

# Emerging Infections Program

## Healthcare-Associated Infections–Community Interface Report

### *Clostridioides difficile* Infection Surveillance, 2022

#### Surveillance Catchment Areas

California (1 county San Francisco area), Colorado (5 county Denver area); Connecticut (1 county New Haven area); Georgia (8 county Atlanta area); Maryland (9 Eastern Shore and 2 western counties); Minnesota (5 counties); New Mexico (1 county Albuquerque area); New York (1 county Rochester area); Oregon (1 rural county); and Tennessee (1 county Nashville area).

#### Population

The surveillance area represents 12,158,781 persons.

Source: U.S. Census Bureau, Population Division, Vintage 2021 Special Tabulation for Connecticut's catchment area and Vintage 2022 Special Tabulation for all other states' catchment areas. In 2022, Connecticut adopted nine planning regions as county-equivalent geographic units; as health data were not available in the new county-equivalent units for 2022, county-level data for Connecticut have been calculated using the 2021 (Vintage 2021 Special Tabulation) population estimates released by the Census Bureau's Population Estimates Program.

#### Case Definition

An incident case of *Clostridioides difficile* infection (CDI) was defined as a *C. difficile*-positive stool test (toxin or molecular assay) from a person  $\geq 1$  year old with no positive test in the prior 8 weeks.

#### Methods

Case finding was active, laboratory-based, and population-based. Laboratories serving the surveillance catchment areas reported positive *C. difficile* tests to EIP staff and were routinely audited with a goal of complete case ascertainment. An initial chart review was performed on all CDI cases in eight EIP sites and on all pediatric cases and a 1/3 random sample of cases age 18 years and older in the two remaining EIP sites with the largest surveillance catchment areas (CO and GA). A subsequent comprehensive chart review was performed on all community-onset cases and a subset of healthcare-facility onset cases.

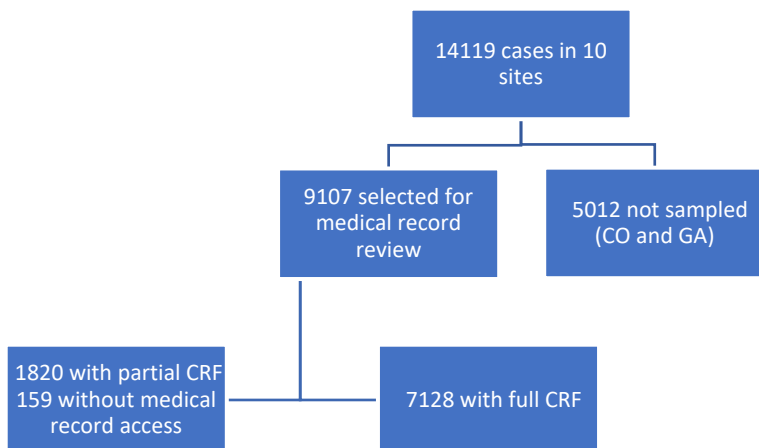
A standardized case report form (CRF) was completed for each incident case through review of medical records. Inpatient and outpatient medical records were reviewed for information on patient demographics, clinical syndrome, outcome of illness, and relevant healthcare exposures.

A convenience sample of stool specimens and swabs was sent to reference laboratories for *C. difficile* isolation. Recovered isolates were sent to CDC for molecular typing and characterization. From 2012–2018, PCR-ribotyping was used for EIP strain typing. Beginning in 2018, whole genome sequencing (WGS) and analysis were used for the molecular characterization of *C. difficile* isolates. *C. difficile* isolates were sequenced (Illumina MiSeq or NovaSeq) by the CDC or the

Minnesota Department of Health Public Health Laboratory. Assembly and multi-locus sequence typing (MLST) were performed using CDC's in-house Portable Healthcare Nextgen Informatics (PHoeNix) pipeline (<https://github.com/CDCgov/phoenix>).

A CDI case was classified as community-associated (CA) if the *C. difficile*-positive stool specimen was collected on an outpatient basis or within 3 days after hospital admission in a person with no documented overnight stay in a healthcare facility in the preceding 12 weeks. All CDI cases that did not meet the aforementioned criteria were classified as healthcare-associated (HA). HA cases with disease onset outside of a healthcare facility but with documented overnight stay in a healthcare facility in the preceding 12 weeks were classified as community-onset, healthcare-facility associated (CO-HCFA). HA cases with disease onset in a healthcare facility were classified as healthcare-facility onset (HCFO). HCFO cases were further classified into hospital onset or long-term care facility onset. Incidence rates were calculated using US Census population estimates.

CDI surveillance data undergo regular data cleaning to ensure accuracy and completeness. Patients with case data as of 03/08/2024 were included in this analysis. Because data can be updated as needed, analyses of datasets generated on a different date may yield slightly different results.



## Results

**Table 1 – Reported Number of CDI Cases and Crude Incidence by Sex, Age Group, Race, and Epidemiologic Classification Among the 10 EIP Sites**

Sex	Population ≥1 Year of Age	Community-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Community-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	Healthcare-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Healthcare-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	All CDI, No. <sup>c</sup>	All CDI, Incidence <sup>b</sup>
Male	5,988,433	2803	46.8	3036	50.7	5839	97.5
Female	6,170,348	4748	77.0	3532	57.2	8280	134.2

Age group	Population ≥1 Year of Age	Community-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Community-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	Healthcare-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Healthcare-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	All CDI, No. <sup>c</sup>	All CDI, Incidence <sup>b</sup>
1-17 years	2,460,011	518	21.0	198	8.1	716	29.1
18-44 years	4,789,790	1849	38.6	781	16.3	2630	54.9
45-49 years	756,028	381	50.4	275	36.4	656	86.8
50-54 years	793,578	469	59.1	397	50.0	866	109.1
55-59 years	762,007	629	82.5	474	62.2	1103	144.7
60-64 years	729,698	667	91.4	684	93.8	1351	185.1
65-70 years	618,467	746	120.6	727	117.6	1473	238.2
70-74 years	498,673	699	140.3	830	166.4	1529	306.6
75-79 years	342,956	671	195.8	788	229.7	1459	425.4
80+ years	407,573	922	226.2	1414	346.9	2336	573.1

Race <sup>a</sup>	Population ≥1 Year of Age	Community-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Community-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	Healthcare-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Healthcare-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	All CDI, No. <sup>c</sup>	All CDI, Incidence <sup>b</sup>
White	8,001,337	5850	73.1	4617	57.7	10467	130.8
Other	4,157,444	1701	40.9	1951	46.9	3652	87.8

Total	Population ≥1 Year of Age	Community-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Community-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	Healthcare-Associated CDI <sup>a</sup> , No. <sup>c</sup>	Healthcare-Associated CDI <sup>a</sup> , Incidence <sup>b</sup>	All CDI, No. <sup>c</sup>	All CDI, Incidence <sup>b</sup>
Total	12,158,781	7552	62.1	6567	54.0	14119	116.1

<sup>a</sup> The epidemiologic classification was statistically imputed for 2% of the CDI cases selected for medical record review, and race was statistically imputed for 13% of the CDI cases selected for medical record review. The weighted frequency of cases in Colorado and Georgia was based on 33% random sampling for cases aged ≥18 years.

<sup>b</sup> Cases per 100,000 persons.

<sup>c</sup> Subcategories may not add to total due to rounding.

**Table 2 – Diagnostic Assay Results of CDI Cases (N=14119)**

<b>Diagnostic assay</b>	<b>N</b>	<b>%</b>
Toxin positive	4324	31
Nucleic acid amplification test (NAAT) positive/toxin negative	4830	34
NAAT positive/toxin result unknown <sup>a</sup>	4951	35
Unspecified assay	6	<1

<sup>a</sup> Includes cases diagnosed mainly by NAAT or multiplex PCR panel (i.e., toxin enzyme immunoassay or cell cytotoxicity assay was not performed) or by NAAT as part of a multistep algorithm where the toxin result was not readily known

**Table 3 – CDI Cases by Epidemiologic Classification (N=14119)**

<b>Epidemiologic classification</b>	<b>N</b>	<b>%</b>
Hospital onset	1783	13
LTCF onset	610	4
COHCFA	1754	12
CA	4792	34
Unknown <sup>a</sup>	5180	37

<sup>a</sup> Includes 5012 non-sampled cases

**Table 4 – CDI Cases by Race and Ethnicity (N=14119)**

<b>Race/Ethnicity</b>	<b>N</b>	<b>%</b>
Hispanic, any race	956	7
Not known to be Hispanic <sup>a</sup> - White <sup>b</sup>	6905	49
Not known to be Hispanic <sup>a</sup> - Black or African American <sup>c</sup>	2194	16
Not known to be Hispanic <sup>a</sup> - Asian <sup>d</sup>	401	3
Not known to be Hispanic <sup>a</sup> - Other or multiple races <sup>e</sup>	150	1
Non-Hispanic- Unknown race	195	1
Unknown ethnicity and race	3318	24

<sup>a</sup> Records either indicated ethnicity was non-Hispanic, or ethnicity was not known.

<sup>b</sup> 558 cases with unknown ethnicity

<sup>c</sup> 98 cases with unknown ethnicity

<sup>d</sup> 42 cases with unknown ethnicity

<sup>e</sup> American Indian or Alaska Native, Native Hawaiian or Other Pacific Islander, or ≥2 races reported; 16 cases with unknown ethnicity

**Table 5 – Location of CDI Cases on the Third Calendar Day Before Incident Specimen Collection (N=9107)**

<b>Location of patient before incident specimen collection</b>	<b>N</b>	<b>%</b>
Private residence	6470	71
Long-term care facility	620	7
Acute-care hospital (inpatient)	1705	19
Long-term care acute care hospital	43	<1
Homeless	82	<1
Incarcerated	7	<1
Other	5	<1
Unknown	175	2

**Table 6 – Location of CDI Cases at Time of Incident Specimen Collection (N=9107)**

Location of incident specimen collection	N	%
Outpatient setting or emergency department	4850	53
Acute care hospital	3659	40
Long-term care facility	393	4
Long-term acute care hospital	35	<1
Other	2	<1
Unknown	168	2

**Table 7 – Selected Clinical Characteristics of CDI Cases (N=7128, except where indicated)**

Clinical characteristic	N	%
Charlson comorbidity index - 0	2937	41
Charlson comorbidity index - 1	1300	18
Charlson comorbidity index - $\geq 2$	2891	41
Underlying conditions - Cardiovascular disease <sup>a,b</sup>	1514	21
Underlying conditions - Diabetes mellitus <sup>a</sup>	1493	21
Underlying conditions - Chronic pulmonary disease <sup>a,c</sup>	1431	20
Underlying conditions - Gastrointestinal disease <sup>a,d</sup>	1704	24
Underlying conditions - Gastrointestinal disease – Diverticular disease <sup>a</sup>	719	10
Underlying conditions - Gastrointestinal disease – Inflammatory bowel disease <sup>a</sup>	529	7
Underlying conditions - Gastrointestinal disease – Peptic ulcer disease <sup>a</sup>	172	2
Underlying conditions - Gastrointestinal disease – Short gut syndrome <sup>a</sup>	15	<1
Underlying conditions - Gastrointestinal disease – Liver disease <sup>a</sup>	441	6
Underlying conditions - Chronic renal disease <sup>a</sup>	1371	19
Underlying conditions - Neurologic condition, any <sup>a</sup>	1386	19
Underlying conditions - Malignancy (hematologic or solid organ) <sup>a</sup>	1209	17
Underlying conditions - Transplant (hematopoietic stem cell or solid organ) <sup>a</sup>	270	4
Positive test for SARS-CoV-2 during hospitalization and on or before date of incident specimen collection <sup>e</sup>	170	6

<sup>a</sup> Underlying conditions are not mutually exclusive.

<sup>b</sup> Defined as myocardial infarction, congestive heart failure, congenital heart disease, stroke, transient ischemic attack, or peripheral vascular disease.

<sup>c</sup> Defined as cystic fibrosis or any chronic respiratory condition resulting in symptomatic dyspnea.

<sup>d</sup> Defined as diverticular disease, inflammatory bowel disease, peptic ulcer disease, short gut syndrome, or liver disease.

<sup>e</sup> Among patients in the hospital on the date of incident specimen collection (N=2873). Excludes patients who were admitted to the hospital after the date of incident specimen collection. A positive SARS-CoV-2 test was defined as any positive viral test for SARS-CoV-2, including antigen and nucleic acid amplification tests.

**Table 8 – Selected Healthcare Exposures and Risk Factors of Incident CDI Cases in the 12 Weeks Before the Date of Incident Specimen Collection by Epidemiologic Classification (N=7128)<sup>a</sup>**

Healthcare Exposure <sup>a</sup>	CA (N=4792)		COHCFA (N=1754)		HCFO (N=573)	
	N	%	N	%	N	%
Acute care hospitalization	0	0	1726	98	286	50
Long-term care facility residence	0	0	187	11	226	39
Long-term acute care hospitalization	0	0	8	<1	14	2
Surgery	198	5	441	25	156	27
Emergency room	1010	21	621	35	156	27
Observation unit	62	2	54	3	15	3
Chronic dialysis	119	2	153	9	64	11

<sup>a</sup> Excludes 9 cases with unknown epiclass

<sup>b</sup> Healthcare exposure categories are not mutually exclusive.

**Table 9 – Antibiotic Use in the 12 Weeks Before the Date of Incident Specimen Collection (N=7128)**

Antibiotic <sup>a</sup>	N	%
Any antibiotic	4026	56
Aminoglycosides	65	<1
Beta-lactam / beta-lactamase inhibitor combinations	1461	20
Carbapenems	199	3
Cephalosporins	199	3
Clindamycin	401	6
Fluoroquinolones	733	10
Glycopeptides	1287	18
Macrolides	237	3
Monobactam	15	<1
Penicillins	389	5
Trimethoprim or Trimethoprim/Sulfamethoxazole	375	5
Tetracyclines	279	4
Other antibiotic	1200	17

<sup>a</sup> Antibiotic use categories are not mutually exclusive.

**Table 10 – Treatment of Incident CDI Cases (N=7128)**

Treatment <sup>a</sup>	N	%
Any treatment <sup>b</sup>	5738	80
Oral or rectal vancomycin (excluding vancomycin tapers) <sup>c</sup>	4636	65
Vancomycin tapers	317	4
Metronidazole	865	12
Fidaxomicin	890	12
Bezlotoxumab	26	<1
Stool transplant	32	<1

<sup>a</sup> Treatment categories are not mutually exclusive.

<sup>b</sup> Includes any course of CDI antibiotic therapy, bezlotoxumab, or stool transplant.

<sup>c</sup> Includes 9 patients receiving vancomycin prophylaxis after treatment of incident CDI.

**Table 11 – Outcomes of Incident CDI Cases (N=7128, except where indicated)**

Outcome	N	%
Toxic megacolon <sup>a</sup>	16	<1
Ileus <sup>a</sup>	125	2
Pseudomembranous colitis <sup>a</sup>	25	<1
White blood cell count $\geq 15,000/\mu\text{l}$ <sup>a</sup>	1131	16
Recurrent infection <sup>a</sup>	811	11
Hospitalization on the day of or within 6 days after the date of incident specimen collection <sup>a, b</sup>	2982	42
ICU admission one day before, the day of, or within 6 days after the date of incident specimen collection <sup>a</sup>	396	6
In-hospital death <sup>a</sup>	174	2
Discharge location after acute-care hospitalization among patients who survived <sup>c</sup> - Private Residence	2309	82
Discharge location after acute-care hospitalization among patients who survived <sup>c</sup> - Long-term care facility	412	15
Discharge location after acute-care hospitalization among patients who survived <sup>c</sup> - Long-term acute care hospital	14	<1
Discharge location after acute-care hospitalization among patients who survived <sup>c</sup> - Other	64	2
Discharge location after acute-care hospitalization among patients who survived <sup>c</sup> - Unknown	9	<1

<sup>a</sup> Outcomes, except for location of discharge from acute care hospitalization, are not mutually exclusive.

<sup>b</sup> Data include 399 cases considered to be hospital-onset.

<sup>c</sup> N=2808

## Laboratory Characterization

In 2022, 1013 *C. difficile* isolates were characterized by CDC. The total number of isolates received from each site ranged from 41 to 270, with a median of 75.5. Most isolates (94%) were collected from patients residing in metropolitan areas. One isolate was from a case with unknown epidemiologic classification.

Among all isolates submitted, 105 distinct sequence types were detected. Among the 551 community-associated isolates, 83 distinct STs were observed. ST2 was most common (12.3%), followed by ST42 (11.3%) and ST8 (10.3%) (Table 12). Among the 461 healthcare-associated isolates, 67 distinct STs were observed. ST42 was most common (12.8%), followed by ST2 (10.2%), ST1 (9.1%), ST8 (6.9%), and ST3 (4.3%) (Table 13). A crosswalk to assist with evaluation of ST data with previous ribotype data is provided in the appendix.

**Table 12 – Frequency of Sequence Types Among Community-Associated *C. difficile* Isolates, 2022 (N=551)**

Sequence Type (ST)	Number of Isolates	Percentage of Isolates
ST2	68	12.3%
ST42	62	11.3%
ST8	57	10.3%
ST53	21	3.8%

ST3	20	3.6%
ST43	19	3.4%
ST14	19	3.4%
ST1	18	3.3%
ST58	17	3.1%
ST10	16	2.9%
All Other STs	234	42.5%

**Table 13 – Frequency of Sequence Types Among Healthcare-Associated *C. difficile* Isolates, 2022 (N=461)**

Sequence Type (ST)	Number of Isolates	Percentage of Isolates
ST42	59	12.8%
ST2	47	10.2%
ST1	42	9.1%
ST8	32	6.9%
ST3	20	4.3%
ST10	18	3.9%
ST53	17	3.7%
ST43	17	3.7%
ST14	17	3.7%
ST58	16	3.5%
All Other STs	176	38.2%

## Summary

Surveillance data from 2022 represent the twelfth year of population-based surveillance for CDI conducted among all 10 Emerging Infections Program sites. The crude overall incidence rate of CDI in 2022 was 116.1 cases per 100,000 persons, with a higher incidence of community associated cases (62.1 cases per 100,000 persons) compared with healthcare-associated cases (54.0 cases per 100,000 persons). The incidence rate of CDI increased with age and was higher in women than in men and higher in White persons than in persons of other races.

Underlying conditions were commonly reported among CDI cases, with 41 percent having a Charlson comorbidity index of  $\geq 2$ . Antibiotic use in the prior 12 weeks was reported for 56 percent of CDI cases. Eighty percent of CDI cases were treated, with vancomycin being the most common treatment given. CDI-related complications, such as toxic megacolon and ileus, were rare.

Historically, ST1 was the predominant US strain type, but since 2017-2019, it has been replaced by a distribution of different STs in both community- and healthcare-associated isolates. Both ST42 and ST2 remain the most common sequence types in both community- and healthcare-associated CDI isolates.

## Citation

Centers for Disease Control and Prevention. 2024. Emerging Infections Program, Healthcare-Associated Infections – Community Interface Surveillance Report, *Clostridioides difficile* infection (CDI), 2022. Available at:

<https://www.cdc.gov/healthcare-associated-infections/media/pdfs/2022-CDI-Report-508.pdf>.

### For more information, visit our web sites:

- *Clostridioides difficile* Infection (CDI) Tracking [[Clostridioides difficile Infection \(CDI\) Surveillance | HAIs | CDC](#)]([https://www.cdc.gov/healthcare-associated-infections/php/haic-eip/cdiff.html?CDC\\_AAref\\_Val=https://www.cdc.gov/hai/eip/cdiff-tracking.html](https://www.cdc.gov/healthcare-associated-infections/php/haic-eip/cdiff.html?CDC_AAref_Val=https://www.cdc.gov/hai/eip/cdiff-tracking.html))
- Emerging Infections Program A.R. & Patient Safety Portal Data [[Emerging Infections Program | A.R. & Patient Safety Portal](#)] (<https://arpsp.cdc.gov/profile/eip?tab=eip>)
- *Clostridioides difficile* Infection [[About C. diff](#) | [C. diff](#) | [CDC](#)] ( [https://www.cdc.gov/cdiff/about/?CDC\\_AAref\\_Val=https://www.cdc.gov/HAI/organisms/cdiff/Cdiff\\_infect.html](https://www.cdc.gov/cdiff/about/?CDC_AAref_Val=https://www.cdc.gov/HAI/organisms/cdiff/Cdiff_infect.html))

## Appendix

A collection of isolates representing common ribotypes observed from previous EIP surveillance years underwent whole genome sequencing and MLST. Some STs corresponded to a single ribotype and some to multiple or overlapping ribotypes. Table A1 represents a crosswalk to assist with evaluation of previous ribotype data for the top community-associated and healthcare-associated STs observed from 2018–2022.

**Table A1. *C. difficile* Multi-locus Sequence Types and Associated PCR Ribotype(s)**

<b>Sequence Type (ST)</b>	<b>Associated PCR Ribotype(s)</b>
ST1	027, 036, A75
ST2	014, 020, 076, 077, 207, A27, A30
ST3	001_072, 009, 305
ST8	002
ST10	015
ST11	078, 126
ST14	014, 077, 207, A27
ST34	056
ST41	106, 153, 171, A32, B14
ST42	106, 002, 077
ST43	054
ST53	024, 103, 351
ST55	070, A12
ST58	056, A05
ST110	014, 020, 076, 154, 207, A27