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Shiga Toxin–Producing *Escherichia coli* O157:H7 Illness Outbreak Associated with Untreated, Pressurized, Municipal Irrigation Water — Utah, 2023

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Abstract

During July–September 2023, an outbreak of Shiga toxin–producing *Escherichia coli* O157:H7 illness among children in city A, Utah, caused 13 confirmed illnesses; seven patients were hospitalized, including two with hemolytic uremic syndrome. Local, state, and federal public health partners investigating the outbreak linked the illnesses to untreated, pressurized, municipal irrigation water (UPMIW) exposure in city A; 12 of 13 ill children reported playing in or drinking UPMIW. Clinical isolates were genetically highly related to one another and to environmental isolates from multiple locations within city A's UPMIW system. Microbial source tracking, a method to indicate possible contamination sources, identified birds and ruminants as potential sources of fecal contamination of UPMIW. Public health and city A officials issued multiple press releases regarding the outbreak reminding residents that UPMIW is not intended for drinking or recreation. Public education and UPMIW management and operations interventions, including assessing and mitigating potential contamination sources, covering UPMIW sources and reservoirs, indicating UPMIW lines and spigots with a designated color, and providing conspicuous signage to communicate risk and intended use might help prevent future UPMIW-associated illnesses.

Investigation and Results

Identification of the Outbreak and Characteristics of Cases

Shiga toxin–producing *Escherichia coli* (STEC) O157:H7 is an enteric illness that can cause hemolytic uremic syndrome (HUS), a severe, life-threatening condition which affects the kidneys; young children (aged <5 years) are among the most susceptible to HUS. During July 25–30, 2023, six cases of STEC O157:H7 illness in children were reported to the Utah County Health Department (UCHD), with onset during July 22–27. All six ill children lived in city A, Utah. UCHD investigators interviewed the identified children's parents using standard case investigation forms to assess various exposures before illness onset. Preliminary whole genome sequencing (WGS) found that two ill children's clinical isolates were zero alleles different from each other, suggesting that an outbreak was occurring. On July 31, an outbreak investigation was initiated.

Investigators identified 13 children with confirmed STEC O157:H7 illness linked to this outbreak, with illness onsets during July 22–August 31 (Figure 1). The median patient age was 4 years (range = 1–15 years). Seven patients were hospitalized, including two with HUS; no deaths were reported.

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This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.*

Association of Outbreak with Exposure to Untreated, Pressurized, Municipal Irrigation Water

Investigators developed a questionnaire to obtain additional exposure information for these cases and those that were later identified, including details regarding exposure to untreated, pressurized, municipal irrigation water (UPMIW), which had frequently been reported in preliminary interviews. UPMIW is surface water piped from reservoirs to homes; it is intended for outdoor landscapes (lawns and gardens) and is not suitable for drinking or recreational activities. UPMIW is not routinely monitored or tested.

All city A residences and businesses have outdoor connections to the UPMIW system. City A's UPMIW is primarily sourced from mountain snow melt and is carried >30 miles (>48 km) by a river and an underground pipeline to several open UPMIW reservoirs within city A and surrounding communities before being pumped to residential connections. Secondary sources of city A's UPMIW system comprise public wells and natural surface waters, including nearby rivers and creeks.

Twelve of 13 ill persons reported UPMIW exposure in city A during the week before symptom onset, including playing with hose water (five), inflatable lawn water toys (three), and water tables (two); drinking (two); and running through sprinklers (one). Among seven ill persons with discrete UPMIW exposure dates, the median incubation period was 3 days (range = 1–5 days). The one ill person who did not report UPMIW exposure was not a city A resident but did report spending time in city A during the week preceding symptom onset. No ill persons are known to have eaten noncommercial produce irrigated with UPMIW.

Environmental Investigation

On August 14, investigators conducted an environmental investigation at two of city A's UPMIW reservoirs and nine sites where persons with confirmed illness reported UPMIW exposure, including private homes. Investigators collected large-volume water samples by dead-end ultrafiltration and grab samples (unfiltered water collected in 1 liter bottles according to Environmental Protection Agency and CDC protocols†); samples of sediment and bird feces from the reservoirs; and swabs of spigots, hoses, toys, and other surfaces likely to have had contact with UPMIW. Investigators observed birds on and around UPMIW reservoirs during the environmental investigation; no other animals or obvious potential sources of STEC O157:H7 were observed during sampling.

* 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

† https://cfpub.epa.gov/si/si_public_record_Report.cfm?dirEntryId=355726&Lab=CESER

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Laboratory Investigation

Investigators submitted samples of bird feces to the Utah Public Health Laboratory for STEC O157:H7 culture and submitted all other environmental samples to CDC for culture of STEC O157:H7 (*1*–*3*), followed by WGS of confirmed STEC O157:H7 isolates. Grab water samples were tested for generic *E. coli* and total coliforms per 100 mL. Microbial source tracking was performed for all dead-end ultrafiltration samples and both reservoir sediment samples (*4*–*6*). Microbial source tracking is used to detect microbial markers specific to the feces of avian species, ruminants (such as cattle, sheep, and deer), and humans (all known fecal shedders of STEC).[§] Clinical laboratories submitted stool samples from ill persons to the Utah Public Health Laboratory for STEC O157:H7 culture, isolation, and WGS.

STEC O157:H7 was isolated from UPMIW reservoir sediment and dead-end ultrafiltration water samples from five of nine exposure sites. STEC O157:H7 was not detected in any other environmental samples collected.

WGS results indicated clinical isolates were within 0–1 allele difference of each other, and the environmental isolates were all within 0–2 allele differences of the clinical isolates by core genome multilocus sequence typing (Figure 2).[¶] All sequencing analysis was conducted using the WGS analysis software platform (version 7.6; BioNumerics). Results from generic *E. coli* and total coliform testing performed on water grab samples were variable (Table), and two exposure sites with detectable STEC O157:H7 had no detectable coliforms or generic *E. coli* (<1 most probable number per 100 mL). Of 12 samples analyzed by microbial source tracking (10 dead-end ultrafiltration and two sediment), avian, ruminant, and human fecal markers were detected in 10, six, and one dead-end ultrafiltration samples, respectively, and the avian marker was detected in both sediment samples.

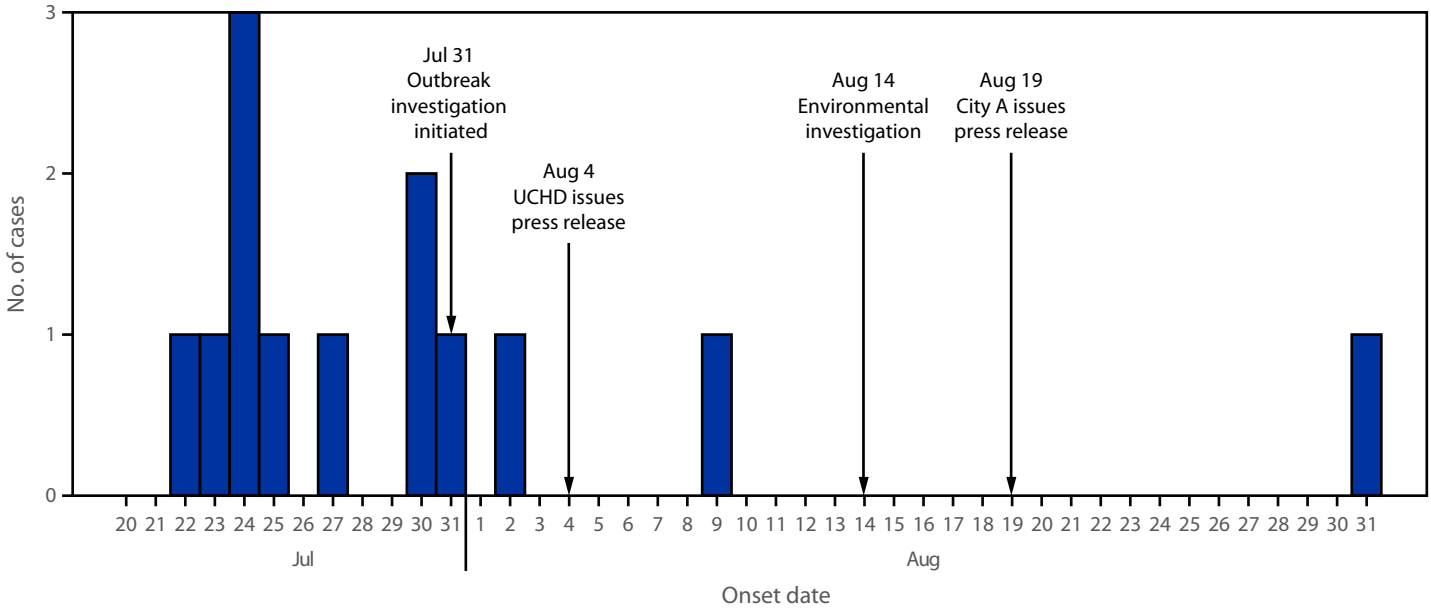
[§] https://cfpub.epa.gov/si/si_public_record_Report.cfm?Lab=NRMRL&dirEntryID=133523

[¶] https://www.applied-maths.com/bionumerics

Public Health Response

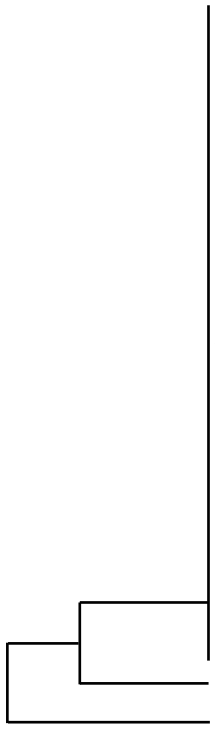
UCHD issued a press release on August 4 (after identification of the first eight cases), before the environmental investigation, notifying the public of the outbreak, and warning against drinking or playing in UPMIW. After the press release, two additional cases were reported. On August 19, city A issued a second press release, stating that STEC O157:H7 had been detected in UPMIW samples and recommending that residents cook homegrown produce and avoid watering lawns and renewed warnings not to drink or play in UPMIW. City A distributed mailers on August 28, further informing residents of the risks associated with using UPMIW for drinking or recreation. City A is also assessing other prevention strategies, including water treatment and reservoir cleaning.

FIGURE 1. Cases of reported Shiga toxin–producing *Escherichia coli* O157:H7 illnesses, by onset date* (N = 13) — city A, Utah, July–August 2023



Abbreviation: UCHD = Utah County Health Department.
* At the time of the August 4 press release, only eight cases had been reported to public health officials.

FIGURE 2. Genetic relatedness* of clinical and environmental isolates from samples collected during the outbreak investigation — city A, Utah, July–August 2023



Case/Site	Sample type	Collection date	NCBI accession
A	Human	Jul 24	SAMN36828866
B	Human	Jul 26	SAMN36828864
C	Human	Jul 27	SAMN36841952
D	Human	Jul 27	SAMN36938186
F	Human	Jul 30	SAMN36938187
G	Human	Aug 1	SAMN36984461
H	Human	Aug 2	SAMN36938185
I	Human	Jul 28	SAMN36872530
J	Human	Aug 6	SAMN36984457
K	Human	Aug 12	SAMN37047336
L	Human	Aug 3	SAMN36984458
M	Human	Sep 2	SAMN37413894
A	Environmental	Aug 14	SAMN37216954
D	Environmental	Aug 14	SAMN37216374
G	Environmental	Aug 14	SAMN37216376
I	Environmental	Aug 14	SAMN37216378
Reservoir	Environmental	Aug 14	SAMN37216381
E	Human	Jul 29	SAMN36841951
C	Environmental	Aug 14	SAMN37216372

Abbreviation: NCBI = National Center for Biotechnology Information.
* Isolates from cases A–M and environmental samples A, D, G, and I and from the reservoir differ from case E and environmental sample C by a median of zero alleles (range = 0–1) and a median of zero alleles (range = 0–2), respectively, by core genome multilocus sequence typing.

The Utah Department of Health and Human Services issued a Health Alert Network message about the outbreak on August 22, encouraging health care providers to perform stool testing for persons with diarrheal illness, educating providers about signs and symptoms of HUS, and warning against antibiotic treatment for STEC infections because treatment might increase the risk for HUS (*7*).

Discussion

UPMIW systems are generally uncommon in the United States; however, they are used in some Utah communities to irrigate residential outdoor landscapes. These systems were designed to conserve drinking water and reduce water treatment costs. Utah UPMIW systems are not intended for drinking or recreation, are not monitored or tested for water quality, and, except for 2022 state legislation requiring metering,** are not currently regulated by state or local authorities.

City A installed an upgraded drinking water system in 1989 and, subsequently, established its UPMIW system by converting its previous drinking water system to a UPMIW system. Because UPMIW is also used by city A for fire suppression, it remains available to residents year-round, although its use is only encouraged during landscape irrigation season, usually mid-April through mid-October.

Epidemiologic and laboratory evidence confirmed UPMIW as the vehicle of this community STEC O157:H7 outbreak. In 2010 and 2015, two other Utah cities experienced campylobacteriosis outbreaks that were suspected to have been caused by cross-connections between UPMIW and drinking water lines (Utah Department of Health and Human Services, unpublished data, 2010 and 2015). Data from city A's outbreak did not specifically implicate homegrown produce as an illness-causing vehicle, but previous outbreaks demonstrated that produce grown with water containing STEC O157:H7 can cause illness (*8*,*9*). Additional data are needed to understand risks associated with consuming noncommercial produce irrigated with UPMIW.

** https://le.utah.gov/~2022/bills/static/HB0242.html#73-10-34.5

TABLE. Environmental testing results of a Shiga toxin–producing *Escherichia coli* O157:H7 outbreak investigation — city A, Utah, July–August 2023

	Grab water samples (MPN/100 mL)		Dead-end ultrafiltration water samples	
Site*	**Total coliforms†**	***E. coli*†**	**Microbial source tracking§**	***E. coli* O157:H7**
Exposure site A	<1	<1	Avian: detected Ruminant: ND Human: ND	Detected
Exposure site C	344.8	5.1	Avian: detected Ruminant: detected Human: ND	Detected
Exposure site D	866.4	8.5	Avian: detected Ruminant: ND Human: ND	Detected
Exposure sites E and F	5.2	<1	Avian: detected Ruminant: ND Human: ND	ND
Exposure site G	NC	NC	Avian: detected Ruminant: detected Human: detected	Detected
Exposures site H	686.7	3.1	Avian: detected Ruminant: detected Human: ND	ND
Exposure site I	<1	<1	Avian: detected Ruminant: detected Human: ND	Detected
Exposure site J	285.1	4.1	Avian: detected Ruminant: detected Human: ND	ND
Exposure site K	228.2	10.8	Avian: detected Ruminant: detected Human: ND	ND
City A UPMIW reservoir	Grab #1: 33.1 Grab #2: 613.1	Grab #1: 2.0 Grab #2: 9.6	Avian: detected Ruminant: ND Human: ND	ND
City A UPMIW reservoir sediment #1	NA	NA	Avian: detected Ruminant: ND Human: ND	ND
City A UPMIW reservoir sediment #2	NA	NA	Avian: detected Ruminant: ND Human: ND	Detected

Abbreviations: *E. coli* = *Escherichia coli;* MPN = most probable number; NA = not applicable; NC = not collected; ND = not detected; UPMIW = untreated, pressurized, municipal irrigation water.

* Exposure sites A–K were named based on the location of each ill person's reported UPMIW exposure.

† Total coliforms and *E. coli* (fecal indicator bacteria) were measured using Environmental Protection Agency standard methods, IDEXX Colilert-18 or Enterolert, on 100-mL grab water samples paired with dead-end ultrafiltration water samples. Sediment was not tested for total coliforms and *E. coli*.

§ Microbial source tracking assays were conducted using methods described in https://journals.asm.org/doi/10.1128/aem.04137-13, https://academic.oup.com/jambio/article/108/3/974/6720002?login=true, and https://www.frontiersin.org/articles/10.3389/fsufs.2019.00124/full.

¶ Detection of *E. coli* O157:H7 in environmental samples was determined using methods from https://assets.publishing.service.gov.uk/media/5be99537ed915d6a203046fd/SCA_Blue_Book_236.pdf, https://assets.publishing.service.gov.uk/media/5be9964e40f0b667b363e25d/MoDWPart4-223MAYh.pdf, and https://pubmed.ncbi.nlm.nih.gov/19363065/.

Notably, two exposure sites (A and I) where STEC O157:H7 was detected had undetectable levels of generic *E. coli* and total coliforms. Similarly, STEC O157:H7 was detected in produce irrigation water with low generic *E. coli* and total coliform levels during an investigation into a 2018 multistate outbreak associated with romaine lettuce.†† This finding is not surprising, given that generic *E. coli* testing cannot detect STEC O157:H7 (*10*). Thus, this testing, although widely used as an indicator of water quality, is not a reliable indicator of the presence of STEC O157:H7.

Although UPMIW is not intended for recreation, all but one child with UPMIW exposure in this outbreak reported some kind of play in the water. Utah water providers have previously instructed residents to not drink or play in UPMIW; however, recent population growth within city A might have resulted in residents who arrived more recently being uninformed about UPMIW-associated risks. This outbreak demonstrates the need for ongoing educational efforts and reminders. Educating residents of communities with UPMIW systems, especially those at higher risk for severe illness (including older adults, children, and persons with compromised immune systems) about the

†† https://www.fda.gov/media/117512/download?attachment

Summary

What is already known about this topic?

Municipal irrigation water systems are underrecognized possible sources of waterborne illnesses.

What is added by this report?

In 2023, at least 13 children in Utah became ill during an outbreak of Shiga toxin–producing *Escherichia coli* O157:H7 associated with untreated, pressurized, municipal irrigation water. Seven children were hospitalized, including two with hemolytic uremic syndrome. Nearly all children (12 of 13) reported using this untreated water for unintended purposes, including recreation and drinking.

What are the implications for public health practice?

Educating residents of communities with these irrigation systems about the risks of playing in or drinking untreated water and improving management and operations risk mitigation of these untreated water systems could help prevent the occurrence of waterborne illness outbreaks.

importance of using UPMIW for its intended purposes as well as the risks associated with drinking and recreational exposure, could prevent future cases of UPMIW-associated waterborne illness. In addition, water utilities could assess UPMIW systems for potential contamination sources and consider risk mitigation interventions, including covering UPMIW sources and reservoirs, more prominent labeling of UPMIW at public sites, distributing conspicuous signage for residents to use in their yards, and color coding UPMIW spigots and lines, as is recommended for other nonpotable water sources to prevent the occurrence of waterborne illness.[§§]

[§§] https://www.epa.gov/sites/default/files/2019-08/documents/2012-guidelines-water-reuse.pdf

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Notes from the Field

Increases in Imported Malaria Cases — Three Southern U.S. Border Jurisdictions, 2023

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Summary

What is already known about this topic?

Approximately 2,000 malaria cases are imported into the United States annually, mostly among U.S. residents with recent travel to areas with endemic malaria.

What is added by this report?

In 2023, reports of imported malaria in three U.S. southern border jurisdictions increased from cases reported in 2022. Enhanced case investigations documenting traveler residency indicated higher percentages of malaria infections among new arrivals to the United States who traveled through at least one country with endemic malaria, including crossing land borders.

What are the implications for public health practice?

Outreach and education about malaria should be provided to local health care professionals and new arrivals, including migrants, with travel through areas with endemic malaria, to facilitate identification of cases, initiation of prompt treatment, and reduction in morbidity.

Introduction

Malaria is a severe and potentially fatal mosquitoborne disease caused by infection with *Plasmodium* spp. parasites. Although malaria is no longer endemic in the United States, imported infections are reported annually; the primary risk group has been U.S. residents traveling to areas where malaria is endemic (*1*). In 2023, sporadic locally acquired mosquito-transmitted malaria cases were reported in several U.S. states (*2*,*3*). This report describes increases in imported malaria cases in 2023 compared with 2022 in three public health jurisdictions along the U.S. southern border.

Investigation and Outcomes

During January–December 2023, a total of 68 imported malaria cases were identified from reportable disease surveillance systems in Pima, Arizona (18), San Diego, California (27), and El Paso, Texas (23), compared with 28 cases in 2022 (three in Pima, 12 in San Diego, and 13 in El Paso) (Table). Because malaria case counts were higher than expected, enhanced case investigations were initiated. Malaria cases were defined according to CDC case definitions.* To describe imported malaria cases in these three jurisdictions, this report summarized patient travel and illness characteristics by U.S. residence status. New arrivals were non–U.S.-born persons who had arrived in the United States within the preceding 6 months and were classified into the following three subgroups: 1) newly arrived refugees (i.e., officially admitted to the United States as part of the U.S. Refugee Admissions Program), 2) other new arrivals (including asylum seekers and other migrants), and 3) persons whose immigration status was unknown. Among jurisdictions, differences were identified in epidemiologic investigation protocols for patients without a local address and whether they were included in local surveillance case counts. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.†

Among the 68 imported malaria cases identified in 2023, 15 (22%) occurred among U.S. residents, two (3%) among newly arrived refugees, 49 (72%) among other newly arrived migrants (i.e., asylum seekers and other migrants), and two (3%) among travelers with unknown immigration status. The local public health jurisdictions attempted an interview with 61 (90%) patients. Among the 68 patients with malaria, 33 (49%) met residence criteria for inclusion in local surveillance case counts (i.e., the 15 U.S. residents, two newly arrived refugees, and 16 [33%] of the 49 other newly arrived migrants). The U.S. residents and refugees traveled directly from another country with endemic malaria to the United States. Among the 49 other newly arrived migrants, 46 (94%) had traveled through one or more countries with endemic malaria, including the country of origin (complex travel). The median travel duration was 29 days (range = 8–85 days), and 36 (73%) persons reported having traversed land borders. Overall, 63 (91%) patients with malaria were hospitalized; no deaths were reported. Nearly one third (21; 31%) of patients with malaria experienced severe disease (*1*), of which *Plasmodium vivax* was reported among 11 (52%), *P. falciparum* among six (29%), and another or unknown *Plasmodium* spp. parasite among four patients. Severe malaria was more common among other newly arrived migrants (18 of 49; 37%) than among U.S. residents (one of 15; 7%).

* https://ndc.services.cdc.gov/case-definitions/malaria-2014/
† 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

TABLE. Characteristics of imported malaria cases reported among patients, by U.S. residency and new arrival visa status — three southern U.S. border jurisdictions,*,† 2023

Characteristic	No. (row %)				
	Total	U.S. residents	Newly arrived refugees§	Other new arrivals¶	New arrivals with unknown immigration status**
Total	**68**	**15 (22)**	**2 (3)**	**49 (72)**	**2 (3)**
Surveillance and data collection					
Patient interview attempted	**61 (90)**	15 (100)	2 (100)	42 (86)	2 (100)
Case investigation completed††	**61 (90)**	14 (93)	2 (100)	44 (90)	1 (50)
Case included in local surveillance data§§	**33 (49)**	15 (100)	2 (100)	16 (33)	0 (—)
Travel type					
Land border crossing only	**26 (38)**	0 (—)	0 (—)	26 (53)	0 (—)
Air travel only	**20 (29)**	15 (100)	2 (100)	2 (4)	1 (50)
Air travel and land border crossing	**10 (15)**	0 (—)	0 (—)	10 (20)	0 (—)
Unknown	**12 (18)**	0 (—)	0 (—)	11 (22)	1 (50)
Complexity of travel					
Direct travel to U.S. destination from country with endemic malaria	**18 (27)**	15 (100)	2 (100)	0 (—)	1 (50)
Transit through one or more country with endemic malaria	**46 (68)**	0 (—)	0 (—)	46 (94)	0 (—)
Unknown travel	**4 (6)**	0 (—)	0 (—)	3 (6)	1 (50)
Region of travel origin¶¶					
Africa	**29 (43)**	14 (93)	2 (100)	12 (25)	1 (50)
Asia	**9 (13)**	1 (7)	0 (—)	8 (16)	0 (—)
Central America	**3 (4)**	0 (—)	0 (—)	2 (4)	1 (50)
South America	**27 (40)**	0 (—)	0 (—)	27 (55)	0 (—)
No. of regions traveled through					
1	**19 (28)**	14 (93)	2 (100)	2 (4)	1 (50)
≥2	**47 (69)**	1 (7)	0 (—)	46 (94)	0 (—)
Unknown	**2 (3)**	0 (—)	0 (—)	1 (2)	1 (50)
Days from symptom onset to seeking care,* median (IQR)**	**6 (4–11)**	6 (4–7)	18 (10–25)	6 (4–13)	1 (1–1)
Days from symptom onset to diagnosis,* median (IQR)**	**7 (4–13)**	7 (5–11)	21 (15–26)	7 (4–14)	7 (7–7)
Malaria species reported					
Plasmodium vivax	**34 (50)**	2 (13)	0 (—)	31 (63)	1 (50)
Plasmodium falciparum	**21 (31)**	10 (67)	0 (—)	11 (22)	0 (—)
Plasmodium malariae	**4 (6)**	0 (—)	2 (100)	1 (2)	1 (50)
Plasmodium ovale	**1 (2)**	0 (—)	0 (—)	1 (2)	0 (—)
Undetermined	**8 (12)**	3 (20)	0 (—)	5 (10)	0 (—)
Hospitalization					
Hospitalized	**62 (91)**	12 (80)	1 (50)	47 (96)	2 (100)
Not hospitalized	**5 (7)**	3 (20)	1 (50)	1 (2)	0 (—)
Unknown	**1 (2)**	0 (—)	0 (—)	1 (2)	0 (—)
Disease severity					
Severe malaria†††	**21 (31)**	1 (7)	0 (—)	18 (37)	2 (100)
Severity unknown	**10 (15)**	3 (20)	0 (—)	7 (14)	0 (—)
Death	**0 (—)**	0 (—)	0 (—)	0 (—)	0 (—)
Available for follow-up after treatment	**18 (27)**	10 (67)	1 (50)	7 (14)	0 (—)

* Jurisdictions included Pima, Arizona; San Diego, California; and El Paso, Texas.

† During 2022, a total of 28 imported malaria cases were reported from these three jurisdictions, including 15 (54%) among U.S. residents, zero among newly arrived refugees, 11 (39%) among other new arrivals, and two (7%) among persons with an unknown immigration status.

§ Refugees from areas in sub-Saharan Africa with endemic malaria receive presumptive treatment for malaria during their predeparture health assessment. https://www.cdc.gov/immigrantrefugeehealth/guidelines/overseas-guidelines.html

¶ Asylum seekers and other migrants.

** Includes one short-term traveler to the United States and one patient without enough information to determine their status.

†† Case investigation protocols differed among jurisdictions. Some protocols required interviews for all reported patients, whereas others only required interviews for patients with a local residential address. Reasons for an incomplete case investigation included inability to contact the patient, and loss to follow-up because of missing or incorrect patient contact information or no response.

§§ Inclusion criteria for local surveillance counts differed among jurisdictions. Some jurisdictions did not include patients who were missing a residential address or whose address was outside the local jurisdiction, regardless of case investigation status.

¶¶ Region of travel origin for new arrivals or region of destination for U.S. residents. Regions included the following countries of travel origin: *Africa:* Angola, Côte d'Ivoire, Ethiopia, Guinea, Mauritania, Nigeria, Senegal, Sudan, The Gambia, and Uganda; *Asia:* Afghanistan and China; *Central America:* Nicaragua and Panama; *South America:* Colombia, Ecuador, and Venezuela. CDC provides information about areas with endemic malaria. https://wwwnc.cdc.gov/travel/yellowbook/2024/infections-diseases/malaria

*** Date of care and diagnosis based on care received at a U.S. health care facility.

††† According to the CDC case definition for severe malaria, which includes laboratory confirmation with neurologic symptoms, acute kidney injury, severe anemia (hemoglobin <7g/dL), acute respiratory distress syndrome, or ≥5% parasitemia; treatment for severe malaria (i.e., artesunate or exchange transfusion); or death. https://doi.org/10.15585/mmwr.ss7108a1

Preliminary Conclusions and Actions

Imported malaria in three U.S. southern border jurisdictions increased in 2023, particularly among new arrivals to the United States with recent, complex transit through at least one country with endemic malaria. During the same period, entry of asylum seekers and other migrants into the United States across the southern land border increased.[§] In light of the different jurisdictional protocols used in case investigations, implementation of classifications and consistent investigation and reporting protocols for non-U.S. residents could facilitate better characterization of malaria incidence among new arrival subgroups in different jurisdictions.[¶]

New arrivals to the United States with complex travel through areas with endemic malaria are potentially at higher risk for malaria and, for reasons not fully understood, for more severe illness. Health care professionals should obtain a complete travel history, consider malaria among symptomatic patients with recent travel through areas where malaria is endemic, and initiate prompt testing and, if indicated, treatment.[**] Outreach and education about malaria directed to local health care professionals and to new arrivals with recent travel in areas with endemic malaria are crucial because prompt care seeking, diagnosis, and treatment of malaria will reduce morbidity in this population.

[§] An increase in the entry of asylum seekers and other migrants across the U.S. southern border was identified using annual numbers of persons with credible fear who were released with a notice to appear for immigration court or paroled into the United States as a proxy for asylum seekers and other migrants. Data are publicly available from 2022 and 2023 annual U.S. Customs and Border Protection Southwest border reports. https://www.cbp.gov/newsroom/stats/custody-and-transfer-statistics

[¶] https://cdn.ymaws.com/www.cste.org/resource/resmgr/PS/03-ID-10revised.pdf

[**] https://www.cdc.gov/malaria/diagnosis_treatment/clinicians1.html

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Notes from the Field

Potential Outbreak of Extrapulmonary *Mycobacterium abscessus* subspecies *massiliense* Infections from Stem Cell Treatment Clinics in Mexico — Arizona and Colorado, 2022

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Summary

What is already known about this topic?

Mycobacterium abscessus is a difficult-to-treat nontuberculous mycobacterium; various extrapulmonary infections have been reported associated with medical tourism.

What is added by this report?

In 2022, three patients developed extrapulmonary *M. abscessus* infections after receiving embryonic stem cell injections in three cities in Mexico. Isolates from two patients were identified as *M. abscessus* subspecies *massiliense* of a single clone, distinct from known dominant circulating clones (DCCs), by whole genome sequencing.

What are the implications for public health practice?

Because these isolates were clonal, distinct from known DCCs, and derived from distant cities, a common infected source associated with embryonic stem cell injections is suspected. Vigilance for similar cases and guidance for persons considering medical tourism are advised.

Mycobacterium abscessus is an intrinsically drug-resistant, rapidly growing, nontuberculous mycobacterium; extrapulmonary infections have been reported in association with medical tourism (*1*). During November–December 2022, two Colorado hospitals (hospitals A and B) treated patient A, a Colorado woman aged 30–39 years, for *M. abscessus* meningitis. In October 2022, she had received intrathecal donor embryonic stem cell injections in Baja California, Mexico to treat multiple sclerosis and subsequently experienced headaches and fevers, consistent with meningitis. Her cerebrospinal fluid revealed neutrophilic pleocytosis and grew *M. abscessus* in culture at hospital A. Hospital A's physicians consulted hospital B's infectious diseases (ID) physicians to co-manage this patient (*2*).

In spring 2023, hospital B's ID physicians identified two additional patients with *M. abscessus* infections acquired after receiving stem cell injections performed at different clinics in Mexico. The first of these, patient B, an Arizona man aged 60–69 years, developed a right elbow osteoarticular infection after receiving donor embryonic stem cell injections for psoriatic arthritis at a Baja California, Mexico clinic different from the one that treated patient A, in April 2022. The second, patient C, a Colorado man aged 60–69 years, developed bilateral knee infections after receiving donor embryonic stem cell injections in both knees for osteoarthritis at a clinic in Guadalajara, Mexico, in October 2022.

Investigation and Outcomes

Hospital B's ID physicians requested the isolates but were only able to obtain the original isolates from patients A and B. Whole genome sequencing (WGS) and phylogenetic analysis, performed at hospital B (*3*), revealed that the isolates were clonal *M. abscessus* subspecies *massiliense*, with only one single nucleotide polymorphism (SNP) difference between the two isolate core genomes* and were distinct from the most prevalent characterized dominant circulating clones (*3*) (Figure). These isolates were regrown from their original subcultures to repeat WGS, and the one SNP difference was confirmed. These patients had their stem cell injections performed at clinics 167 miles (269 km) apart in Baja California, Mexico. As of March 28, 2024, treatment is ongoing for all three patients.

The patients' treating physicians informed their state public health departments of their findings. The Colorado Department of Public Health and Environment (CDPHE) interviewed patients A and C, and the Arizona Department of Public Health interviewed patient B. CDPHE searched for similar cases within Colorado and other states and consulted with CDC; as of March 28, 2024, no additional cases have been identified. This activity was reviewed by CDC, deemed not research, and was conducted consistent with applicable federal law and CDC policy.†

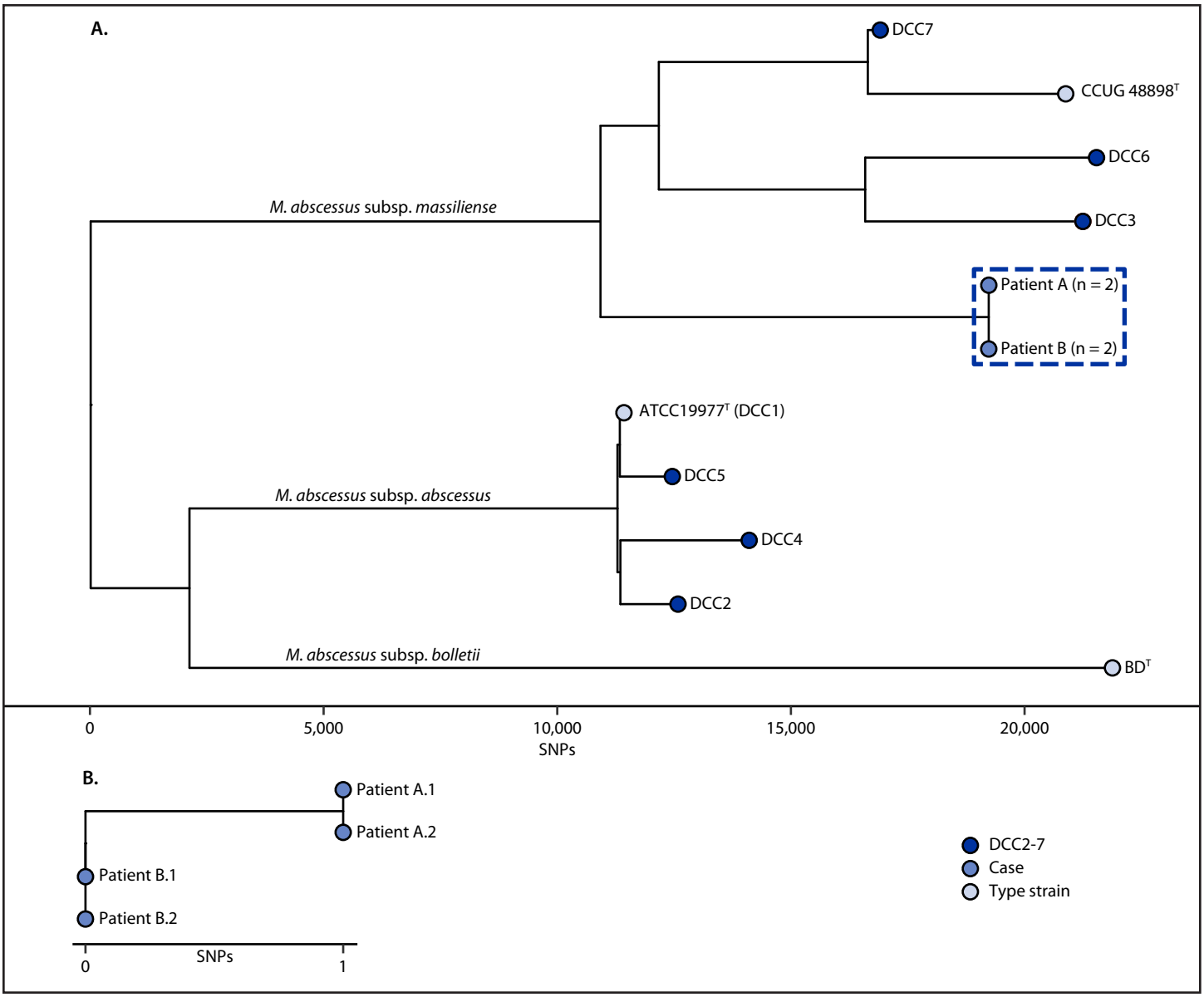
Preliminary Conclusions and Actions

Given that the isolates identified from patients treated at different, distant clinics represent a single clone, the physicians

* WGS for isolates from patients A and B have been deposited in the National Center for Biotechnology Information BioProject, CDC HAI-Seq Nontuberculous mycobacterium (542112).

† 45 C.F.R. part 46.102(l)(2), 21 C.F.R. part 56; 42 U.S.C. Sect. 241(d); 5 U.S.C. Sect. 552a; 44 U.S.C. Sect. 3501 et seq.

FIGURE. *Mycobacterium abscessus* whole genome phylogeny*,† of dominant circulating clones 1–7 and isolates from patients A§ and B¶ (A) and genomic similarity between the first and second whole genome sequencing single nucleotide polymorphisms for isolates from patients A§ and B¶ (B) associated with receipt of stem cell treatment in Mexico — Arizona and Colorado, 2022



Abbreviations: ATCC = American type culture collection; BD = Becton Dickinson; DCC = dominant circulating clone; SNP = single nucleotide polymorphism; WGS = whole genome sequencing.
* WGS was conducted twice to confirm the SNP difference between isolates from patients A and B.
† Superscripted T (T) is the standard designation for a type strain of a taxon.
§ Patient A.1 = isolate from patient A, first WGS result; patient A.2 = isolate from patient A, second WGS result.
¶ Patient B.1 = isolate from patient B, first WGS result; patient B.2 = isolate from patient B, second WGS result.

and CDPHE suspect a common infected source (potentially the product, reagents, or equipment used) for patients A and B. CDPHE's attempts to identify the product or gather details about its administration have been unsuccessful to date. CDPHE attempted to contact clinics that performed the stem cell injections, but received no response. A collaborative process with Mexican health authorities was initiated and is ongoing; however, no new substantial cases have yet been identified.

Next steps include 1) performing WGS on the organism isolated from patient C from newly acquired specimens; 2) sharing genomic information from the WGS analysis with the National Center for Biotechnology Information to ensure that comparisons can be made with additional cases;

and 3) conducting prospective case finding. Historically, stem cell treatments have been linked to bacterial infections (*4*), and procedure-related infection risks associated with medical tourism are known (*1*,*5*). Providers and public health agencies need to be aware of the risk for *M. abscessus* infections from stem cell treatments for indications not approved by the Food and Drug Administration and maintain vigilance for similar cases (*5*). They also are advised to provide guidance for persons considering medical tourism (*5*).

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