Emerging Infections Program
Healthcare-Associated Infections–Community Interface Report
Clostridioides difficile Infection Surveillance, 2023

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 12,212,565 persons.

Source: U.S. Census Bureau, Population Division, Vintage 2021 Special Tabulation for Connecticut's catchment area and Vintage 2023 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 2023, 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 ≥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 areas reported positive *C. difficile* tests to Emerging Infections Program (EIP) staff and were routinely audited with a goal of complete case ascertainment.

An initial chart review using a standardized case report form (CRF) was performed on all CDI cases in eight EIP sites and on all pediatric cases and a 33% age- and sex-stratified random sample of cases aged 18 years and older in the two remaining EIP sites with the largest surveillance areas (Colorado and Georgia). Inpatient and outpatient medical records were reviewed for patient demographics and selected healthcare exposures. A subsequent comprehensive chart review was performed on all community-onset cases and a subset of healthcare-facility onset cases to collect additional healthcare exposures, clinical syndrome, outcome of illness, and treatment. Case address information was geocoded to its corresponding census tract.

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 these 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.

Race/ethnicity was considered missing if a patient had unknown ethnicity (regardless of reported race) or if a patient had unknown race and was not Hispanic or Latino. New for 2023 data, Bayesian Improved Surname Geocoding (BISG) was used to impute missing race/ethnicity [1]. BISG applies Bayes' Theorem to calculate a patient's probability of identifying with each racial/ethnic group given their surname and home census tract or county. Probabilities for patients with known race/ethnicity were set to 1 for their reported race/ethnicity group and 0 for all other racial/ethnic groups. Race/ethnicity-stratified case counts were calculated by summing the probabilities for each racial/ethnic group.

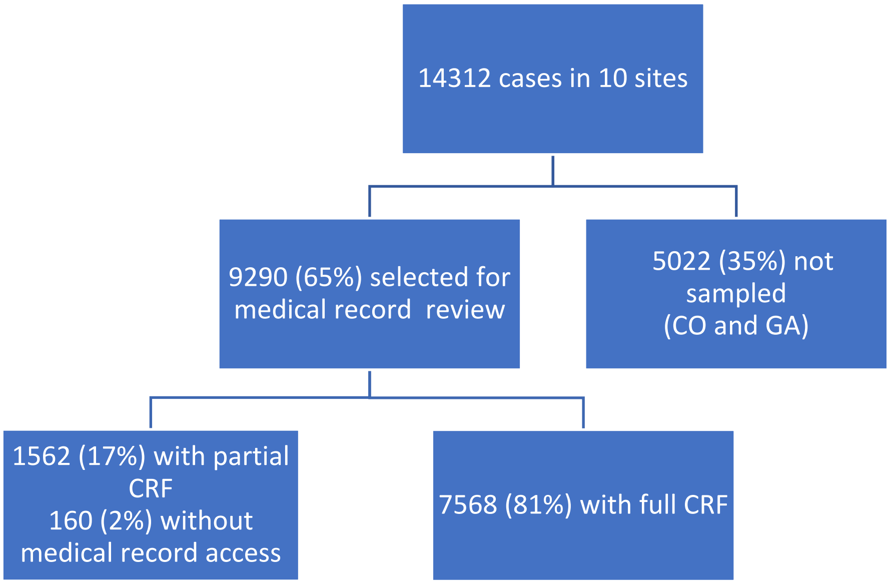
Multiple imputation analysis was performed for missing epidemiologic class variables (community-associated versus healthcare-associated) using the Fully Conditional Specification method [2], with the logistic regression incorporating race/ethnicity, age, sex, and EIP site as predictors. For Colorado and Georgia, where cases underwent sampling for medical record review, the total case counts for each epidemiologic class were estimated based on the stratified random sampling scheme described above. Post-stratification weighting was applied to adjust the estimated counts, ensuring alignment with the total CDI cases across each race/ethnicity, age, and sex stratum, so that the estimates accurately reflect the distribution of these demographic characteristics within the overall population. Incidence rates for all cases and by demographic groups were calculated using US Census population estimates.

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 CDC or the Minnesota Department of Health Public Health Laboratory.

Assembly and multi-locus sequence typing were performed using CDC's in-house Portable Healthcare Nextgen Informatics (PHoeNIx) pipeline [3].

CDI surveillance data undergo regular data cleaning to ensure accuracy and completeness. Patients with case data as of 6/20/2025 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.

Figure. Flow diagram depicting the selection of *Clostridioides difficile* infection cases for medical record review, Emerging Infections Program, 2023



Abbreviations: CO, Colorado; GA, Georgia; CRF, case report form

Results

Table 1 – Reported Number of *Clostridioides difficile* Infection Cases and Crude Incidence by Sex, Age Group, Race, and Epidemiologic Classification Among the 10 Emerging Infections Program Sites, 2023

Sex	**Population ≥1 Year of Age**	**Community-Associated CDI[a], No.[c]**	**Community-Associated CDI[a], Incidence[b]**	**Healthcare-Associated CDI[a], No.[c]**	**Healthcare-Associated CDI[a], Incidence[b]**	**All CDI, No.[c]**	**All CDI, Incidence[b]**
Male	6,004,472	2933	48.8	3062	51.0	5994	99.8
Female	6,208,093	4677	75.3	3641	58.7	8318	134.0

Age group	**Population ≥1 Year of Age**	**Community-Associated CDI[a], No.[c]**	**Community-Associated CDI[a], Incidence[b]**	**Healthcare-Associated CDI[a], No.[c]**	**Healthcare-Associated CDI[a], Incidence[b]**	**All CDI, No.[c]**	**All CDI, Incidence[b]**
1-17 years	2,471,237	662	26.8	194	7.8	856	34.6
18-44 years	4,798,318	1981	41.3	843	17.6	2823	58.8
45-49 years	759,818	356	46.8	263	34.6	619	81.5
50-54 years	789,123	437	55.3	426	54.0	863	109.4
55-59 years	750,869	542	72.2	505	67.2	1047	139.4
60-64 years	734,346	663	90.3	662	90.1	1325	180.4
65-70 years	631,425	657	104.0	785	124.3	1442	228.4
70-74 years	509,226	682	133.9	819	160.8	1501	294.8
75-79 years	361,141	647	179.0	826	228.9	1473	407.9
80+ years	407,062	983	241.5	1380	339.0	2363	580.3

Race[d]	**Population ≥1 Year of Age**	**Community-Associated CDI[a], No.[c]**	**Community-Associated CDI[a], Incidence [b]**	**Healthcare-Associated CDI[a], No.[c]**	**Healthcare-Associated CDI[a], Incidence[b]**	**All CDI, No.[c]**	**All CDI, Incidence[b]**
Hispanic or Latino, any race	2,196,153	888	40.4	782	35.6	1670	76.0
Not Hispanic or Latino - Asian and/or Native Hawaiian/Other Pacific Islander[e]	935,785	316	33.8	260	27.8	576	61.5
Not Hispanic or Latino - Asian only[f]	923,466	N/A	N/A	N/A	N/A	383	41.5
Not Hispanic or Latino - Native Hawaiian/Other Pacific Islander only[f]	12,319	N/A	N/A	N/A	N/A	18	146.1
Not Hispanic or Latino – Black or African American	2,561,189	1177	46.0	1568	61.2	2745	107.2
Not Hispanic or Latino – White	6,156,686	5023	81.6	3961	64.3	8983	145.9

Not Hispanic or Latino – American Indian or Alaska Native or Multiracial	362,752	206	56.7	132	36.4	338	93.1
Not Hispanic or Latino – American Indian or Alaska Native only[f]	63,206	N/A	N/A	N/A	N/A	53	83.9
Not Hispanic or Latino – Multiracial only[f]	299,546	N/A	N/A	N/A	N/A	72	24.0

Total	**Population ≥1 Year of Age**	**Community-Associated CDI[a], No.[c]**	**Community-Associated CDI[a], Incidence[b]**	**Healthcare-Associated CDI[a], No.[c]**	**Healthcare-Associated CDI[a], Incidence[b]**	**All CDI, No.[c]**	**All CDI, Incidence[b]**
Total	12,212,565	7610	62.3	6702	54.9	14312	117.2

Abbreviations: CDI, *Clostridioides difficile* infection; N/A, Not applicable (refer to corresponding footnote).

[a] The epidemiologic classification was statistically imputed for 2% of the CDI cases that underwent medical record review.

[b] Cases per 100,000 persons.

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

[d] Race/ethnicity was imputed for cases with missing race/ethnicity (26.7%, n=3,826) using BISG, as described in the methods section. The number of cases reported (i.e., non- missing) by race/ethnicity were 1,105 (Hispanic or Latino, any race), 401 (not Hispanic or Latino – Asian and/or Native Hawaiian/Other Pacific Islander), 2,284 (Not Hispanic or Latino – Black or African American), 6,571 (Not Hispanic or Latino – White), and 125 (Not Hispanic or Latino – American Indian or Alaska Native or Multiracial).

[e] A small proportion of patients with missing race/ethnicity who are multiracial (Asian and NH/PI) may have been imputed as Non-Hispanic or Latino – Asian and/or Native Hawaiian/Other Pacific Islander using the BISG method, which does not distinguish between these two racial/ethnic groups.

[f] Case counts include reported (i.e., non-missing) data only. Missing data for these racial/ethnic groups were not separately imputed because BISG combines each of these groups with another racial/ethnic group. Thus, since missing epidemiologic class data were imputed using BISG-imputed race/ethnicity data, incidence rates by epidemiologic class could not be calculated for these racial/ethnic groups.

Table 2 – Diagnostic Assay Results of *Clostridioides difficile* infection Cases (N=14312), Emerging Infections Program, 2023

Diagnostic assay	N	%
Toxin positive	4164	29
Nucleic acid amplification test (NAAT) positive/toxin negative	5599	39
NAAT positive/toxin result unknown[a]	4545	32
Unspecified assay	4	<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.

Table 3 – *Clostridioides difficile* infection Cases by Epidemiologic Classification (N=14312), Emerging Infections Program, 2023

Epidemiologic classification	N	%
Hospital onset	1744	12
Long-term care-facility onset	603	4
Community-onset, healthcare-facility associated	1920	13
Community-associated	4849	34
Unknown[a]	5196	36

[a] Includes 5022 non-sampled cases.

Table 4 – Location of *Clostridioides difficile* infection Cases on the Third Calendar Day Before Incident Specimen Collection, Emerging Infections Program, 2023 (N=9290)

Location of patient before incident specimen collection	N	%
Private residence	6661	72
Long-term care facility	608	7
Acute-care hospital (inpatient)	1717	18
Long-term care acute care hospital	29	<1
Homeless	85	1
Incarcerated	6	<1
Other	5	<1
Unknown	179	2

Table 5 – Location of *Clostridioides difficile* infection Cases at Time of Incident Specimen Collection, Emerging Infections Program, 2023 (N=9290)

Location of incident specimen collection	N	%
Outpatient setting or emergency department	5176	56
Acute care hospital	3567	38
Long-term care facility	348	4
Long-term acute care hospital	23	<1
Other	3	<1
Unknown	173	2

Table 6 – Selected Clinical Characteristics of *Clostridioides difficile* infection Cases, Emerging Infections Program, 2023 (N=7568, except where indicated)

Clinical characteristic	N	%
Charlson comorbidity index - 0	2941	39
Charlson comorbidity index - 1	1411	19
Charlson comorbidity index - ≥2	3216	42
Underlying conditions - Cardiovascular disease[a,b]	1802	24

Underlying conditions - Diabetes mellitus[a]	1666	22
Underlying conditions - Chronic pulmonary disease[a,c]	1662	22
Underlying conditions - Gastrointestinal disease[a,d]	1960	26
Underlying conditions - Gastrointestinal disease – Diverticular disease[a]	849	11
Underlying conditions - Gastrointestinal disease – Inflammatory bowel disease[a]	578	8
Underlying conditions - Gastrointestinal disease – Peptic ulcer disease[a]	206	3
Underlying conditions - Gastrointestinal disease – Short gut syndrome[a]	11	<1
Underlying conditions - Gastrointestinal disease – Liver disease[a]	531	7
Underlying conditions - Chronic renal disease[a]	1528	20
Underlying conditions - Neurologic condition, any[a]	1808	24
Underlying conditions - Malignancy (hematologic or solid organ)[a]	1317	17
Underlying conditions - Transplant (hematopoietic stem cell or solid organ)[a]	283	4
Positive test for SARS-CoV-2 during hospitalization and on or before date of incident specimen collection[e]	95	3

[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=3112). 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 7 – Selected Healthcare Exposures and Risk Factors of Incident *Clostridioides difficile* infection Cases in the 12 Weeks Before the Date of Incident Specimen Collection by Epidemiologic Classification, Emerging Infections Program, 2023 (N=7568)[a]

	CA (N=4833)		**COHCFA (N=1920)**		**HCFO (N=811)**	
Healthcare Exposure[a, b]	**N**	**%**	**N**	**%**	**N**	**%**
Acute care hospitalization	0	0	1889	98	406	50
Long-term care facility residence	0	0	208	11	310	38
Long-term acute care hospitalization	0	0	14	1	18	2
Surgery	209	4	495	26	251	31
Emergency room	1113	23	705	37	224	28
Observation unit	62	1	70	4	17	2
Chronic dialysis	140	3	159	8	79	10

Abbreviations: CA, community-associated; COHCFA, community-onset, healthcare-facility associated; HCFO, healthcare-facility onset

[a] Excludes 4 cases with unknown epidemiologic classification.

[b] Healthcare exposure categories are not mutually exclusive.

Table 8 – Antibiotic Use in the 12 Weeks Before the Date of Incident Specimen Collection, Emerging Infections Program, 2023 (N=7568)

Antibiotic [a]	N	%
Any antibiotic	4764	63
Aminoglycosides	92	1
Beta-lactam / beta-lactamase inhibitor combinations	1775	23
Carbapenems	241	3
Cephalosporins	2571	34
Clindamycin	425	6
Fluoroquinolones	821	11
Glycopeptides	1457	19
Macrolides	319	4
Monobactam	14	<1
Penicillins	496	7
Trimethoprim or Trimethoprim/Sulfamethoxazole	423	6
Tetracyclines	406	5
Other antibiotic	1417	19

[a] Antibiotic use categories are not mutually exclusive.

Table 9 – Treatment of Incident *Clostridioides difficile* infection Cases, Emerging Infections Program, 2023 (N=7568)

Treatment[a]	N	%
Any treatment[b]	6074	80
Oral or rectal vancomycin (excluding vancomycin tapers)[c]	4791	63
Vancomycin tapers	317	4
Metronidazole[d]	877	12
Fidaxomicin[e]	1135	15
Bezlotoxumab	33	<1
Microbiota-based therapy (excluding stool transplant)	14	<1
Stool transplant	40	1

[a] Treatment categories are not mutually exclusive.

[b] Includes any course of *C. difficile infection* (CDI) antibiotic therapy, bezlotoxumab, or microbiota-based therapy (REBYOTA, VOWST, or stool transplant).

[c] Includes 57 patients receiving vancomycin prophylaxis after treatment of incident CDI.

[d] Includes 3 patients receiving metronidazole prophylaxis after treatment of incident CDI.

[e] Includes 1 patient receiving fidaxomicin prophylaxis after treatment of incident CDI.

Table 10 – Clinical Course and Outcomes of Incident *Clostridioides difficile* infection Cases, Emerging Infections Program, 2023 (N=7568, except where indicated)

Clinical course and outcome	N	%
Toxic megacolon[a]	18	<1
Ileus[a]	192	3
Pseudomembranous colitis[a]	20	<1
White blood cell count >= 15,000/µl[a]	1220	16
Recurrent infection[a]	843	11
Hospitalization on the day of or within 6 days after the date of incident specimen collection[a, b]	3240	43
ICU admission one day before, the day of, or within 6 days after the date of incident specimen collection [a]	464	6
In-hospital death[a]	193	3
Discharge location after acute-care hospitalization among patients who survived[c] - Private Residence	2407	79
Discharge location after acute-care hospitalization among patients who survived[c] - Long-term care facility	550	18
Discharge location after acute-care hospitalization among patients who survived[c] - Long-term acute care hospital	14	<1
Discharge location after acute-care hospitalization among patients who survived[c] - Other	64	2
Discharge location after acute-care hospitalization among patients who survived[c] - Unknown	11	<1

Abbreviations: ICU, intensive care unit

[a] Clinical course and outcomes, except for location of discharge from acute care hospitalization, are not mutually exclusive.

[b] Data include 587 cases considered to be hospital-onset.

[c] N=3046

Laboratory Characterization

In 2023, 999 *C. difficile* isolates were characterized by CDC. The total number of isolates received from each site ranged from 39 to 317, with a median of 50. Most isolates (95%) were collected from patients residing in metropolitan areas. Two isolates were from cases with unknown epidemiologic classification.

Among all isolates submitted, 111 distinct sequence types were detected. Among the 516 community-associated isolates, 86 distinct STs were observed. ST42 was most common (11.4%), followed by ST2 (10.7%), ST8 (7.6%), ST53 (4.3%), and ST58 (4.1%) (Table 12). Among the 481 healthcare-associated isolates, 72 distinct STs were observed. ST42 was most common (12.9%), followed by ST2 (11.2%), ST8 (10.0%), ST1 (6.9%), ST58 (4.8%), and ST3 (4.2%) (Table 13). A crosswalk to assist with comparison of ST data to previous ribotype data is provided in the appendix.

Table 12 – Frequency of Sequence Types Among Community-Associated *C. difficile* Isolates, 2023 (N=516)

Sequence Type (ST)	Number of Isolates	Percentage of Isolates
ST42	59	11.4%
ST2	55	10.7%
ST8	39	7.6%
ST53	22	4.3%
ST58	21	4.1%
ST43	19	3.7%
ST3	16	3.1%
ST14	16	3.1%
ST34	15	2.9%
ST110	15	2.9%
All Other STs	239	46.3%

Table 13 – Frequency of Sequence Types Among Healthcare-Associated *C. difficile* Isolates, 2023 (N=481)

Sequence Type (ST)	Number of Isolates	Percentage of Isolates
ST42	62	12.9%
ST2	54	11.2%
ST8	48	10.0%
ST1	33	6.9%
ST58	23	4.8%
ST3	20	4.2%
ST110	18	3.7%
ST14	17	3.5%
ST53	15	3.1%
ST43	15	3.1%
All Other STs	176	36.6%

Summary

Surveillance data from 2023 represent the thirteenth year of population-based surveillance for CDI conducted in 10 Emerging Infections Program sites. The crude overall incidence rate of CDI in 2023 was 117.2 cases per 100,000 persons, similar to the overall incidence rate of 116.1 cases per 100,000 persons in 2022. These estimates do not account for potential changes in diagnostic testing practices over time. The incidence of community-associated CDI cases (62.3 cases per 100,000 persons) was higher compared with healthcare-associated cases (54.9 cases per 100,000 persons). The incidence rate of CDI increased with age and was higher in women than in men and highest in persons who were Native Hawaiian/Other Pacific Islander or White, compared to persons of other racial/ethnic groups.

Underlying conditions were commonly reported among CDI cases, with 42 percent having a Charlson comorbidity index of ≥2. Antibiotic use in the prior 12 weeks was reported for 63 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 variety of different STs; this shift has been observed among both community- and healthcare-associated isolates. In 2023, both ST42 and ST2 remain the most common sequence types in both community- and healthcare-associated CDI isolates. The percentage of ST1 isolates continues to fall; in 2023, ST1 accounted for 2.5% of community-associated isolates and 6.9% of healthcare-associated isolates.

References

1. Elliott MN, Morrison PA, Fremont A, McCaffrey DF, Pantoja P, Lurie N. Using the Census Bureau's Surname List to Improve Estimates of Race/Ethnicity and Associated Disparities. RAND website. Available at: Using the Census Bureau's Surname List to Improve Estimates of Race/Ethnicity and Associated Disparities | RAND (https://www.rand.org/pubs/external_publications/EP20090611.html#document-details) Accessed September 19, 2025.
2. Buuren SV, Brand JPL, Groothuis-Oudshoorn CGM, Rubin DB. Fully conditional specification in multivariate imputation. Stat Comput Sim 2006;76:1049–1064.
3. Hagey JV, Vlachos N, Kent AG, Masters T, Qi P, and Halpin AL. (2025). CDCgov/phoenix: v2.2.0 (v2.2.0). Zenodo. https://doi.org/10.5281/zenodo.8147510

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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)
- 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/c-diff/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; resulting data were used to perform multi-locus sequence typing. Some STs correspond 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 community-associated and healthcare-associated STs observed from 2018–2023.

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

Sequence Type (ST)	Associated PCR Ribotype(s)
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