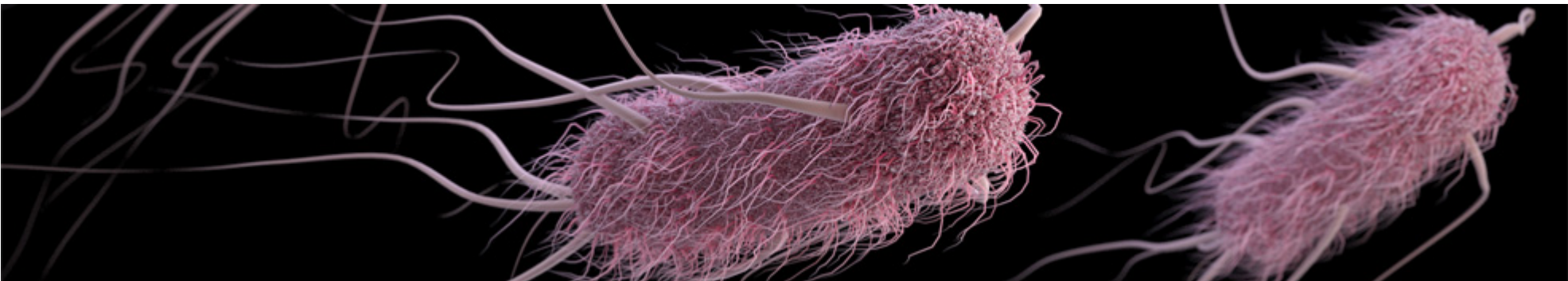# Division of Foodborne, Waterborne, and Environmental Diseases (DFWED)

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Persistent Strain of *E. coli* O157:H7 (REPEXH01) Linked to Multiple Sources

Posted February 8, 2023

REPEXH01

REPEXH01 is a persistent strain of Shiga toxin-producing *E. coli* O157:H7 bacteria that has caused illnesses and outbreaks in the United States.

Illness caused by this strain was first reported to PulseNet in 2017. Illnesses caused by this strain occur year-round but are less common in winter.

In the past, the REPEXH01 strain has spread to people through contaminated food and contaminated recreational water.

This strain is relatively diverse genetically. Bacteria in this strain are within 21 allele differences of one another by whole genome sequencing, which is more diverse than typical multistate foodborne outbreaks where bacteria generally fall within 10 allele differences of one another.

What is a persistent strain?

CDC uses "persistent" to describe some strains of bacteria that have caused illness for years. The strains continue to cause illness, even though the number of illnesses they cause might vary over time. The strains are sometimes linked to more than one source, making them harder to control.

Learn about these strains and CDC's efforts to control them

Fast Facts

Bacteria	*Escherichia coli*
Serotype	O157:H7
Shiga Toxin Type ⧉	Stx2a and/or Stx2c
Persistent Strain	REPEXH01
First Detection	April 2017
Illnesses Reported in PulseNet	634
Outbreaks Investigated	14
Identified outbreak sources* *Confirmed sources were implicated by epidemiologic plus traceback or laboratory data. Suspected sources were implicated by epidemiologic data only. More info	• Recreational water (confirmed): 1 outbreak • Romaine lettuce (confirmed): 1 outbreak • Leafy greens (suspected): 1 outbreak • Ground beef (suspected): 2 outbreaks

Outbreaks and Outbreak-Related Illnesses

Although most enteric illnesses – including those caused by REPEXH01 – are not part of an outbreak, investigation of outbreaks provides information that increases our understanding of germs, sources, settings, and factors that contribute to illness. Moreover, lab-confirmed cases comprise only a small portion of the true number of illnesses that occur because most people do not seek medical care and even fewer submit a stool specimen.

Starting in 2017, CDC and local, state, and federal health and regulatory partners have investigated several outbreaks of *E. coli* O157:H7 illnesses caused by the REPEXH01 strain.

Summary of Selected Multistate Outbreaks

Outbreak	Dates People Got Sick*	Outbreak Source†	Geographic Location of Outbreak Source**	Reported Illnesses	Number of States with Illnesses	More Information
Outbreak A	July 2017	Recreational water (confirmed)	California	10	1	
Outbreak B	March 2018–August 2018	Romaine lettuce (confirmed)	Arizona	238	37	CDC Food Safety Alert Peer-reviewed article 🔗
Outbreak C	August 2018–October 2018	Ground beef (suspected)	Unknown	12	4	
Outbreak D	October 2018–December 2018	Leafy greens (suspected)	Unknown	25	10	
Outbreak E	May 2019–October 2019	Ground beef (suspected)	Unknown	44	12	
Outbreak F	December 2020–January 2021	Unknown	Unknown	22	7	CDC Investigation Notice
Outbreak G	April 2021–June 2021	Unknown	Unknown	5	3	

* Outbreak dates are based on reported or estimated illness onset dates.

† Confirmed sources were implicated by epidemiologic plus traceback or laboratory data. Suspected sources were implicated by epidemiologic data only. More info

** The geographic location of a confirmed outbreak source may not always be known. This can happen when a food containing multiple ingredients (e.g., bagged salad blend) is confirmed as the source, but the evidence cannot implicate a specific food, or when evidence confirms an outbreak source but traceback cannot pinpoint the exact geographic location of the source.

Timeline

This chart, called an epidemiologic curve, shows when people got sick.
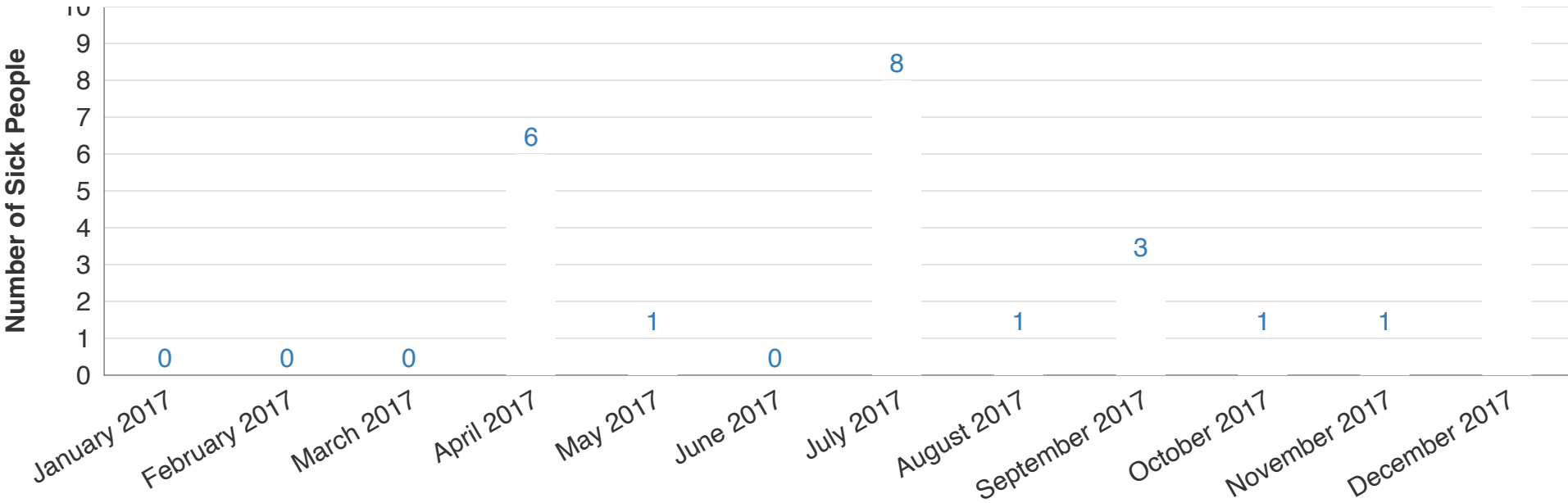
People with *E. coli* O157:H7 illnesses caused by the REPEXH01 strain, by date illness began and by outbreak, 2017–2022*,†

Select Year

[2017 ⌄]

Apply Filters   Reset All

Number of Sick People (y-axis)

| Month	Number
January 2017	0
February 2017	0
March 2017	0
April 2017	
May 2017	6
June 2017	0
July 2017	1
August 2017	8
September 2017	1
October 2017	3
November 2017	1
December 2017	1

Data Table +

[*] N=634 for whom information was reported as of September 2, 2022. Some illness onset dates have been estimated from other reported information.

[†] PulseNet transitioned to using whole genome sequencing (WGS) as the standard subtyping method for STEC in July 2019. Before then, not all STEC isolates reported to PulseNet had WGS data available. Isolates are identified as part of this strain based on WGS. As a result, the number of people with lab-confirmed illness caused by this strain before 2019 may be underrepresented.

Map

This map shows where sick people lived.

E. coli O157:H7 illnesses caused by the REPEXH01 strain, by state, 2017–2022*
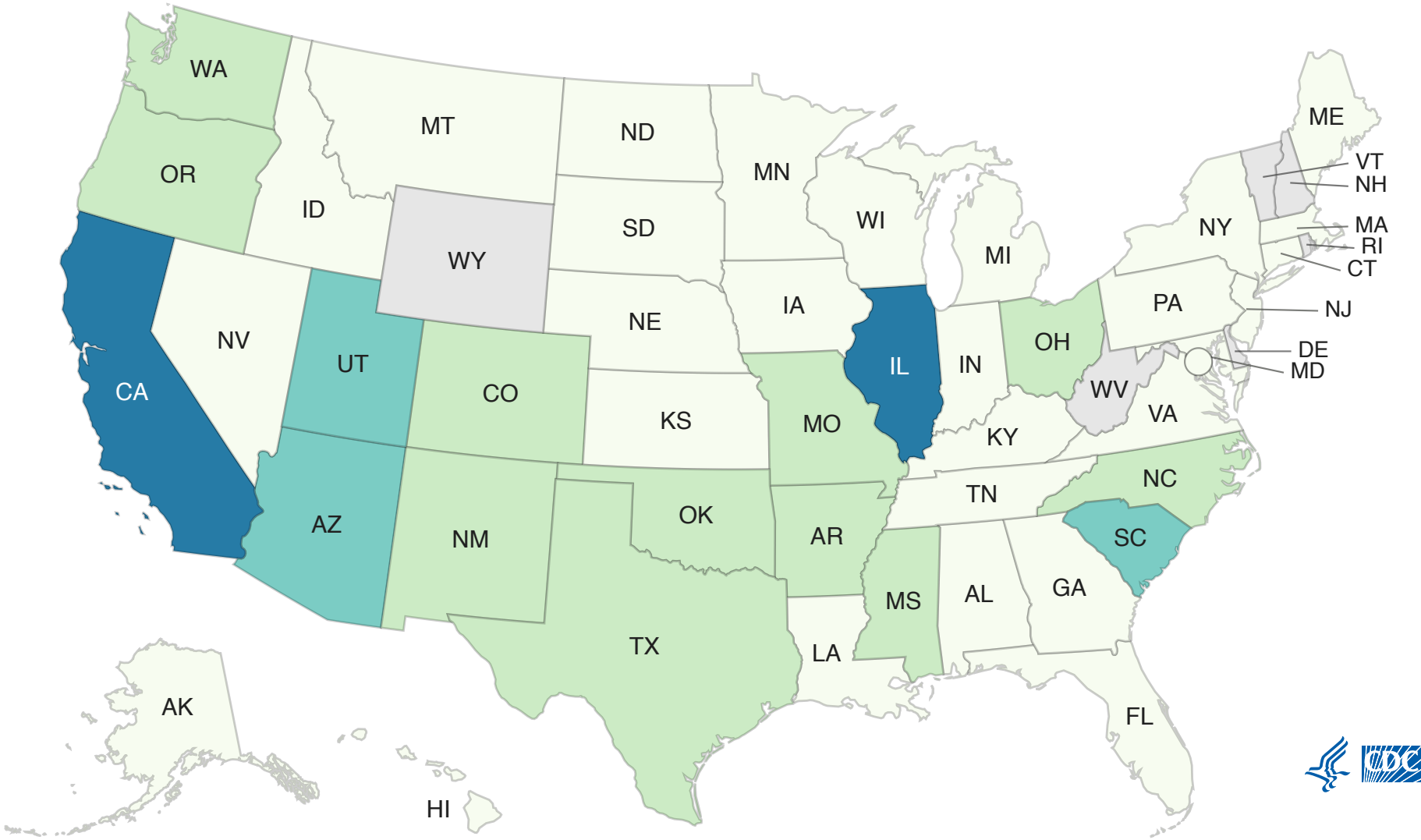
Number of Sick People

○ 1 to 9   ○ 10 to 19

○ 20 to 39   ○ 40 to 350

Data Table +

Laboratory data

WGS analysis

Bacteria in this strain are within 21 allele differences of one another by core genome multilocus sequence typing (cgMLST) ⬈, which is more diverse than typical multistate foodborne outbreaks where bacteria generally fall within 10 allele differences of one another.

This strain includes two major genetic subclusters. Each has caused at least two outbreaks linked to different sources and geographic regions. Possible reasons for the differences among genetic subclusters are still being investigated. More research is needed to determine if any genetic subclusters are associated with specific foods, animal populations, or geographic regions.

Isolates from food, animal, and environmental samples

Year	Number of Isolates	Isolate Type	Geographic Location of Source	Reason Collected
2017	1	Goose feces	California	Outbreak A
2017	2	Lake sediment	California	Outbreak A
2017	4	Lake water	California	Outbreak A
2018	24	Agricultural irrigation water	Arizona	Outbreak B
2019	1	Ground beef	California	Routine Sampling

Genomic information

The National Center for Biotechnology Information (NCBI) advances science and health by providing access to biomedical and genomic information.
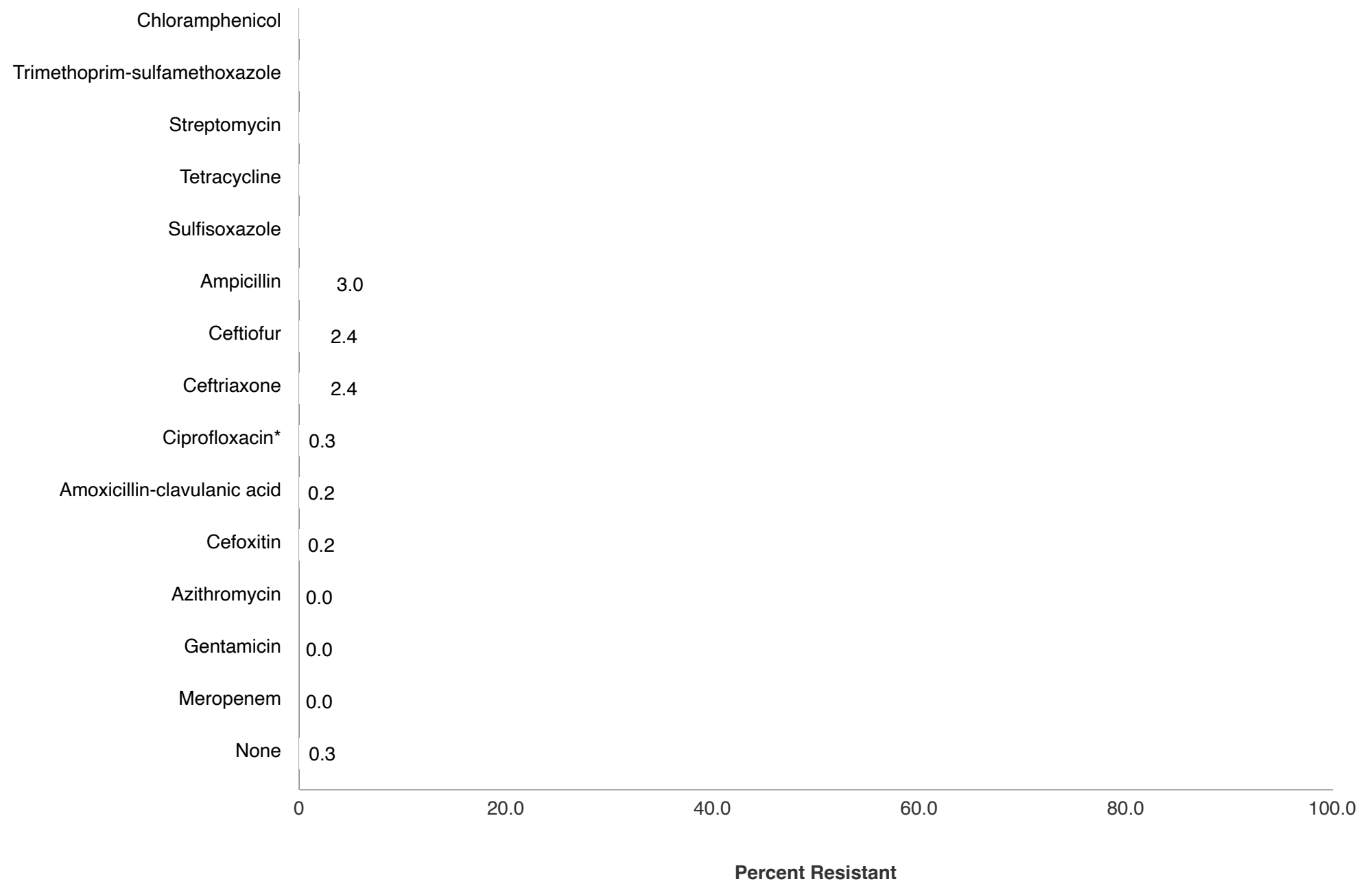
SNP Cluster*: PDS000059979.158 ⬈

* The SNP (Single Nucleotide Polymorphism) tree provided by NCBI's Pathogen Detection Pipeline in the link above may include isolates that are not considered part of this strain. The difference in thresholds and allele/SNP differences occur because NCBI's Pathogen Detection Pipeline uses an analysis pipeline different from CDC PulseNet. The link is provided to give context to the overall genetic relatedness of the strain reported on this page, as well as to provide links to raw sequence files. Moreover, the SNP trees on NCBI's Pathogen Detection Pipeline are updated more frequently than this web page.

Antimicrobial resistance information

The National Antimicrobial Resistance Monitoring System (NARMS) is a national public health surveillance system that tracks antimicrobial resistance for certain intestinal bacteria from sick people (CDC), retail meats ⬈ (FDA), and food animals ⬈ (USDA) in the United States. The NARMS program helps protect public health by providing information about emerging antimicrobial resistance, the ways in which resistance is spread, and how resistant infections differ from susceptible infections.

Bacteria from most sick people's samples showed resistance to the antimicrobials chloramphenicol, streptomycin, sulfisoxazole, tetracycline, and trimethoprim-sulfamethoxazole. These findings do not affect treatment guidance because antimicrobials are not recommended for patients with *E. coli* O157:H7 infection.

Figure: Percentage of *E. coli* O157:H7 REPEXH01 isolates from ill people that were antimicrobial resistant, by antimicrobial (n = 596), as of August 31, 2022 — National Antimicrobial Resistance Monitoring System

Chloramphenicol	
Trimethoprim-sulfamethoxazole	
Streptomycin	
Tetracycline	
Sulfisoxazole	
Ampicillin	3.0
Ceftiofur	2.4
Ceftriaxone	2.4
Ciprofloxacin*	0.3
Amoxicillin-clavulanic acid	0.2
Cefoxitin	0.2
Azithromycin	0.0
Gentamicin	0.0
Meropenem	0.0
None	0.3

Percent Resistant

| Data Table | + |

Note: Resistance was determined based on the results of antimicrobial susceptibility testing when available (n = 73 isolates); otherwise, resistance was predicted based on whole genome sequencing (n = 523).

[*] Includes isolates carrying a single quinolone resistance gene (n = 2; 0.3%); a single gene may result in interpretation of "intermediate" or "susceptible" for ciprofloxacin on antimicrobial susceptibility testing.

Collaboration

Interested in collaborating on a project related to this strain? Contact CDC at REPStrains@cdc.gov.

Last Reviewed: February 8, 2023