Emerging Infections Program
Healthcare-Associated Infections–Community Interface Report
Clostridioides difficile infection, 2018

In 2018, a total of 15,591 cases of *C. difficile* infection (CDI) were reported to the Emerging Infections Program (EIP) in 35 counties in 10 states (California, Colorado, Connecticut, Georgia, Maryland, Minnesota, New Mexico, New York, Oregon, and Tennessee).

The overall distribution of EIP CDI cases and crude incidence by selected demographic factors and epidemiologic classification is presented in Table 1. Data in this report are not intended to be directly compared to annual reports from other years and should not be used to determine annual changes in EIP CDI incidence rates because single year calculations do not account for changes in testing practices by reporting facilities.

Table 1. Reported Number of CDI Cases and Crude Incidence by Sex, Age Group, Race, and Epidemiologic Classification Among the 10 EIP Sites[a]

Demographic Characteristic	Population ≥1 Year of Age	Community Associated CDI[b] No.	Community-Associated CDI[b] Incidence[d]	Healthcare-Associated CDI[b] No.	Healthcare-Associated CDI[b] Incidence[d]	All CDI[c] No.	All CDI[c] Incidence[d]
Male	5,866,907	2905	49.52	3640	62.04	6545	111.56
Female	6,116,019	4995	81.68	4051	66.23	9046	147.91
1-17 years	2,526,903	675	26.70	228	9.03	903	35.74
18-44 years	4,691,190	1951	41.59	836	17.82	2787	59.41
45-64 years	3,088,096	2443	79.11	2227	72.12	4670	151.23
≥65 years	1,676,737	2832	168.91	4399	262.35	7231	431.25
White	8,053,029	6330	78.60	5600	69.54	11930	148.14
Other	3,929,897	1571	39.98	2090	53.18	3661	93.16
Total[c]	11,982,926	7901	65.93	7690	64.18	15591	130.11

[a] The epidemiologic classification was statistically imputed for 1.5% of the observed CDI cases, and race was statistically imputed for 18.7% of the observed CDI cases. The weighted frequency of cases in Colorado and Georgia was based on 33% random sampling for cases aged ≥18 years.

[b] A CDI case was classified as community-associated 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 do not meet the aforementioned criteria were classified as healthcare-associated.

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

[d] Cases per 100,000 persons.

Diagnostic testing

In 2018, 87% of participating laboratories reported routinely using a nucleic acid amplification test (NAAT) either alone or as part of a multistep testing algorithm for CDI diagnosis. Among all CDI cases identified in 2018, 23% were toxin positive (diagnosed by toxin enzyme immunoassay or cell cytotoxicity assay), 22% were NAAT positive but toxin negative, 55% were positive by NAAT but no information was available regarding toxin positivity (e.g., diagnosed by a laboratory that only utilized NAAT), and 0.1% were diagnosed by other methods (e.g., culture).

Laboratory Characterization of *C. difficile* Isolates

From 2012-2018, PCR-ribotyping was the primary method used for EIP *C. difficile* 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 Minnesota 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).

In 2018, a total of 1076 *C. difficile* isolates were submitted to CDC for further analysis. The total number of isolates received from each site ranged from 23 to 278, with a median of 76.5. The majority of the isolates (97%) were collected in metropolitan areas.

Among all isolates submitted, 137 distinct ribotypes were detected. Ribotype 106 was the most common ribotype among community-associated *C. difficile* isolates, followed by 002, 014, and 076 (Table 2). Among healthcare-associated *C. difficile* isolates, ribotype 027 predominated, followed by 106, 002 and 014 (Table 3). An overall decline in ribotype 027 has been observed since 2012 among both community-associated (17% vs. 4%; $p<0.0001$) and healthcare-associated (21% vs. 16%; $p=0.06$) isolates. In contrast, our data demonstrate a continued increase in ribotype 106 among community-associated isolates between 2012 and 2018 (9% vs 16%; $p=0.0007$).

Twenty-two percent of the isolates harbored a deletion in *tcdC.* Twenty percent of the isolates were binary toxin-positive, and among these, ribotypes 027, 078, and 019 predominated.

Table 2. Frequency of Ribotypes Among Community-Associated *C. difficile* Isolates, 2018 (n=555)

Ribotype	Number of Isolates	% Isolates
106	91	16%
002	42	8%
014	35	6%
076	25	5%
020	22	4%
027	21	4%
A12	19	3%
056	18	3%
054	17	3%
009	15	3%
Others	250	45%

Table 3. Frequency of Ribotypes Among Community-Associated *C. difficile* Isolates, 2018 (n=521)

Ribotype	Number of Isolates	% Isolates
027	82	16%
106	65	12%
002	38	7%
014	34	7%
020	33	6%
076	19	4%
056	18	3%
001_072	14	3%
015	12	2%
017	12	2%
Others	194	37%

Sequencing was successfully performed for 1071 (99.5%) of 1076 isolates. Among the 1071 isolates sequenced, 99 known multi-locus sequence types (STs) were detected; one isolate had an unknown ST. Of the 550 community-associated isolates, 82 STs were observed and ST42 (78/550, 14.2%) was predominant, followed by ST2 (11.6%), ST8 (8.0%), ST3 (4.5%), ST14 (4.0%); all other STs consisted of <4% of isolates (Table 4). Of the 521 healthcare-associated isolates, 65 STs were observed and ST1 was predominant (82/521, 15.7%), followed by ST2 (12.1%), ST42 (10.9%), ST8 (7.7%), and ST3 (5.0%); all other STs consisted of ≤4% of isolates (Table 5). ST42 is associated with ribotype 106 and ST1 is associated with ribotype 027, the predominant ribotypes observed in 2018 among community-associated and healthcare-associated isolates, respectively. A crosswalk to assist with evaluation of ST data with previous ribotype data is provided in Appendix 2.

Table 4. Frequency of Sequence Types Among Community-Associated *C. difficile* Isolates, 2018 (n=550)

Sequence Type (ST)	Number of Isolates	% Isolates
ST42	78	14%
ST2	64	12%
ST8	44	8%
ST3	25	5%
ST14	22	4%
ST1	20	4%
ST53	19	4%
ST55	19	4%
ST11	17	3%
ST41	17	3%
All Other STs	225	41%

Table 5. Frequency of Sequence Types Among Healthcare-Associated *C. difficile* Isolates, 2018 (n=521)

Sequence Type (ST)	Number of Isolates	% Isolates
ST1	82	16%
ST2	63	12%
ST42	57	11%
ST8	40	8%
ST3	26	5%
ST110	21	4%
ST34	16	3%
ST53	15	3%
ST11	13	3%
ST14	13	3%
All Other STs	175	34%

Citation

Centers for Disease Control and Prevention. 2022. Emerging Infections Program, Healthcare-Associated Infections – Community Interface Surveillance Report, *Clostridioides difficile* infection (CDI), 2018. Available at: https://www.cdc.gov/healthcare-associated-infections/media/pdfs/2018-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 1*

An initial chart review was performed on all CDI cases in eight EIP sites and on a random sample of cases in the two remaining EIP sites with the largest surveillance catchment areas (CO and GA).[1] A subsequent comprehensive chart review was performed on all community-associated cases and a subset of healthcare-associated cases. Of 7418 cases with data available, 7091 (95.6%) received CDI treatment. These included 4798 (67.7%) cases treated with vancomycin (excluding vancomycin tapers), 366 (5.2%) with vancomycin tapers, 3268 (46.1%) with metronidazole, and 188 (2.7%) with fidaxomicin. Bezlotoxumab was administered to 7 cases. Overall, the average duration of therapy was 14 days (range: 1–104 days).

Of the 7091 treated cases, 3334 (47.0%) either required hospitalization for their CDI or were already hospitalized at the time of their CDI diagnosis. The average length of hospital stay was 8 days (range: 0–365 days). Among 3126 hospitalized cases with treatment dates available: 2664 (85.2%) were treated with vancomycin (excluding vancomycin taper), and on average, received 49.5% (range: 0% to 100%) of their therapy as inpatient and 50.5% (range: 0% to 100%) as outpatient; 1443 (46.2%) were treated with metronidazole, and on average, received 76.2% (range: 0% to 100%) of their therapy as inpatient and 23.8% (range: 0% to 100%) as outpatient; and 72 (2.3%) were treated with fidaxomicin, and on average, received 61.7% (range: 0% to 100%) of their therapy as inpatient, and 38.4% (range: 0% to 100%) as outpatient.

References

[1]Centers for Disease Control and Prevention. Healthcare-Associated Infections - Community Interface (HAIC). *Clostridioides difficile* infection (CDI) Surveillance. Available at: https://www.cdc.gov/healthcare-associated-infections/php/haic-eip/cdiff.html Accessed August 16, 2024.

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

Appendix 2*

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 ribotypes. Table A1 represents a crosswalk to assist with evaluation of previous ribotype data for the top ten Community-Associated and Healthcare-AssociatedSTs observed in 2018.

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
ST11	078, 126
ST14	014, 077, 207, A27
ST34	056
ST41	106, 153, 171, A32, B14
ST42	106, 002, 077
ST53	024, 103, 351
ST55	070, A12
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.

Note: The dataset analyzed for this report was generated on March 17, 2020. Diagnostic testing information was updated on March 31, 2022, and laboratory data were updated on March 31, 2022, and January 17, 2025.