Emerging Infections Program
Healthcare-Associated Infections–Community Interface Report
Clostridioides difficile infection, 2020

Note: The COVID-19 pandemic caused significant delays in 2020 case identification, data collection, data entry, data cleaning, and isolate collection and submission in all EIP sites. However, overall completeness of data collection for *Clostridioides difficile* infection cases in 2020 was similar to pre-pandemic years.

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 12,104,962 persons.
Source: U.S. Census Bureau, Population Division, Vintage 2020 Special Tabulation.

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 ≥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 all positive *C. difficile* tests to EIP staff and were routinely audited to ensure 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-associated cases and a subset of healthcare-facility onset cases.

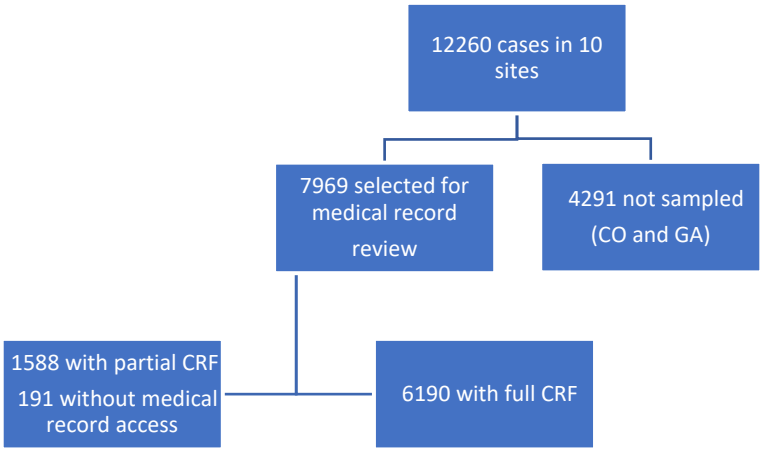
A standardized case report form (CRF) was completed for each incident case through review of medical records. Inpatient and outpatient medical records were reviewed for information on patient demographics, clinical syndrome, outcome of illness, and relevant healthcare exposures.

A convenience sample of stool specimens or 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 and NovaSeq) by CDC or the MN Department of Health Public Health Laboratory. Assembly and multi-locus sequence typing (MLST) were performed using CDC's in-house 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 complete case report form data as of 12/07/2022 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[a], No.[b]	Community-Associated CDI[a], Incidence[c]	Healthcare-Associated CDI[a], No.[b]	Healthcare-Associated CDI[a], Incidence[c]	All CDI[a], No.[b]	All CDI[a], Incidence[c]
Male	5,921,841	2316	39.1	2823	47.7	5139	86.8
Female	6,183,121	3882	62.8	3239	52.4	7121	115.2

Age group	Population ≥1 Year of Age	Community-Associated CDI[a], No.[b]	Community-Associated CDI[a], Incidence[c]	Healthcare-Associated CDI[a], No.[b]	Healthcare-Associated CDI[a], Incidence[c]	All CDI[a], No.[b]	All CDI[a], Incidence[c]
1-17 years	2,497,437	351	14.1	153	6.1	504	20.2
18-44 years	4,755,297	1551	32.6	791	16.6	2342	49.3
45-49 years	780,305	360	46.1	271	34.8	631	80.9
50-54 years	776,740	456	58.7	325	41.9	781	100.5
55-59 years	783,418	501	63.9	521	66.5	1022	130.5
60-64 years	720,234	619	85.9	609	84.6	1228	170.5
65-70 years	597,748	555	92.9	750	125.4	1305	218.3
70-74 years	480,445	588	122.4	809	168.4	1397	290.8
75-79 years	309,638	506	163.5	616	198.9	1122	362.4
80+ years	403,700	711	176.2	1217	301.4	1928	477.6

Race[a]	Population ≥1 Year of Age	Community-Associated CDI[a], No.[b]	Community-Associated CDI[a], Incidence[c]	Healthcare-Associated CDI[a], No.[b]	Healthcare-Associated CDI[a], Incidence[c]	All CDI[a], No.[b]	All CDI[a], Incidence[c]
White	8,052,023	4879	60.6	4457	55.3	9336	115.9
Other	4,052,939	1318	32.5	1606	39.6	2924	72.1

Total	Population ≥1 Year of Age	Community-Associated CDI[a], No.[b]	Community-Associated CDI[a], Incidence[c]	Healthcare-Associated CDI[a], No.[b]	Healthcare-Associated CDI[a], Incidence[c]	All CDI[a], No.[b]	All CDI[a], Incidence[c]
Total	12,104,962	6198	51.2	6062	50.1	12260	101.3

[a] The epidemiologic classification was statistically imputed for 2% of the CDI cases selected for medical record review, and race was statistically imputed for 16% 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.

[b] Cases per 100,000 persons.

[c] Subcategories may not add to total due to rounding.

Table 2 – Diagnostic Assay Results of CDI Cases (N=12260)

Diagnostic assay	N	%
Toxin positive	3901	32
Nucleic acid amplification test (NAAT) positive/toxin negative	3789	31
NAAT positive/toxin result unknown[a]	4555	37
Other methods[b]	15	<1

[a]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
[b]Includes cases diagnosed by culture or unspecified assay

Table 3 – CDI Cases by Epidemiologic Classification (N=12260)

Epidemiologic classification	N	%
Hospital onset	1464	12
LTCF onset	726	6
COHCFA	1674	14
CA	3914	32
Unknown[a]	4482	37

[a] Includes 4291 non-sampled cases

Table 4 – CDI Cases by Race and Ethnicity (N=12260)

Race/Ethnicity	N	%
Hispanic, any race	879	7
Not known to be Hispanic[a] - White[b]	6003	49
Not known to be Hispanic[a] - Black or African American[c]	1807	15
Not known to be Hispanic[a] - Asian[d]	262	2
Not known to be Hispanic[a] - Other or multiple races[e]	156	1
Non-Hispanic- Unknown race	176	1
Unknown ethnicity and race	2977	24

[a] Records either indicated ethnicity was non-Hispanic, or ethnicity was not known
[b] 635 cases with unknown ethnicity
[c] 134 cases with unknown ethnicity
[d] 36 cases with unknown ethnicity
[e] American Indian or Alaska Native, Native Hawaiian or Other Pacific Islander, or ≥2 races reported; 68 cases with unknown ethnicity

Table 5 – Location of CDI Cases on the Third Calendar Day Before Incident Specimen Collection (N=7969)

Location of patient before incident specimen collection	N	%
Private residence	5535	69
Long-term care facility	743	9
Acute-care hospital (inpatient)	1372	17
Long-term care acute care hospital	38	<1
Homeless	83	1
Incarcerated	5	<1
Other	1	<1
Unknown	192	2

Table 6 – Location of CDI Cases at Time of Incident Specimen Collection (N=7969)

Location of incident specimen collection	N	%
Outpatient setting or emergency department	4055	51
Acute care hospital	3166	40
Long-term care facility	514	6
Long-term acute care hospital	41	<1
Other	1	<1
Unknown	192	2

Table 7 – Selected Clinical Characteristics of CDI Cases (N=6190, except where indicated)

Clinical characteristic	N	%
Charlson comorbidity index - 0	2486	40
Charlson comorbidity index - 1	1136	18
Charlson comorbidity index - ≥2	2568	41
Underlying conditions - Cardiovascular disease[a,b]	1319	21
Underlying conditions - Diabetes mellitus[a]	1394	23
Underlying conditions - Chronic pulmonary disease[a,c]	1279	21
Underlying conditions - Gastrointestinal disease[a,d]	1461	24
Underlying conditions - Gastrointestinal disease – Diverticular disease[a]	579	9
Underlying conditions - Gastrointestinal disease – Inflammatory bowel disease[a]	459	7
Underlying conditions - Gastrointestinal disease – Peptic ulcer disease[a]	164	3
Underlying conditions - Gastrointestinal disease – Short gut syndrome[a]	19	<1
Underlying conditions - Gastrointestinal disease – Liver disease[a]	377	6
Underlying conditions - Chronic renal disease[a]	1181	19
Underlying conditions - Neurologic condition, any[a]	1126	18
Underlying conditions - Malignancy (hematologic or solid organ)[a]	1081	17
Underlying conditions - Transplant (hematopoietic stem cell or solid organ)[a]	215	3
Positive test for SARS-CoV-2 during hospitalization and on or before date of incident specimen collection[e]	94	4

[a] Underlying conditions are not mutually exclusive

[b] Defined as myocardial infarction, congestive heart failure, congenital heart disease, stroke, transient ischemic attack, or peripheral vascular disease

[c] Defined as cystic fibrosis or any chronic respiratory condition resulting in symptomatic dyspnea

[d] Defined as diverticular disease, inflammatory bowel disease, peptic ulcer disease, short gut syndrome, or liver disease

[e] Among patients in the hospital on the date of incident specimen collection (N=2665). 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=6190)

Healthcare Exposure[a]	CA (N=3914) N (%)	COHCFA (N=1674) N (%)	HCFO (N=602) N (%)
Acute care hospitalization	0 (0)	1645 (98)	305 (51)
Long-term care facility residence	0 (0)	159 (9)	231 (38)
Long-term acute care hospitalization	0 (0)	10 (<1)	16 (3)
Surgery	155 (4)	446 (27)	172 (29)
Emergency room	764 (20)	666 (40)	190 (32)
Observation unit	55 (1)	80 (5)	33 (5)
Chronic dialysis	112 (3)	137 (8)	60 (10)

[a] Healthcare exposure categories are not mutually exclusive.

Table 9 – Antibiotic Use in the 12 Weeks Before the Date of Incident Specimen Collection (N=6190)

Antibiotic [a]	N	%
Any antibiotic	3758	61
Aminoglycosides	76	1
Beta-lactam / beta-lactamase inhibitor combinations	1240	20
Carbapenems	186	3
Cephalosporins	1887	30
Clindamycins	461	7
Fluoroquinolones	793	13
Glycopeptides	1203	19
Macrolides	262	4
Monobactam	21	<1
Penicillins	319	5
Trimethoprim or Trimethoprim/Sulfamethoxazole	364	6
Tetracyclines	255	4
Other antibiotic	1045	17

[a] Antibiotic use categories are not mutually exclusive.

Table 10 – Treatment of Incident CDI Cases (N=6190)

Treatment[a]	N	%
Any treatment[b]	5227	84
Oral or rectal vancomycin (excluding vancomycin tapers)	4402	71
Vancomycin tapers	331	5
Metronidazole	1169	19
Fidaxomicin	192	3
Bezlotoxumab	9	<1
Stool transplant	26	<1

[a] Treatment categories are not mutually exclusive.

[b] Includes any course of CDI antibiotic therapy, bezlotoxumab, or stool transplant.

Table 11 – Outcomes of Incident CDI Cases (N=6190, except where indicated)

Outcome	N	%
Toxic megacolon[a]	20	<1
Ileus[a]	142	2
Pseudomembranous colitis[a]	29	<1
White blood cell count >= 15,000/µl[a]	1071	17
Recurrent infection[a]	659	11
Hospitalization on the day of or within 6 days after the date of incident specimen collection[a, b]	2807	45
ICU admission one day before, the day of, or within 6 days after the date of incident specimen collection [a]	407	7
In-hospital death[a]	163	3
Discharge location after acute-care hospitalization among patients who survived[c] - Private Residence	2114	80
Discharge location after acute-care hospitalization among patients who survived[c] - Long-term care facility	422	16
Discharge location after acute-care hospitalization among patients who survived[c] - Long-term acute care hospital	39	1
Discharge location after acute-care hospitalization among patients who survived[c] - Other	61	2
Discharge location after acute-care hospitalization among patients who survived[c] - Unknown	8	<1

[a] Outcomes, except for location of discharge from acute care hospitalization, are not mutually exclusive.
[b] Data include 407 cases considered to be hospital-onset.
[c] N=2644

Laboratory Characterization of *C. difficile* isolates

In 2020, 1007 *C. difficile* isolates were characterized by CDC. The total number of isolates received from each site ranged from 43 to 295, with a median of 70.5. Most isolates (95%) were collected in metropolitan areas.

Among all isolates submitted, 102 distinct multi-locus sequence types (STs) were detected. Of the 497 community-associated isolates, 72 STs were observed and ST42 (60/497, 12.1%) and ST2 (59/497, 11.9%) were predominant, followed by ST8 (9.1%), and ST1 (4.6%); all other STs consisted of <4% of isolates (Table 12). Of the 510 healthcare-associated isolates, 70 STs were observed and ST42 was predominant (66/510, 12.9%), followed by ST8 (11.2%), ST1 (10.8%), ST2 (9.0%), and ST53 (5.5%); all other STs consisted of <4% of isolates (Table 13).

Historically, ST1 was the predominant US strain type, but it has been replaced by a distribution of different STs in both community- and healthcare-associated isolates. 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, 2020 (N=497)

Sequence Type (ST)	Number of Isolates	% Isolates
ST42	60	12
ST2	59	12
ST8	45	9
ST1	23	5
ST110	19	4
ST3	19	4
ST34	19	4
ST41	17	3
ST14	16	3
ST58	15	3
All Other STs	205	41

Table 13 – Frequency of Sequence Types Among Healthcare-Associated *C. difficile* Isolates, 2020 (N=510)

Sequence Type (ST)	Number of Isolates	% Isolates
ST42	66	13
ST8	57	11
ST1	55	11
ST2	46	9
ST53	28	6
ST110	19	4
ST14	18	4
ST43	18	4
ST3	15	3
ST34	14	3
All Other STs	174	34

Summary

Surveillance data from 2020 represent the tenth year of population-based surveillance for CDI conducted among all 10 Emerging Infections Program sites. The crude overall incidence rate of CDI in 2020 was 101.3 cases per 100,000 persons, with a slightly higher incidence of community associated cases (51.2 cases per 100,000 persons) compared with healthcare-associated cases (50.1 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 40 percent having a Charlson comorbidity index of ≥2. Antibiotic use in the prior 12 weeks was reported for 61 percent of CDI cases. Eighty-

four 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.

Citation

Centers for Disease Control and Prevention. 2025. Emerging Infections Program, Healthcare-Associated Infections – Community Interface Surveillance Report, *Clostridioides difficile* infection (CDI), 2020. Available at: https://www.cdc.gov/healthcare-associated-infections/media/pdfs/2020-CDI-Report-P.pdf.

For more information, visit our web sites:

- *Clostridioides difficile* Infection (CDI) Tracking (https://www.cdc.gov/healthcare-associated-infections/php/haic-eip/cdiff.html)
- Healthcare-Associated Infections - Community Interface Data Visualization (HAICViz) (https://www.cdc.gov/healthcare-associated-infections/php/haic-eip/haicviz.html)
- *Clostridioides difficile* Infection (https://www.cdc.gov/c-diff/about/)

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 and/or overlapping ribotypess. Table A1 represents a crosswalk to assist with evaluation of previous ribotype data for the top ten Community-Associated and Healthcare-Associated STs observed in 2020.

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

MLST (ST)	Associated PCR Ribotype(s)
ST1	027, 036, A75
ST2	014, 020, 076, 077, 207, A27, A30
ST3	001_072, 009, 305
ST8	002
ST14	014, 077, 207, A27
ST34	056
ST41	106, 153, 171, A32, B14
ST42	106, 002, 077
ST43	054
ST53	024, 103, 351
ST58	056, A05
ST110	014, 020, 076, 154, 207, A27

*The appendix includes results of special analyses that are requested or of interest during a particular surveillance year.