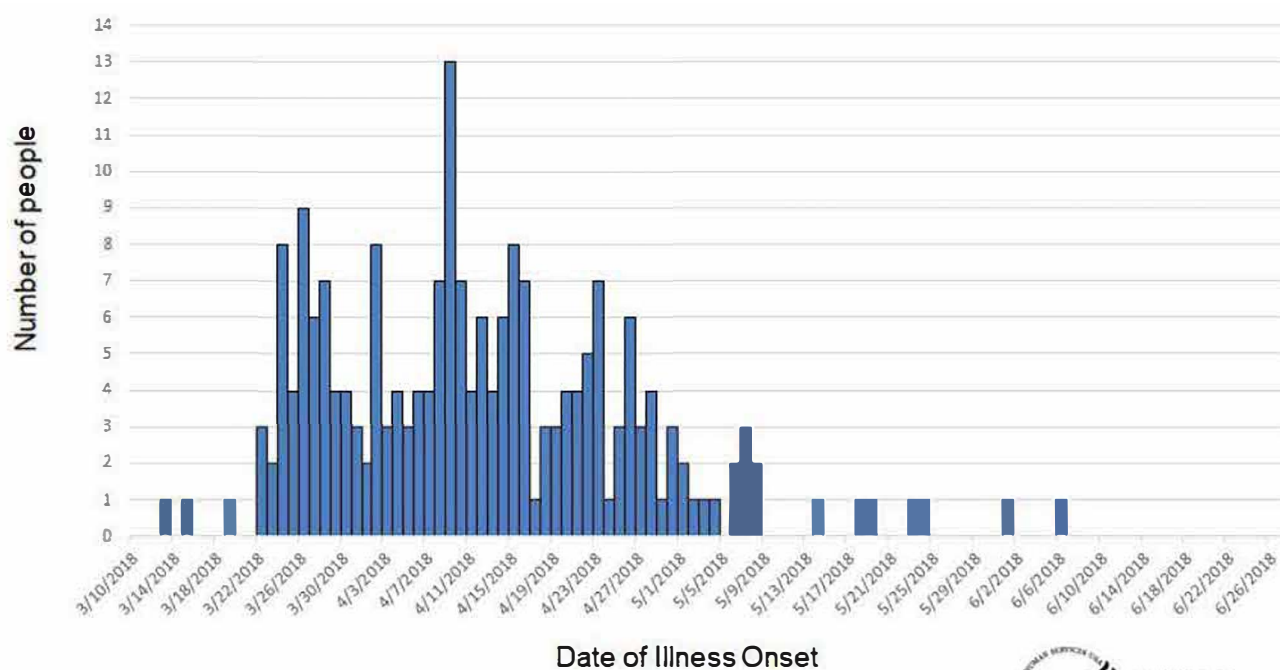


More Information

- Advice to Consumers, Restaurants, Retailers, and Clinicians
- Signs & Symptoms
- Key Resources



[CLICK TO VIEW CASE COUNT MAPS](#)



CLICK TO VIEW EPI CURVE GRAPHS

Related Links

Multistate Foodborne Outbreaks (<http://www.cdc.gov/foodsafety/outbreaks/multistate-outbreaks/outbreaks-list.html>)

Estimates of Foodborne Illness (<http://www.cdc.gov/foodborneburden/index.html>)

Food Safety at CDC (<http://www.cdc.gov/foodsafety/cdc-and-food-safety.html>)

Foodborne disease (<http://www.cdc.gov/foodsafety/facts.html>)

Travelers' Health: Safe Food & Water (<http://wwwnc.cdc.gov/travel/>)

Healthy Swimming (<http://www.cdc.gov/healthywater/swimming/index.html>)

E. coli Infection & Farm Animals

File Formats Help:

How do I view different file formats (PDF, DOC, PPT, MPEG) on this site?

(<https://www.cdc.gov/Other/plugins/>)

(<https://www.cdc.gov/Other/plugins/#pdf>)

Page last reviewed: April 13, 2018

Page last updated: June 28, 2018

Content source: Centers for Disease Control and Prevention (/)

National Center for Emerging and Zoonotic Infectious Diseases (NCEZID) (/ncezid/)

Division of Foodborne, Waterborne, and Environmental Diseases (DFWED) (/ncezid/dfwed/index.html)

Key	SourceState	Serotype	PFGE-XbaI-pattern	PFGE-BlnI-pattern	Outbreak	SourceCountry	SourceCity	SourceCountry	SourceType	SourceSite	TypeDetails	PatientAge
b6	AK	Undetermined:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		16
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		18
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		26
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		29
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		30
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		34
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		43
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		44
b6	AK	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		44
b6	AL	E. coli O157:H7	EXHX01.7171	EXHA26.5294	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	AL	E. coli O157:H7	EXHX01.7171	EXHA26.5294	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	AL	E. coli O157:H7	EXHX01.7171	EXHA26.5294	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	AR	E. coli O157:H7	EXHX01.1486	EXHA26.5274	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	AZ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		6
b6	AZ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		7
b6	AZ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		10
b6	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		17
b6	AZ	E. coli O157:Pending	EXHX01.1486	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		19
b6	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		41
b6	AZ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		45
b6	AZ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		65
b6	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		82
CDC__2018C-3900a	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3900b	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3900c	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3900d	AZ	E. coli O157:H7	EXHX01.1486	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3900e	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3900f	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3900g	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3900h	AZ	E. coli O157:H7	EXHX01.1486	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3901a	AZ	E. coli O157:H7	EXHX01.2951	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3901b	AZ	E. coli O157:H7	EXHX01.1486	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3901 c	AZ	E. coli O157:H7	EXHX01.2951	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3901d	AZ	E. coli O157:H7	EXHX01.2951	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3901e	AZ	E. coli O157:H7	EXHX01.2951	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3901f	AZ	E. coli O157:H7	EXHX01.2951	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902a	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902b	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902 c	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902d	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902e	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902f	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902g	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902h	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		

Key	SourceState	Serotype	PFGE-XbaI-pattern	PFGE-BlnI-pattern	Outbreak	SourceCountry	SourceCity	SourceCountry	SourceType	SourceSite	TypeDetails	PatientAge
CDC__2018C-3902i	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-3902j	AZ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Environmental	Water		
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		1
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		1
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		1
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		1
b6	CA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		1
b6	CA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		2
b6	CA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		2
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		3
b6	CA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		3
b6	CA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		4
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		6
b6	CA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		6
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		7
b6	CA	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		7
b6	CA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		8
b6	CA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		8
b6	CA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		8
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		13
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		13
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		13
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		14
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b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		14
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		14
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		14
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		14
b6	CA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		16
b6	CA	E. coli O157:Pending	EXHX01.0277	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		16
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		17
b6	CA	E. coli O157:Pending	EXHX01.1040	EXHA26.5148	1804MLEXH-1	b6	b6	USA	Human	Stool		17
b6	CA	E. coli O157:Pending	EXHX01.2951	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		17
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		18
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		20
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		21
b6	CA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		23
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		24
b6	CA	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		24
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		25
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		27
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		28
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		28
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		28

Key	SourceState	Serotype	PFGE-XbaI-pattern	PFGE-BlnI-pattern	Outbreak	SourceCountry	SourceCity	SourceCountry	SourceType	SourceSite	TypeDetails	PatientAge
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		35
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		36
b6	CA	E. coli O157:Pending	EXHX01.0277	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		36
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		36
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		37
b6	CA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		41
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		48
b6	CA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		57
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		60
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		62
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		63
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		72
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		75
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		75
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		76
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		87
b6	CA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		88
CDC__2018C-4267a	CA	E. coli O157:H7	EXHX01.7319	EXHA26.5432	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4267b	CA	E. coli O157:NM	EXHX01.7323	EXHA26.5433	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4267c	CA	E. coli O157:H7	EXHX01.7321	EXHA26.0929	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4267d	CA	E. coli O157:H7	EXHX01.7321	EXHA26.0929	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4267e	CA	E. coli O157:H7	EXHX01.7321	EXHA26.0929	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4267g	CA	E. coli O157:H7	EXHX01.0995	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4267h	CA	E. coli O157:H7	EXHX01.7321	EXHA26.0929	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4267i	CA	E. coli O157:H7	EXHX01.3227	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268a	CA	E. coli O157:H7	EXHX01.5440	EXHA26.5432	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268b	CA	E. coli O157:H7	EXHX01.5440	EXHA26.5432	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268c	CA	E. coli O157:H7	EXHX01.3227	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268d	CA	E. coli O157:H7	EXHX01.3227	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268e	CA	E. coli O157:H7	EXHX01.5440	EXHA26.5432	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268f	CA	E. coli O157:H7	EXHX01.3227	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268g	CA	E. coli O157:H7	EXHX01.3227	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268h	CA	E. coli O157:H7	EXHX01.5440	EXHA26.5432	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268i	CA	E. coli O157:H7	EXHX01.3227	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
CDC__2018C-4268j	CA	E. coli O157:H7	EXHX01.3227	EXHA26.0675	1804MLEXH-1			USA	Environmental	Water		
b6	CO	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Human	Stool		b6
b6	CO	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Human	Stool		b6
b6	CO	E. coli O157:H7	EXHX01.1486	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	CO	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Human	Stool		b6
b6	CO	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1			USA	Human	Stool		b6
b6	CT	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	FL	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		b6
b6	FL	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		b6
b6	FL	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		b6

Key	SourceState	Serotype	PFGE-XbaI-pattern	PFGE-BlnI-pattern	Outbreak	SourceCountry	SourceCity	SourceCountry	SourceType	SourceSite	TypeDetails	PatientAge
b6	GA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		b6
b6	GA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	GA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	GA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	IA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Urine		b6
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		12
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		23
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		26
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		36
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		37
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		50
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		51
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		52
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		57
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		58
b6	ID	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		64
b6	IL	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	IL	Pending:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	KS	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	KY	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	LA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MI	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MI	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MI	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MI	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MI	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		15
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		21
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		22
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		32
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		40
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		45
b6	MN	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		46
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		55
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		59
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		68
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		71
b6	MN	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		82
b6	MO	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6

Key	SourceState	Serotype	PFGE-Xbal-pattern	PFGE-BlnI-pattern	Outbreak	SourceCountry	SourceCity	SourceCountry	SourceType	SourceSite	TypeDetails	PatientAge
b6	MS	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		19
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		31
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		34
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		38
b6	MT	E. coli O157:H7	EXHX01.1486	EXHA26.5274	1804MLEXH-1	b6	b6	USA	Human	Stool		61
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		67
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		68
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		79
b6	MT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		85
b6	NC	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	ND	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	ND	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	ND	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	NE	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	NJ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		18
b6	NJ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		28
b6	NJ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		37
b6	NJ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		43
b6	NJ	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		46
b6	NJ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		55
b6	NJ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		66
b6	NJ	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		84
b6	NY	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		17
b6	NY	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		22
b6	NY	E. coli O157:H7	EXHX01.0124	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		23
b6	NY	E. coli O157:Pending	EXHX01.1486	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		24
b6	NY	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		29
b6	NY	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		36
b6	NY	E. coli O157:NM	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		41
b6	NY	E. coli O157:H7	EXHX01.0124	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		44
b6	NY	E. coli O157:NM	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		48
b6	NY	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		65
b6	NY	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		84
b6	OH	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		7
b6	OH	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		10
b6	OH	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		12
b6	OH	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		15
b6	OH	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		18
b6	OH	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		24
b6	OH	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		24
b6	OK	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	OR	E. coli O157:NM	EXHX01.1486	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Unknown		b6
b6	OR	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6

Key	SourceState	Serotype	PFGE-Xbal-pattern	PFGE-BlnI-pattern	Outbreak	SourceCountry	SourceCity	SourceCountry	SourceType	SourceSite	TypeDetails	PatientAge
b6	PA	E. coli O157:NM	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		12
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		12
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		13
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		13
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		14
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		14
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.5277	1804MLEXH-1	b6	b6	USA	Human	Stool		16
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		23
b6	PA	E. coli O157:NM	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		24
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		24
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		28
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		29
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.5277	1804MLEXH-1	b6	b6	USA	Human	Stool		29
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		30
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		32
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		38
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		39
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		42
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		61
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		63
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		68
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		70
b6	PA	E. coli O157:H7	EXHX01.1486	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		75
b6	PA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		80
b6	SD	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	SD	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	TN	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	TN	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	TN	Pending:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	TX	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	TX	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	TX	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	TX	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	UT	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	VA	E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	WA	Pending:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		1
b6	WA	Pending:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		2
b6	WA	Pending:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		3
b6	WA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		5
b6	WA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		7
b6	WA	E. coli O157:Undetermined	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		8
b6	WA	Pending:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		21
b6	WA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		31
b6	WA	E. coli O157:Pending	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		54

Key	SourceState	Serotype	PFGE-XbaI-pattern	PFGE-BlnI-pattern	Outbreak	SourceCountry	SourceCity	SourceCountry	SourceType	SourceSite	TypeDetails	PatientAge
b6	WI	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	WI	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6	WI	E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6		E. coli O157:H7	EXHX01.2401	EXHA26.0626	1804MLEXH-1	b6	b6		Human	Stool		b6
b6		E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6		E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	Australia	Human	Stool		b6
b6		E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6		E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6		Human	Stool		b6
b6		E. coli O157:HNT	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	USA	Human	Stool		b6
b6		E. coli O157:H7	EXHX01.0047	EXHA26.0626	1804MLEXH-1	b6	b6	Canada	Human	Stool		b6

Key	PatientSex	IsolatDate	ReceivedDate	UploadDate
b6	FEMALE	8/8/2018	8/10/2018	8/14/2018
b6	MALE	4/15/2018	4/23/2018	4/25/2018
b6	MALE	4/10/2018	4/16/2018	4/17/2018
b6	MALE	4/15/2018	4/23/2018	4/25/2018
b6	MALE	4/10/2018	4/16/2018	4/17/2018
b6	MALE	4/23/2018	4/23/2018	4/25/2018
b6	MALE	4/11/2018	4/16/2018	4/17/2018
b6	MALE	4/9/2018	4/13/2018	4/14/2018
b6	MALE	4/11/2018	4/16/2018	4/17/2018
b6	FEMALE	4/26/2018	5/11/2018	5/14/2018
b6	FEMALE	4/26/2018	5/11/2018	5/14/2018
b6	FEMALE	4/26/2018	5/11/2018	5/14/2018
b6	FEMALE	4/22/2018	5/1/2018	5/3/2018
b6	FEMALE	4/20/2018	4/26/2018	4/27/2018
b6	FEMALE	4/18/2018	4/26/2018	4/27/2018
b6	FEMALE	3/26/2018	4/10/2018	4/12/2018
b6	FEMALE	3/28/2018	4/11/2018	4/13/2018
b6	MALE	4/26/2018	5/22/2018	5/24/2018
b6	FEMALE	4/3/2018	4/17/2018	4/18/2018
b6	FEMALE	3/27/2018	4/10/2018	4/12/2018
b6	FEMALE	4/19/2018	4/26/2018	4/27/2018
b6	FEMALE	4/12/2018	4/19/2018	4/20/2018
CDC__2018C-3900a		6/5/2018		6/25/2018
CDC__2018C-3900b		6/5/2018		6/25/2018
CDC__2018C-3900c		6/5/2018		6/25/2018
CDC__2018C-3900d		6/5/2018		6/25/2018
CDC__2018C-3900e		6/5/2018		6/25/2018
CDC__2018C-3900f		6/5/2018		6/25/2018
CDC__2018C-3900g		6/5/2018		6/25/2018
CDC__2018C-3900h		6/5/2018		6/25/2018
CDC__2018C-3901a		6/5/2018		6/25/2018
CDC__2018C-3901b		6/5/2018		6/25/2018
CDC__2018C-3901c		6/5/2018		6/22/2018
CDC__2018C-3901d		6/5/2018		6/22/2018
CDC__2018C-3901e		6/5/2018		6/22/2018
CDC__2018C-3901f		6/5/2018		6/27/2018
CDC__2018C-3902a		6/5/2018		6/22/2018
CDC__2018C-3902b		6/5/2018		6/22/2018
CDC__2018C-3902c		6/5/2018		6/22/2018
CDC__2018C-3902d		6/5/2018		6/22/2018
CDC__2018C-3902e		6/5/2018		6/22/2018
CDC__2018C-3902f		6/5/2018		6/22/2018
CDC__2018C-3902g		6/5/2018		6/22/2018
CDC__2018C-3902h		6/5/2018		6/27/2018

Key	PatientSex	IsolatDate	ReceivedDate	UploadDate
CDC__2018C-3902i		6/5/2018		6/27/2018
CDC__2018C-3902j		6/5/2018		6/27/2018
b6	MALE	3/28/2018	4/12/2018	4/17/2018
b6	FEMALE	5/11/2018	5/17/2018	5/21/2018
b6	FEMALE	5/23/2018	6/5/2018	6/8/2018
b6	FEMALE	7/10/2018	8/3/2018	8/8/2018
b6	MALE	7/4/2018	7/10/2018	7/13/2018
b6	FEMALE	5/4/2018	5/17/2018	5/22/2018
b6	MALE	4/27/2018	5/10/2018	5/14/2018
b6	FEMALE	4/18/2018	4/26/2018	4/30/2018
b6	MALE	4/16/2018	5/4/2018	5/9/2018
b6	MALE	5/20/2018	5/25/2018	6/1/2018
b6	MALE	4/15/2018	5/4/2018	5/9/2018
b6	UNKNOWN	5/9/2018	8/10/2018	8/15/2018
b6	FEMALE	4/16/2018	4/25/2018	4/27/2018
b6	MALE	5/8/2018	5/21/2018	5/24/2018
b6	FEMALE	7/22/2018	7/27/2018	8/6/2018
b6	MALE	7/23/2018	8/10/2018	8/15/2018
b6	MALE	4/12/2018	5/1/2018	5/3/2018
b6	FEMALE	4/13/2018	4/19/2018	4/23/2018
b6	MALE	4/13/2018	4/20/2018	4/24/2018
b6	MALE	4/17/2018	4/26/2018	5/3/2018
b6	FEMALE	4/8/2018	4/17/2018	4/19/2018
b6	FEMALE	4/11/2018	4/19/2018	4/23/2018
b6	FEMALE	4/14/2018	4/19/2018	4/23/2018
b6	MALE	4/16/2018	4/25/2018	4/27/2018
b6	FEMALE	4/21/2018	5/3/2018	5/8/2018
b6	MALE	6/5/2018	6/13/2018	6/18/2018
b6	FEMALE	4/9/2018	4/17/2018	4/20/2018
b6	FEMALE	4/12/2018	4/27/2018	5/2/2018
b6	MALE	4/9/2018	4/17/2018	4/19/2018
b6	MALE	4/15/2018	4/25/2018	4/27/2018
b6	MALE	5/1/2018	5/16/2018	5/21/2018
b6	FEMALE	4/2/2018	4/10/2018	4/13/2018
b6	FEMALE	4/23/2018	5/2/2018	5/4/2018
b6	FEMALE	6/22/2018	7/2/2018	7/6/2018
b6	FEMALE	4/14/2018	5/4/2018	5/9/2018
b6	MALE	4/11/2018	5/4/2018	5/9/2018
b6	MALE	4/7/2018	4/16/2018	4/18/2018
b6	MALE	4/23/2018	5/1/2018	5/3/2018
b6	FEMALE	6/30/2018	7/5/2018	7/10/2018
b6	FEMALE	4/13/2018	4/19/2018	4/23/2018
b6	FEMALE	4/15/2018	4/20/2018	4/24/2018
b6	FEMALE	4/12/2018	5/4/2018	5/9/2018

Key	PatientSex	IsolatDate	ReceivedDate	UploadDate
b6	FEMALE	4/23/2018	5/2/2018	5/4/2018
b6	FEMALE	4/11/2018	4/25/2018	4/30/2018
b6	FEMALE	4/17/2018	5/4/2018	5/9/2018
b6	FEMALE	7/3/2018	7/11/2018	7/13/2018
b6	FEMALE	4/19/2018	4/26/2018	4/30/2018
b6	MALE	7/30/2018	8/7/2018	8/10/2018
b6	FEMALE	4/23/2018	4/27/2018	5/2/2018
b6	FEMALE	4/11/2018	5/4/2018	5/9/2018
b6	MALE	4/17/2018	4/23/2018	4/26/2018
b6	FEMALE	4/12/2018	4/18/2018	4/23/2018
b6	FEMALE	4/17/2018	5/4/2018	5/9/2018
b6	FEMALE	4/15/2018	4/24/2018	4/26/2018
b6	FEMALE	4/13/2018	4/19/2018	4/23/2018
b6	MALE	4/11/2018	4/25/2018	4/30/2018
b6	FEMALE	6/29/2018	7/19/2018	7/24/2018
b6	MALE	4/3/2018	4/19/2018	4/24/2018
b6	FEMALE	4/8/2018	4/13/2018	4/17/2018
CDC__2018C-4267a		7/12/2018		8/1/2018
CDC__2018C-4267b		7/12/2018		8/1/2018
CDC__2018C-4267c		7/12/2018		8/1/2018
CDC__2018C-4267d		7/12/2018		8/1/2018
CDC__2018C-4267e		7/12/2018		8/1/2018
CDC__2018C-4267g		7/12/2018		8/17/2018
CDC__2018C-4267h		7/12/2018		8/17/2018
CDC__2018C-4267i		7/12/2018		8/17/2018
CDC__2018C-4268a		7/12/2018		8/1/2018
CDC__2018C-4268b		7/12/2018		8/1/2018
CDC__2018C-4268c		7/12/2018		8/1/2018
CDC__2018C-4268d		7/12/2018		8/1/2018
CDC__2018C-4268e		7/12/2018		8/1/2018
CDC__2018C-4268f		7/12/2018		8/17/2018
CDC__2018C-4268g		7/12/2018		8/17/2018
CDC__2018C-4268h		7/12/2018		8/17/2018
CDC__2018C-4268i		7/12/2018		8/17/2018
CDC__2018C-4268j		7/12/2018		8/17/2018
b6	FEMALE	6/20/2018	6/25/2018	6/27/2018
b6	MALE	6/22/2018	6/27/2018	6/29/2018
b6	MALE	4/29/2018	5/8/2018	5/10/2018
b6	MALE	4/14/2018	4/19/2018	4/23/2018
b6	FEMALE	4/7/2018	4/17/2018	4/19/2018
b6	FEMALE	3/25/2018	3/29/2018	4/3/2018
b6	MALE	5/17/2018	6/13/2018	6/19/2018
b6	MALE	5/9/2018	6/13/2018	6/19/2018
b6	MALE	3/28/2018	5/3/2018	5/7/2018

Key	PatientSex	IsolatDate	Received Date	UploadDate
b6	FEMALE	4/13/2018	4/24/2018	4/26/2018
b6	FEMALE	3/31/2018	4/17/2018	4/20/2018
b6	MALE	4/14/2018	4/24/2018	4/26/2018
b6	UNKNOWN	4/17/2018	4/24/2018	4/26/2018
b6	FEMALE	4/27/2018	5/3/2018	5/8/2018
b6	FEMALE	4/4/2018	4/5/2018	4/10/2018
b6	MALE	4/3/2018	4/4/2018	4/10/2018
b6	FEMALE	4/2/2018	4/3/2018	4/6/2018
b6	FEMALE	4/5/2018	4/6/2018	4/10/2018
b6	MALE	4/3/2018	4/4/2018	4/6/2018
b6	MALE	4/3/2018	4/4/2018	4/6/2018
b6	FEMALE	4/20/2018	4/23/2018	4/25/2018
b6	FEMALE	4/5/2018	4/6/2018	4/10/2018
b6	MALE	4/2/2018	4/3/2018	4/6/2018
b6	FEMALE	4/10/2018	4/11/2018	4/16/2018
b6	FEMALE	4/9/2018	4/10/2018	4/12/2018
b6	FEMALE	4/19/2018	4/27/2018	5/1/2018
b6	FEMALE	4/5/2018	4/5/2018	4/10/2018
b6	FEMALE		8/16/2018	8/17/2018
b6	MALE	4/18/2018	4/25/2018	4/27/2018
b6	FEMALE		4/10/2018	4/13/2018
b6	FEMALE	4/26/2018	5/3/2018	5/7/2018
b6	FEMALE	4/20/2018	4/26/2018	4/30/2018
b6	MALE	3/29/2018	4/2/2018	4/6/2018
b6	MALE	4/20/2018	4/26/2018	4/30/2018
b6	FEMALE	5/15/2018	5/23/2018	5/25/2018
b6	FEMALE	4/8/2018	4/13/2018	4/16/2018
b6	MALE	4/18/2018	4/27/2018	4/30/2018
b6	FEMALE	8/6/2018	8/10/2018	8/13/2018
b6	MALE	4/3/2018	4/11/2018	4/12/2018
b6	FEMALE	4/12/2018	4/23/2018	4/24/2018
b6	FEMALE	4/23/2018	4/30/2018	5/3/2018
b6	FEMALE	4/23/2018	5/2/2018	5/3/2018
b6	FEMALE	5/1/2018	5/7/2018	5/8/2018
b6	FEMALE	4/25/2018	5/1/2018	5/2/2018
b6	FEMALE	4/28/2018	5/4/2018	5/7/2018
b6	FEMALE	4/23/2018	4/30/2018	5/1/2018
b6	FEMALE	5/5/2018	5/11/2018	5/14/2018
b6	MALE	4/25/2018	5/2/2018	5/3/2018
b6	FEMALE	4/24/2018	5/1/2018	5/2/2018
b6	FEMALE	4/28/2018	5/4/2018	5/7/2018
b6	FEMALE	4/27/2018	5/4/2018	5/7/2018
b6	FEMALE	5/2/2018	5/9/2018	5/10/2018
b6	FEMALE	3/28/2018	4/3/2018	4/5/2018

Key	PatientSex	IsolatDate	Received Date	UploadDate
b6	FEMALE	4/11/2018	4/23/2018	4/24/2018
b6	FEMALE	4/18/2018	4/23/2018	4/25/2018
b6	MALE	4/2/2018	4/10/2018	4/12/2018
b6	FEMALE	4/7/2018	4/13/2018	4/17/2018
b6	MALE	4/9/2018	4/13/2018	4/17/2018
b6	FEMALE	4/19/2018	4/25/2018	4/27/2018
b6	FEMALE	4/5/2018	4/13/2018	4/19/2018
b6	MALE	4/5/2018	4/10/2018	4/12/2018
b6	FEMALE	4/7/2018	4/13/2018	4/17/2018
b6	FEMALE	4/5/2018	4/10/2018	4/12/2018
b6	FEMALE	5/11/2018	5/23/2018	5/25/2018
b6	MALE	5/4/2018	5/15/2018	5/17/2018
b6	MALE	4/22/2018	4/30/2018	5/2/2018
b6	FEMALE	4/24/2018	5/2/2018	5/4/2018
b6	FEMALE	4/29/2018	5/4/2018	5/8/2018
b6	MALE	3/26/2018	4/5/2018	4/6/2018
b6	FEMALE	3/27/2018	4/5/2018	4/6/2018
b6	FEMALE	4/22/2018	4/30/2018	5/2/2018
b6	FEMALE	3/27/2018	4/5/2018	4/6/2018
b6	FEMALE	3/27/2018	4/3/2018	4/4/2018
b6	FEMALE	4/1/2018	4/10/2018	4/11/2018
b6	FEMALE	3/26/2018	4/5/2018	4/6/2018
b6	FEMALE	3/28/2018	4/5/2018	4/6/2018
b6	FEMALE	3/30/2018	4/5/2018	4/10/2018
b6	FEMALE	3/28/2018	4/10/2018	4/12/2018
b6	FEMALE	4/14/2018	4/27/2018	5/1/2018
b6	MALE	4/18/2018	5/1/2018	5/7/2018
b6	FEMALE	4/24/2018	5/16/2018	5/18/2018
b6	FEMALE	5/8/2018	5/16/2018	5/24/2018
b6	FEMALE	4/28/2018	5/10/2018	5/15/2018
b6	FEMALE	4/14/2018	4/26/2018	4/30/2018
b6	FEMALE	4/27/2018	5/4/2018	5/8/2018
b6	FEMALE	4/14/2018	5/30/2018	6/1/2018
b6	FEMALE	5/1/2018	5/23/2018	5/25/2018
b6	FEMALE	4/29/2018	5/7/2018	5/10/2018
b6	FEMALE	4/30/2018	5/7/2018	5/10/2018
b6	FEMALE	5/9/2018	5/18/2018	5/22/2018
b6	MALE	5/1/2018	5/9/2018	5/11/2018
b6	FEMALE	3/30/2018	4/17/2018	4/18/2018
b6	FEMALE	3/26/2018	4/2/2018	4/4/2018
b6	FEMALE	3/30/2018	4/6/2018	4/10/2018
b6	FEMALE	5/11/2018	5/22/2018	5/24/2018
b6	FEMALE	4/27/2018	5/4/2018	5/10/2018
b6	MALE	7/12/2018	7/18/2018	7/20/2018

Key	PatientSex	IsolatDate	Received Date	UploadDate
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b6	FEMALE	3/30/2018	4/9/2018	4/12/2018
b6	FEMALE	3/28/2018	4/9/2018	4/12/2018
b6	MALE	4/6/2018	4/16/2018	4/19/2018
b6	FEMALE	3/16/2018	4/11/2018	4/16/2018
b6	FEMALE	3/30/2018	4/11/2018	4/16/2018
b6	FEMALE	4/13/2018	4/25/2018	5/1/2018
b6	MALE	4/4/2018	4/16/2018	4/19/2018
b6	FEMALE	3/26/2018	4/2/2018	4/5/2018
b6	MALE	3/28/2018	4/9/2018	4/12/2018
b6	FEMALE	4/7/2018	4/16/2018	4/19/2018
b6	FEMALE	4/2/2018	4/9/2018	4/12/2018
b6	FEMALE	4/13/2018	4/30/2018	5/3/2018
b6	FEMALE	4/3/2018	4/9/2018	4/12/2018
b6	FEMALE	4/9/2018	4/16/2018	4/19/2018
b6	FEMALE	4/12/2018	4/23/2018	4/26/2018
b6	MALE	4/1/2018	4/10/2018	4/12/2018
b6	MALE	5/10/2018	5/21/2018	5/24/2018
b6	MALE	3/29/2018	4/11/2018	4/16/2018
b6	FEMALE	4/17/2018	4/25/2018	5/1/2018
b6	MALE	4/5/2018	4/16/2018	4/19/2018
b6	FEMALE	3/29/2018	5/3/2018	5/8/2018
b6	FEMALE	4/3/2018	4/16/2018	4/19/2018
b6	MALE	3/29/2018	4/9/2018	4/12/2018
b6	FEMALE	7/30/2018	8/2/2018	8/6/2018
b6	MALE	3/29/2018	4/18/2018	4/19/2018
b6	MALE	4/30/2018	5/10/2018	5/14/2018
b6	MALE	3/25/2018	4/23/2018	4/25/2018
b6	FEMALE	4/26/2018	5/4/2018	5/8/2018
b6	FEMALE	5/6/2018	5/17/2018	5/21/2018
b6	MALE	5/26/2018		6/5/2018
b6	FEMALE	4/11/2018	5/1/2018	5/3/2018
b6	FEMALE	4/28/2018	5/11/2018	5/15/2018
b6	MALE	4/22/2018	4/25/2018	4/26/2018
b6	FEMALE	3/29/2018	4/9/2018	4/11/2018
b6	FEMALE	4/21/2018	4/24/2018	4/25/2018
b6	FEMALE	4/14/2018	4/24/2018	4/25/2018
b6	MALE	4/17/2018	4/24/2018	4/25/2018
b6	MALE	4/24/2018	5/1/2018	5/3/2018
b6	FEMALE	7/16/2018	7/26/2018	7/27/2018
b6	MALE	4/12/2018	4/19/2018	4/20/2018
b6	FEMALE	6/8/2018	6/12/2018	6/14/2018
b6	FEMALE	4/16/2018	4/26/2018	4/27/2018
b6	FEMALE	3/26/2018	4/5/2018	4/6/2018

Key	PatientSex	IsolatDate	Received Date	UploadDate
b6	FEMALE	5/2/2018	5/9/2018	5/10/2018
b6	FEMALE	4/15/2018	4/17/2018	4/25/2018
b6	MALE	8/10/2018	8/17/2018	8/20/2018
b6	FEMALE	4/12/2018	4/20/2018	4/23/2018
b6	UNKNOWN	4/18/2018	5/11/2018	5/15/2018
b6	MALE		4/19/2018	4/24/2018
b6	FEMALE	7/30/2018	8/14/2018	8/17/2018
b6	FEMALE	5/31/2018	6/1/2018	6/6/2018
b6	FEMALE	4/27/2018	5/3/2018	5/4/2018
b6	MALE	4/2/2018	4/17/2018	4/18/2018

E. coli O157
Cluster 1804MLEXH-1

June 27, 2018

Agenda

- Roll call
- Slides
- State updates from states with new cases
- FDA update
- Communications
- Case Count Confirmations
- Manuscript
- Final questions or thoughts

Cases of *E. coli* O157 in cluster 1804MLEXH-1, as of June 27, 2018

STATE	COUNT
AL	3
AK	8
AR	1
AZ	9
CA	49
CO	3
CT	2
FL	3
GA	5
IA	1
ID	12
IL	2
KY	1
LA	1
MA	4
MI	5
MN	12
MO	1
MS	1
MT	9
ND	3
NE	1
NJ	8
NY	11
NC	1
OH	7
OK	1
OR	1
PA	24
SD	1
TN	3
TX	4
UT	1
VA	1
WA	8
WI	3
TOTAL	210

- Case definition:
 - Infection with *E. coli* O157, and
 - with isolate matching PFGE pattern combination EXHX01.0047/EXHA26.0626 (204) or EXHX01.0124/EXHA26.0626 (2) or EXHX01.0277/EXHA26.0626 (2) or EXHX01.1486/EXHA26.0626 (8) or EXHX01.2401/EXHA26.0626 (1) or EXHX01.1040/EXHA26.5148 (1) or EXHX01.0047/EXHA26.5277 (2) or EXHX01.1486/EXHA26.5274 (2) or EXHX01.2951/EXHA26.0626 (5) or EXHX01.7171/EXHA26.5294 (3), and
 - with isolation dates during 3/16/2018 – present
- 210 cases from 36 states
- Isolation dates: 3/16/2018 – 6/8/2018
- Reported onset dates (n=195): 3/13/2018 – 6/6/2018

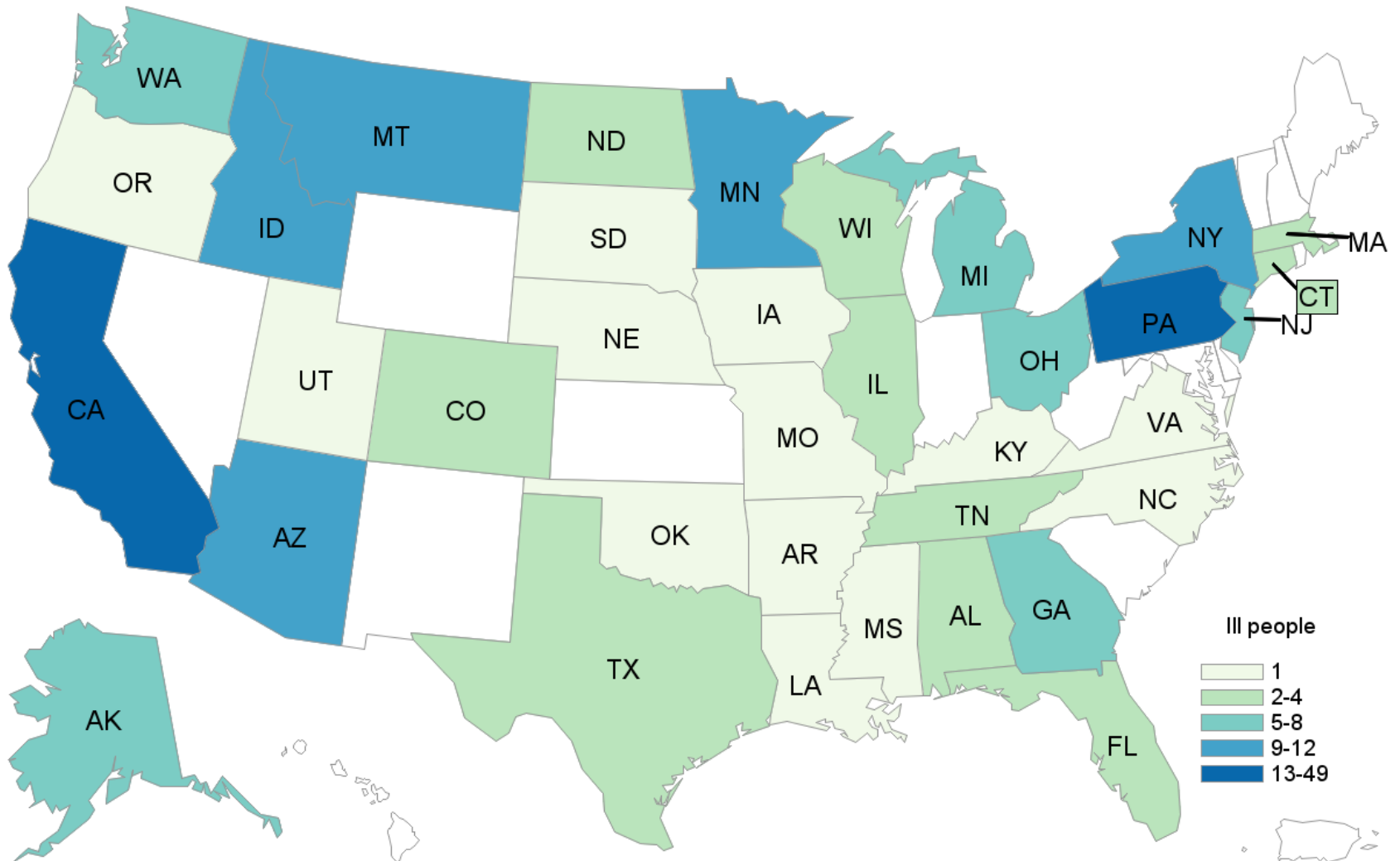
Table 2. Patient demographics in *E. coli* O157 cluster 1804MLEXH-1, as of June 27, 2018

Demographics	
Age range (median), (n=210)	1-88 (28)
Age categories in years (n=210)	n (%)
<5	15 (7)
5 to 17	55 (26)
18 to 59	101 (48)
≥60	39 (19)
Sex (n=210)	n (%)
Female	140 (67)

Table 3. Patient outcomes in *E. coli* O157 cluster 1804MLEXH-1, as of June 27, 2018

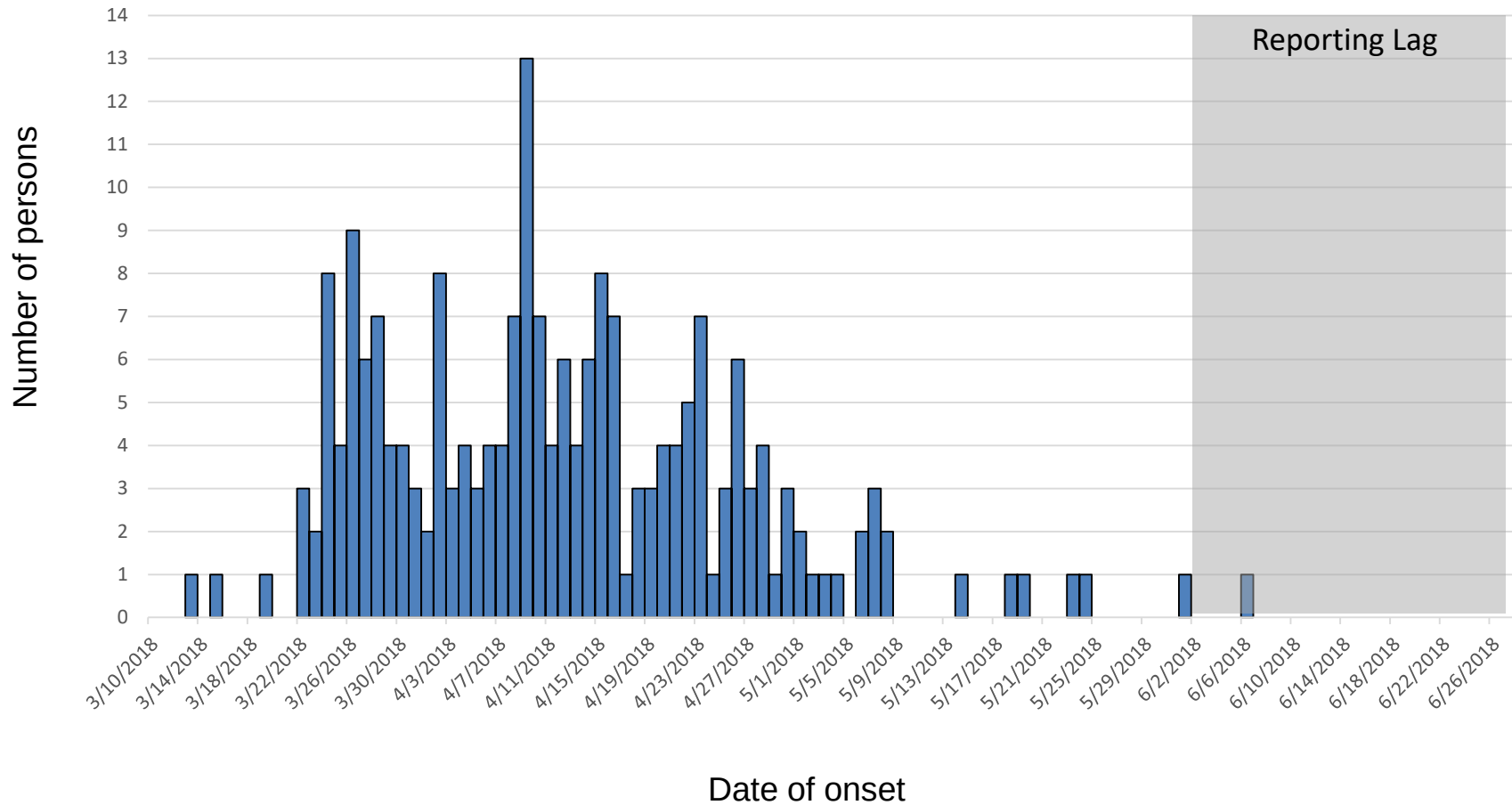
Outcomes	n (%)
Hospitalized (n=198)	93 (47)
HUS (n=185)	27 (15)
Died (n=198)	5 (3)

People infected with the outbreak strain of *E.coli* O157:H7,
by state of residence, as of June 27, 2018 (n=210)



Information for internal use only; not for distribution. Data are preliminary and subject to change

Persons infected with the outbreak strain of *E. coli* O157 (1804MLEXH-1), by date of onset*, as of June 27, 2018



*Some dates are estimated

Information for internal use only; not for distribution. Data are preliminary and subject to change

Interview Data

- Of those interviewed, 171/177 (97%) report leafy green exposures
 - 145/166 (87%) report romaine
- Identified Sub-clusters
 - Panera
 - Applebee's
 - Red Lobster
 - Alaska Prison
 - Chick-Fil-A
 - Papa Murphy's
- Common Stores
 - Shop-Rite
 - Costco
 - Meijer

Environmental Samples

- E. coli O157:H7 has been identified in 50 L irrigation canal water samples (24 isolates) taken from three irrigation canal locations along a 2 mile stretch in the Wellton area
 - Main outbreak strain identified (EXHX01.0047/EXHA26.0626)
 - Secondary outbreak strain identified (EXHX01.1486/EXHA26.0626)
 - Close variant of the outbreak strain identified (EXHX01.2951/EXHA26.0626)
- Whole genome sequencing indicates that these 20 isolates are highly related to clinical isolates
- Additional samples are pending

Clade A: Cases of *E. coli* O157 in cluster 1804MLEXH-1

- **28 new isolates added, but this includes 3 from Clade D and 9 from Clade F**
- **Reported onset dates:** 4/14/2017 – 5/7/2018
- **Subclusters:**
 - Applebee's (8)
 - Buca di Beppo (3)
 - Chick-Fil-A (4)
 - Costco kiosk (2)
 - Hospital Cafeteria (2)
 - ID Local Chain A (2)
 - Moe's (3)
 - Panera (5)
 - Papa Murphy's (4)
 - AK Prison (8)
 - Red Lobster (6)
 - Texas Roadhouse (3)
 - La Madeleine (2)
 - Meijer (2)
 - MN Residential Facilities (3)
- **Historical Isolates or Variants:**

One from 1704MLEXH-1 from CO, 2 from Canada, one from ME from earlier 2018 outbreak, one PA case variant with Panera exposure, 1 MT variant, Lake Wildwood

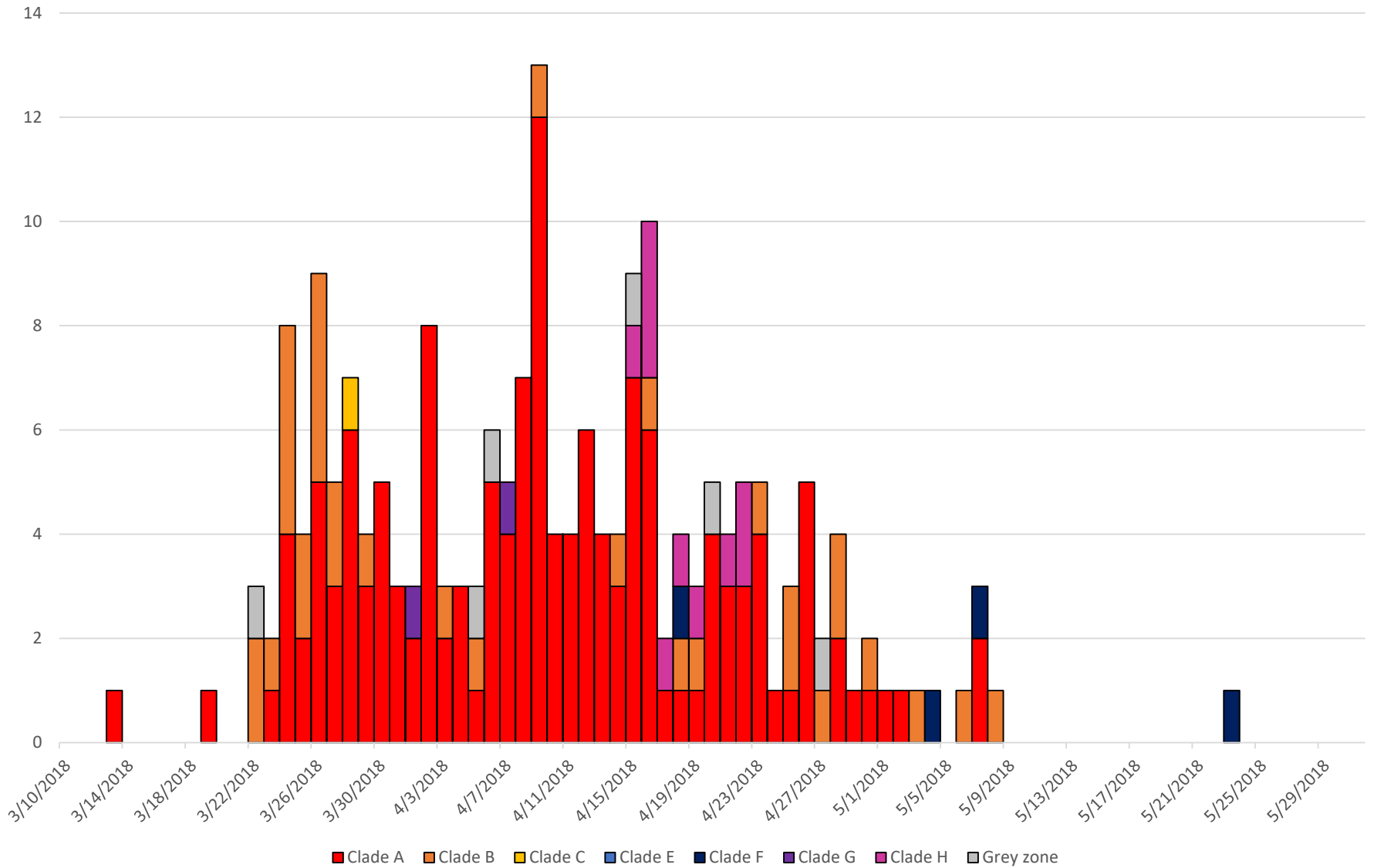
Clade B: Cases of *E. coli* O157 in cluster 1804MLEXH-1

- **13 isolates added**
- **Reported onset dates:** 12/4/2017 – 5/8/2018
- **Subclusters:**
 - Panera (n=12)
 - OH Subway
 - AL High school
- **Panera Locations:**
 - Alliance, OH (1)
 - Bensalem, PA (1)
 - Bethlehem, PA (1)
 - Easton, PA (1)
 - Fenton, MO (1)
 - Flemington, NJ (1)
 - Murrysville, PA (1)
 - Phillipsburg, NJ (1)
 - Raritan, NJ (3; 1 reports no romaine lettuce eaten)
 - Not documented (NJ resident): 1
- **Historical Isolates or variants**
 - One from WI from earlier 2018, one from Canada, one variant from Michigan

Clade F: Cases of *E. coli* O157 in cluster 1804MLEXH-1

- 4 cases from 2 states
- Onsets 4/18/2018 – 5/23/2018
- Two had raw, unpasteurized cheese

Epi Curve by Clade



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