# Emerging Infections Program
# Healthcare-Associated Infections Community Interface Report
# Invasive *Staphylococcus aureus*, 2020

Last Updated: June 12, 2025

*Erratum September 5, 2024: The rates among people on dialysis were corrected. The previous version of this report used an incorrect denominator for calculating these rates.*

*Update June 12, 2025: Laboratory data have been added in this update.*

## Surveillance Catchment Areas

**Methicillin-resistant *Staphylococcus aureus* (MRSA):** California (3 county San Francisco Bay area); Connecticut (Fairfield, Hartford, and New Haven Counties); Georgia (8 county Atlanta area); Maryland (Baltimore City and County); Minnesota (2 county Minneapolis–Saint Paul area); New York (1 Rochester county); Tennessee (1 Nashville county).

**Methicillin-sensitive *Staphylococcus aureus* (MSSA):** California (3 county San Francisco Bay area); Connecticut (New Haven County); Georgia (1 Atlanta county); Maryland (Baltimore City and County); Minnesota (2 county Minneapolis–Saint Paul area); New York (1 Rochester county); Tennessee (1 Nashville county).

## Population

The MRSA surveillance areas represent 15,218,247 persons. The MSSA surveillance areas represent 10,274,147 persons.

Source: U.S. Census Bureau, Population Division, Vintage 2020 Special Tabulation

## Case Definition

Invasive *Staphylococcus aureus* (SA) infection: isolation of SA from a normally sterile site in a resident of the surveillance area in 2020. Cases of infection are classified into one of three epidemiologic classifications.

A case is classified as

- hospital-onset (HO) if the SA culture was obtained on or after the third calendar day of hospitalization, where admission is hospital day 0[1];
- healthcare-associated community-onset (HACO) if the culture was obtained in an outpatient setting or before the third[1] calendar day of hospitalization and had one or more of the following:
    1. a history of hospitalization, surgery, dialysis, or residence in a long-term care facility in the previous year, or

2. the presence of a central vascular catheter (CVC) within 2 days prior to SA culture;

- community-associated (CA) if none of the previously mentioned criteria are met.

Cases were classified as MRSA or MSSA based on results from local clinical microbiology laboratory testing.

[1] Compared to annual summaries from 2005–2017, this case definition represents an update in nomenclature (i.e., switching from “fourth” to “third” day before), but not a change to the case definition

# Methods

Case finding was active, laboratory-based and population-based. Emerging Infections Program (EIP) personnel routinely contacted microbiology laboratories serving healthcare facilities in their area to identify cases. Laboratories serving the surveillance catchment areas were routinely audited to ensure complete case ascertainment.

A standardized case report form was completed for each incident case through review of medical records. Medical records were reviewed for information on demographic characteristics, clinical syndrome, and outcome of illness.

Convenience samples of MSSA and MRSA isolates were collected and sent to CDC for routine testing, including antimicrobial susceptibility testing using reference broth microdilution and, beginning with 2017 isolates, whole genome sequencing (WGS) to perform SCC*mec* typing, *spa* typing, multilocus sequence typing (MLST), clonal complex assignment, and inferred pulsed-field gel electrophoresis (PFGE) typing. Pulsed field type is inferred from WGS based on phylogenetic relatedness, MLST clonal complex, and molecular characteristics of the isolates[1]. Isolates belonging to clonal complex 8 are sub-typed using a single nucleotide polymorphism (SNP) assay that has been modified for use with WGS data, allowing confirmation of isolates identified as USA300[2]. The use of PFGE for all isolates was discontinued in 2008; up until 2012, PFGE was inferred using a validated algorithm based on the following isolate microbiologic characteristics: SCC*mec* type, presence of Panton-Valentine leukocidin and Toxic Shock Syndrome Toxin genes, and antimicrobial susceptibility results[3]. From 2012-2016, *spa* typing was included in routine laboratory testing and MLST clonal complexes were inferred based on *spa* type, allowing for the identification of PFGE types based on MLST clonal complex and molecular characteristics of the isolates[1], with 2016 isolates identified as USA300 confirmed using a SNP assay[2]. In 2020, MRSA isolates were collected in five sites (California, Georgia, Minnesota, New York, and Tennessee) and MSSA isolates in three (Georgia, Minnesota, and New York).

Rates of invasive SA infection among all patients were calculated using population estimates for 2020. Cases with unknown race were assigned race based on distribution of known age, race, and sex by EIP site.

Rates of invasive SA infection among patients who were undergoing chronic dialysis treatment were calculated using the December 31, 2019 point prevalent counts of patients on dialysis from the United States Renal Data System (USRDS) (https://www.niddk.nih.gov/about-niddk/strategic-plans-reports/usrds). The figures depicting the overall invasive SA incidence by epidemiologic class and incidence of invasive HACO SA among persons on dialysis, 2009–2020, are restricted to the continuous catchment area (California [3 county San Francisco Bay area]; Connecticut [Fairfield, Hartford, and New Haven Counties]; Georgia [8 county Atlanta area]; Minnesota [2 county Minneapolis–Saint Paul area]; New York [1 Rochester county]; and Tennessee [1 Nashville county]) for comparison of trends over time.

Invasive SA surveillance data undergo regular data cleaning to ensure accuracy and completeness. Patients with complete case report form data as of September 5, 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.

[1] Inferred Identification of Pulsed Field Types based on MLST clonal complex (CC) (https://archive.cdc.gov/#/details?url=https://www.cdc.gov/hai/settings/lab/ccalgorithm.html)

[2] Improved Subtyping of *Staphylococcus aureus* Clonal Complex 8 Strains Based on Whole-Genome Phylogenetic Analysis [PDF - 15 pages] (https://msphere.asm.org/content/msph/3/3/e00464-17.full.pdf)

[3] Use of an Inferred PFGE Algorithm, Emerging Infections Program/Active Bacterial Core (ABCs) Surveillance Invasive MRSA Project (https://archive.cdc.gov/#/details?url=https://www.cdc.gov/hai/settings/lab/inferred-pfge-algorithm.html)

# Results

## Table 1. MSSA (N=3593) and MRSA (N=3051) Cases by Race, Emerging Infections Program, 2020

| Race | MSSA No. (Rate[a]) | MRSA No. (Rate[a]) |
|---|---|---|
| White | 2202 (35.9) | 1688 (18.8) |
| Black | 1012 (47.4) | 1185 (31.8) |
| Other | 379 (18.9) | 178 (7.1) |
| TOTAL | 3593 (35.0) | 3051 (20.1) |

Unknown race (n= 362 MSSA, n= 236 MRSA) was imputed using age, sex, and dialysis status

[a] Cases per 100,000 population for EIP areas (crude rates)

## Table 2. MSSA (N=3593) and MRSA (N=3051) Case and Death Rate by Epidemiological Classification, Emerging Infections Program, 2020

| Class | No. (Rate[a]) MSSA Cases | No. (Rate) MSSA Deaths | No. (Rate) MRSA Cases | No. (Rate) MRSA Deaths |
|---|---|---|---|---|
| CA | 1307 (12.7) | 131 (1.3) | 665 (4.4) | 78 (0.5) |
| HCA[b] | 2241 (21.8) | 312 (3.0) | 2361 (15.5) | 414 (2.7) |
| HO | 487 (4.7) | 112 (1.1) | 458 (3.0) | 138 (0.9) |
| HACO | 1754 (17.1) | 200 (1.9) | 1903 (12.5) | 276 (1.8) |
| Unknown | 45 (0.4) | 1 (<0.01) | 25 (0.2) | 1 (<0.01) |

[a] Cases per 100,000 population for EIP areas (crude rates) calculated using 2020 U.S. Census Data

[b] HCA: Healthcare-associated invasive SA infection; sum of patients that are classified as either the HO or HACO classes

## Table 3. MSSA (N=3593) and MRSA (N=3051) Cases by Race and Ethnicity, Emerging Infections Program, 2020

| Race/Ethnicity | MSSA | No. (%) | MSSA | No. (%) |
|---|---|---|---|---|
| Hispanic, any race | 315 | (8.8) | 208 | (6.8) |
| Not known to be Hispanic[a] - White[b] | 1906 | (53.1) | 1481 | (48.5) |
| Not known to be Hispanic[a] - Black or African American[c] | 885 | (24.6) | 1082 | (35.5) |
| Not known to be Hispanic[a] - Asian[d] | 242 | (6.7) | 99 | (3.2) |
| Not known to be Hispanic[a] - Other or multiple races[e] | 70 | (1.9) | 49 | (1.6) |
| Not known to be Hispanic[a,f] - Unknown race | 175 | (4.9) | 132 | (4.3) |

[a] Records either indicated ethnicity was non-Hispanic, or ethnicity was not known
[b] 129 MSSA cases and 100 MRSA cases with unknown ethnicity
[c] 48 MSSA cases and 62 MRSA cases with unknown ethnicity
[d] 45 MSSA cases and 12 MRSA cases with unknown ethnicity
[e] American Indian or Alaska Native, Native Hawaiian or Other Pacific Islander, or ≥2 races reported; 8 MSSA cases and 5 MRSA cases with unknown ethnicity
[f] Of cases with unknown race, 102 MSSA and 75 MRSA cases had unknown ethnicity

## Table 4. MRSA Inferred PFGE Type by Epidemiologic Classification, Isolates Tested at CDC (N=469), Emerging Infections Program, 2020

| Class | Total Sequenced | CC5 USA100 No. (%) | Other CC5 No. (%) | CC8 USA300 No. (%) | Other CC8 No. (%) | Other (not CC5 or CC8) No. (%) |
|---|---|---|---|---|---|---|
| CA[a] | 99 | 7 (7.1) | 7 (7.1) | 75 (75.8) | 1 (1.0) | 9 (9.1) |
| HCA[b,c] | 368 | 101 (27.4) | 21 (5.7) | 178 (48.4) | 18 (4.9) | 50 (13.6) |
| HO | 62 | 15 (24.2) | 6 (9.7) | 27 (43.5) | 4 (6.5) | 10 (16.1) |
| HACO | 306 | 86 (28.1) | 15 (4.9) | 151 (49.3) | 14 (4.6) | 40 (13.1) |
| Total | 467 | 108 (23.1) | 28 (6.0) | 253 (54.2) | 19 (4.1) | 59 (12.6) |

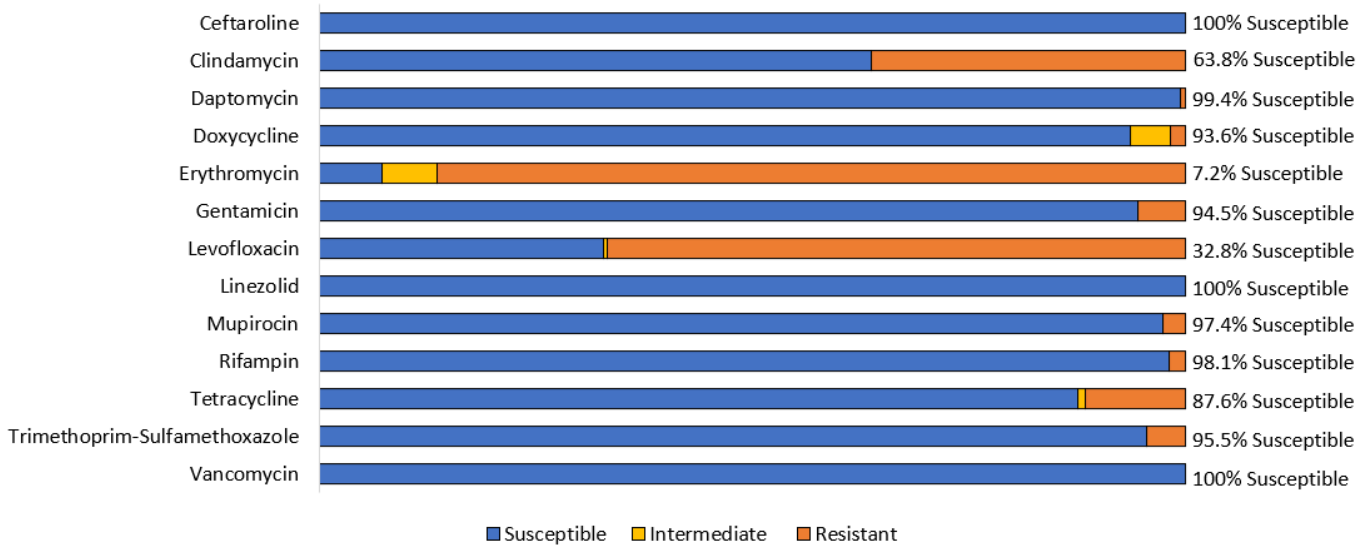
[a] 1 CA isolate failed sequencing

[b] HCA: Healthcare-associated invasive SA infection; sum of patients that are classified as either the HO or HACO classes

[c] 1 HACO isolate failed sequencing

## Figure 1. MRSA Antimicrobial Susceptibility Testing Results by Agent[a,b,c] (N=469 Isolates Tested at CDC), Emerging Infections Program, 2020

Of a chart




[a] High-level mupirocin resistance (MIC >256 µg/mL) depicted in the figure as resistant; isolates without high level mupirocin resistance (i.e., ≤256 µg/mL) shown as susceptible.

[b] Daptomycin non-susceptible isolates are depicted in the figure as resistant

[c] Isolates with inducible resistance to clindamycin are considered resistant

## Table 5. MSSA Clonal Complex[a] by Epidemiologic Classification, Isolates Tested at CDC (N=364), Emerging Infections Program, 2020

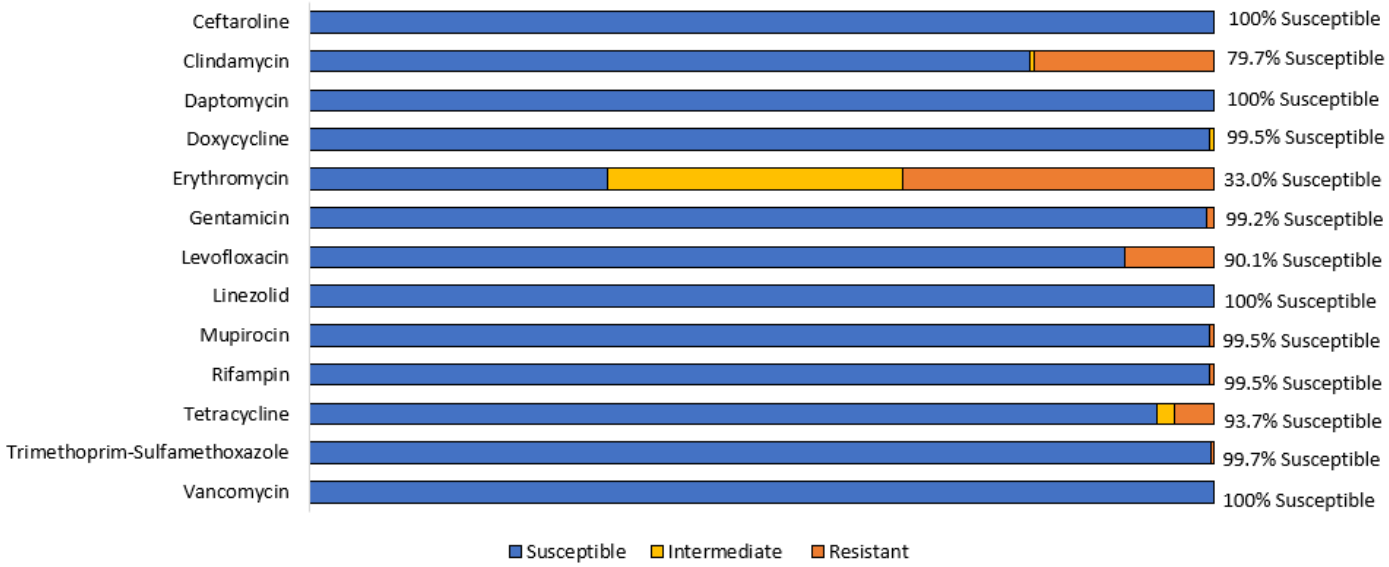
| Class | Total | CC5 No. (%) | CC8 No. (%) | CC30 No. (%) | CC72 No. (%) | Other clonal complex[c] No. (%) |
|---|---|---|---|---|---|---|
| CA | 85 | 17 (20.0) | 14 (16.5) | 15 (17.6) | 3 (3.5) | 36 (42.4) |
| HCA[b] | 279 | 48 (17.2) | 50 (17.9) | 31 (11.1) | 14 (5.0) | 136 (48.7) |
| HO | 79 | 14 (17.7) | 9 (11.4) | 14 (17.7) | 4 (5.1) | 38 (48.1) |
| HACO | 200 | 34 (17.0) | 41 (20.5) | 17 (8.5) | 10 (5.0) | 98 (49.0) |
| Total[c] | 364 | 65 (17.9) | 64 (17.6) | 46 (12.6) | 17 (4.7) | 172 (47.3) |

[a] The four most common clonal complexes are displayed

[b] HCA: Healthcare-associated invasive SA infection; sum of patients that are classified as either the HO or HACO classes

[c] 'Other clonal complex' includes CC15 (n=40), CC45 (n=25), CC398 (n=24), CC1 (n=21), CC59 (n=13), CC97 (n=10), CC20 (n=7), CC1/CC97 (n=4), CC22 (n=3), CC152 (n=3), CC1/CC8/CC97 (n=1), CC8/CC72 (n=1), CC12 (n=1), CC25 (n=1), CC121 (n=1), CC361 (n=1), and unknown CC (n=16)

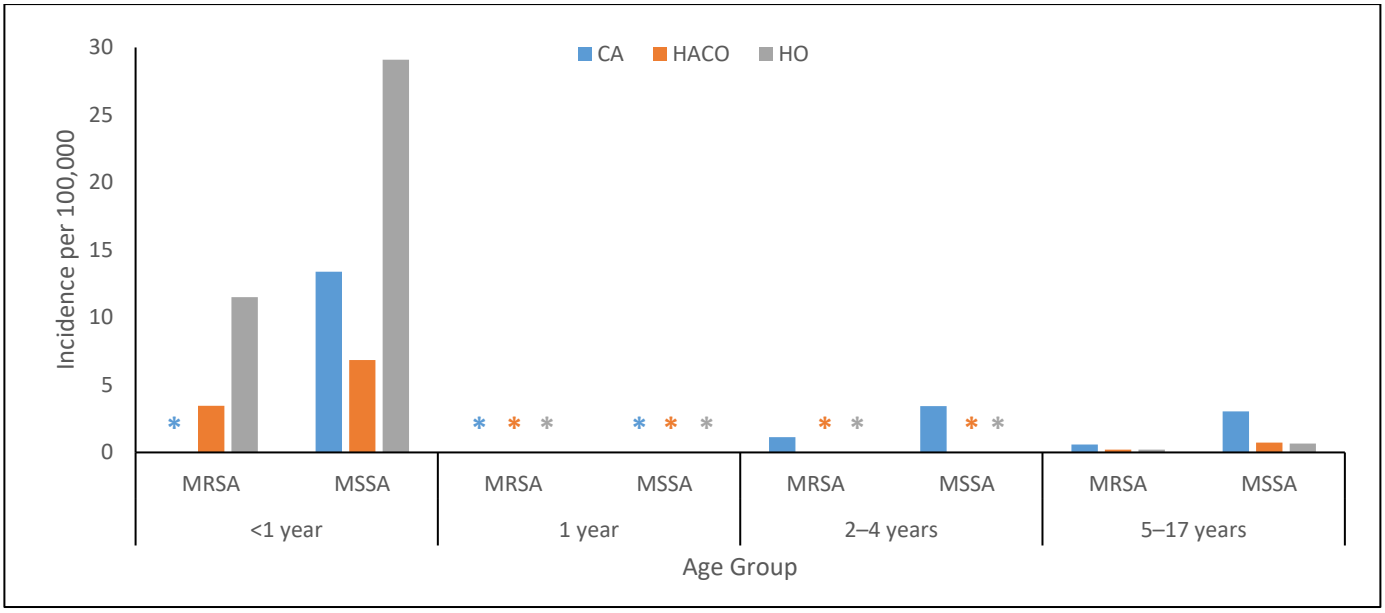
## Figure 2. MSSA Antimicrobial Susceptibility Testing Results by Agent[a,b] (N=364 Isolates Tested at CDC), Emerging Infections Program, 2020




[a] High-level mupirocin resistance (MIC >256 µg/mL) depicted in the figure as resistant; isolates without high level mupirocin resistance (i.e., ≤256 µg/mL) shown as susceptible.

[b] Isolates with inducible resistance to clindamycin are considered resistant

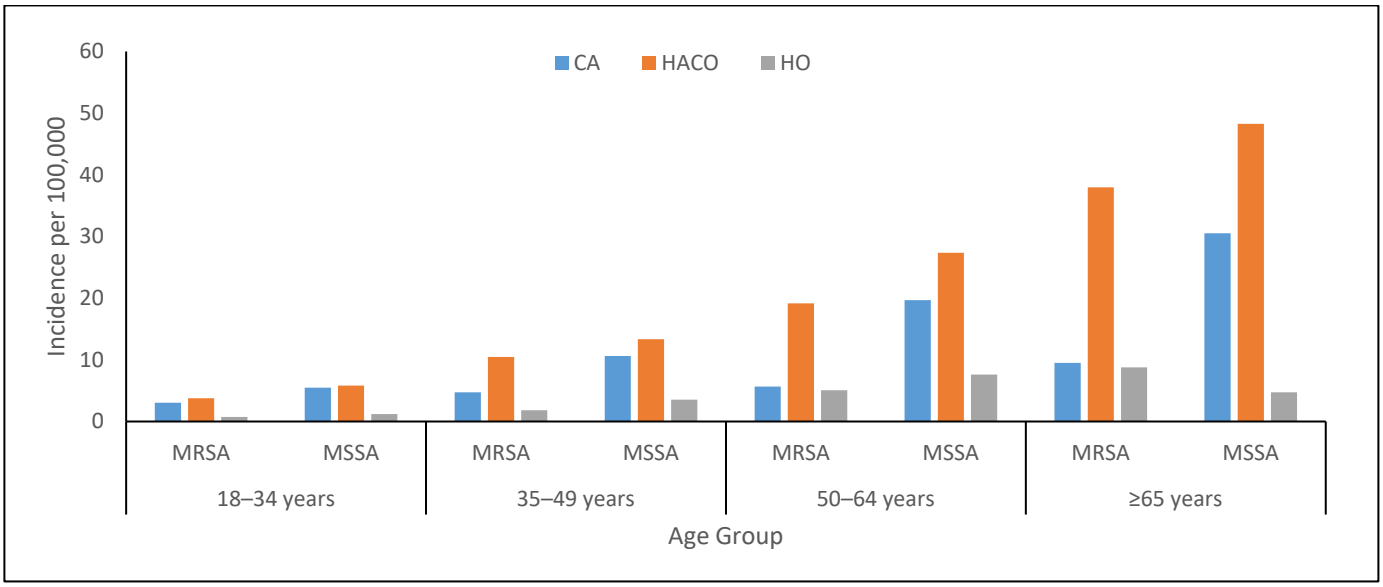
## Figure 3. Incidence[a,b] of Invasive *Staphylococcus aureus*, by Epidemiologic Class, Pediatric Age Groups, and Methicillin-Resistance Status, Emerging Infections Program, 2020




[a] Incidence (no. per 100,000 population per year) calculated using 2020 U.S. Census Data

[b] An asterisk represents a case count of <5; rates for these groups have been suppressed

## Figure 4. Incidence[a] of Invasive *Staphylococcus aureus*, by Epidemiologic Class, Adult Age Groups, and Methicillin-Resistance Status, Emerging Infections Program, 2020




[a] Incidence (no. per 100,000 population per year) calculated using 2020 U.S. Census Data

[b] An asterisk represents a case count of <5; rates for these groups have been suppressed

## Table 6. Location of Invasive MSSA (N=3593) and MRSA (N=3051) Cases Before Incident Specimen Collection, Emerging Infections Program, 2020

| Location of patient before incident specimen collection[a] | MSSA No. (%) | MRSA No. (%) |
|---|---|---|
| Private residence | 2691 (74.9) | 1898 (62.2) |
| Long-term care facility | 237 (6.6) | 543 (17.8) |
| Acute-care hospital (inpatient) | 419 (11.7) | 389 (12.8) |
| Long-term acute care hospital | 5 (0.1) | 14 (0.5) |
| Homeless | 273 (7.6) | 235 (7.7) |
| Other | 11 (0.3) | 18 (0.6) |
| Unknown | 52 (1.4) | 34 (1.1) |

[a] Represents location of the patient three days before incident specimen collection, where date of initial culture is day 0

## Table 7. Location of Invasive MSSA (N=3593) and MRSA (N=3051) Cases at Time of Incident Specimen Collection, Emerging Infections Program, 2020

| Location of incident specimen collection | MRSA | No. (%) | MRSA | No. (%) |
|---|---|---|---|---|
| Outpatient setting or emergency department | 2507 | (69.8) | 2140 | (70.1) |
| Acute care hospital | 1012 | (28.2) | 858 | (28.1) |
| Long-term care facility | 10 | (0.3) | 22 | (0.7) |
| Long-term acute care hospital | 5 | (0.1) | 6 | (0.2) |
| Other | 20 | (0.6) | 3 | (0.1) |
| Unknown | 39 | (1.1) | 22 | (0.7) |

## Table 8. Selected Clinical Characteristics of Invasive MSSA (N=3548[a]) and MRSA (N=3026[a]) Cases by Epidemiological Class, Emerging Infections Program, 2020

| Characteristics | CA, No. (%) MSSA (n=1307) | CA, No. (%) MRSA (n=665) | HACO, No. (%) MSSA (n=1754) | HACO, No. (%) MRSA (n=1903) | HO, No. (%) MSSA (n=487) | HO, No. (%) MRSA (n=458) |
|---|---|---|---|---|---|---|
| Charlson comorbidity index[b] - 0 | 453 (34.9) | 222 (33.7) | 249 (14.3) | 204 (10.7) | 123 (25.4) | 90 (19.7) |
| Charlson comorbidity index[b] - 1 | 382 (29.4) | 193 (29.3) | 283 (16.2) | 333 (17.6) | 90 (18.6) | 64 (14.0) |
| Charlson comorbidity index[b] - ≥2 | 464 (35.7) | 244 (37.0) | 1211 (69.5) | 1359 (71.7) | 271 (56.0) | 303 (66.3) |
| Underlying conditions[b] – Burn/surgical wound | 9 (0.7) | 2 (0.3) | 37 (2.1) | 60 (3.2) | 6 (1.2) | 4 (0.9) |
| Underlying conditions[b] - Chronic pulmonary disease | 189 (14.5) | 126 (19.1) | 314 (18.0) | 464 (24.5) | 100 (20.7) | 116 (25.4) |
| Underlying conditions[b] - Chronic kidney disease | 165 (12.7) | 85 (12.9) | 746 (42.8) | 787 (41.5) | 121 (25.0) | 135 (29.5) |
| Underlying conditions[b] - Decubitus/pressure ulcer | 36 (2.8) | 21 (3.2) | 100 (5.7) | 232 (12.2) | 17 (3.5) | 32 (7.0) |

| | | | | | | |
|---|---|---|---|---|---|---|
| Underlying conditions[b] - Diabetes mellitus | 436 (33.6) | 201 (30.5) | 771 (44.2) | 909 (47.9) | 168 (34.7) | 178 (39.0) |
| Underlying conditions[b] - Hemiplegia | 3 (0.2) | 4 (0.6) | 19 (1.1) | 36 (1.9) | 5 (1.0) | 2 (0.4) |
| Underlying conditions[b] - Injection drug use | 169 (13.0) | 161 (24.4) | 121 (6.9) | 171 (9.0) | 14 (2.9) | 24 (5.3) |
| Underlying conditions[b] - Obesity or morbid obesity | 239 (18.4) | 100 (15.2) | 321 (18.4) | 349 (18.4) | 96 (19.8) | 102 (22.3) |
| Underlying conditions[b] - Other chronic ulcer or chronic wound | 126 (9.7) | 70 (10.6) | 209 (12.0) | 314 (16.6) | 22 (4.6) | 43 (9.4) |
| Underlying conditions[b] - Paraplegia | 6 (0.5) | 10 (1.5) | 11 (0.6) | 63 (3.3) | 1 (0.2) | 7 (1.5) |
| Underlying conditions[b] - Pregnancy | 2 (0.2) | 1 (0.2) | 6 (0.3) | 2 (0.1) | 0 (0.0) | 0 (0.0) |
| Syndrome[c] - Bloodstream infection[d] with other syndrome | 747 (57.1) | 429 (64.5) | 1011 (57.6) | 1224 (64.3) | 194 (39.8) | 221 (48.3) |
| Syndrome[c] - Bloodstream infection with no other syndrome | 315 (24.0) | 137 (20.6) | 528 (30.1) | 507 (26.6) | 219 (45.0) | 159 (34.7) |
| Syndrome[c] - Pneumonia | 123 (9.4) | 105 (15.8) | 172 (9.8) | 266 (14.0) | 86 (17.7) | 106 (23.1) |
| Syndrome[c] - Osteomyelitis | 185 (14.2) | 90 (13.5) | 215 (12.3) | 296 (15.6) | 29 (6.0) | 46 (10.0) |
| Syndrome[c] - Endocarditis | 120 (9.2) | 82 (12.3) | 152 (8.7) | 183 (9.6) | 25 (5.1) | 33 (7.2) |
| Syndrome[c] - Cellulitis | 232(17.8) | 136 (20.5) | 180 (10.3) | 221 (11.6) | 23 (4.7) | 30 (6.6) |

| | | | | | | |
|---|---|---|---|---|---|---|
| Syndrome[c] - Surgical wound[e] | 16 (1.2) | 5 (0.8) | 106 (6.0) | 87 (4.6) | 14 (2.9) | 17 (3.7) |
| Syndrome[c] - Decubitus/pressure ulcer | 22 (1.7) | 9 (1.4) | 43 (2.5) | 80 (4.2) | 7 (1.4) | 14 (3.1) |
| Syndrome[c] - Skin abscess[f] | 101 (7.7) | 66 (9.9) | 93 (5.3) | 104 (5.5) | 16 (3.3) | 18 (3.9) |
| Syndrome[c] - Other wound[g] | 59 (4.5) | 19 (2.9) | 80 (4.6) | 120 (6.3) | 12 (2.5) | 7 (1.5) |
| Syndrome[c] - Traumatic wound | 23 (1.8) | 10 (1.5) | 18 (1.0) | 11 (0.6) | 5 (0.9) | 14 (3.1) |

[a] Excludes 45 MSSA and 25 MRSA cases with unknown epidemiological class

[b] Some case patients had more than one underlying condition. Excludes 8 CA MSSA, 6 CA MRSA, 11 HACO MSSA, 7 HACO MRSA, 3 HO MSSA, and 1 HO MRSA cases with unknown underlying conditions

[c] Some case patients had more than one syndrome

[d] Catheter site infection or AV fistula infection only are included in BSI with other syndrome

[e] Combines deep tissue/organ infection and infection of a surgical wound, post-operatively

[f] Category includes skin abscess, necrotizing fasciitis, gangrene

[g] Category includes non-traumatic and other chronic wound infections

## Table 9. Selected Healthcare Exposures and Risk Factors for Invasive MSSA (N=3593) and MRSA (N=3051), Emerging Infections Program, 2020

| Exposures | MSSA No. (%) | MRSA No. (%) |
|---|---|---|
| Healthcare facility stay in the year before incident specimen collection | 1656 (46.1) | 2012 (66.0) |
| Acute care hospitalization | 1573 (43.8) | 1860 (61.0) |
| Long-term care facility residence | 379 (10.5) | 850 (27.9) |
| Long-term acute care hospitalization | 10 (0.3) | 33 (1.1) |
| Surgery in the year before the date of incident specimen collection | 676 (18.8) | 781 (25.6) |
| Chronic dialysis | 489 (13.6) | 506 (16.6) |
| Peritoneal[a] | 30 (6.1) | 15 (3.0) |
| Hemodialysis[b] | 456 (93.3) | 489 (96.6) |
| AV Fistula/Graft | 226 (49.6) | 180 (36.8) |
| CVC | 232 (50.9) | 306 (62.6) |
| Unknown | 5 (1.1) | 8 (1.6) |
| Unknown dialysis type | 3 (0.6) | 2 (0.4) |
| Central vascular catheter in place at any time in the 2 calendar days before incident specimen collection | 534 (14.9) | 612 (20.1) |
| Unknown | 45 (1.3) | 25 (0.8) |

[a] No cases were reported to receive both peritoneal dialysis and hemodialysis

[b] 7 MSSA and 5 MRSA cases had both AV Fistula/Graft and CVC

## Table 10. Number and Incidence Rates of Invasive MSSA (N=3593) and MRSA (N=3051) Infections by Dialysis Status and Epidemiologic Class, Emerging Infections Program, 2020

| Epidemiologic Class | Dialysis Patients[a] No. (Incidence Rate) MSSA | Dialysis Patients[a] No. (Incidence Rate) MRSA | Non-Dialysis Patients[b] No. (Incidence Rate) MSSA | Non-Dialysis Patients[b] No. (Incidence Rate) MRSA | Total[c] No. (Incidence Rate) MSSA | Total[c] No. (Incidence Rate) MRSA |
|---|---|---|---|---|---|---|
| CA | NA | NA | 1307 (12.7) | 665 (4.4) | 1307 (12.7) | 665 (4.4) |
| HCA[d] | 489 (2607.0) | 506 (1789.6) | 1750 (17.1) | 1852 (12.2) | 2241 (21.8) | 2361 (15.5) |
| HO | 39 (207.9) | 55 (194.5) | 448 (4.4) | 402 (2.6) | 487 (4.7) | 458 (3.0) |
| HACO | 450 (2399.1) | 451 (1595.1) | 1302 (12.7) | 1450 (9.5) | 1754 (17.1) | 1903 (12.5) |
| Overall[e] | 489 (2607.0) | 506 (1789.6) | 3057 (29.8) | 2517 (16.6) | 3593 (35.0) | 3051 (20.0) |

[a] Incidence (no. per 100,000 dialysis patients per year) for dialysis patients calculated using 2019 USRDS point prevalence data

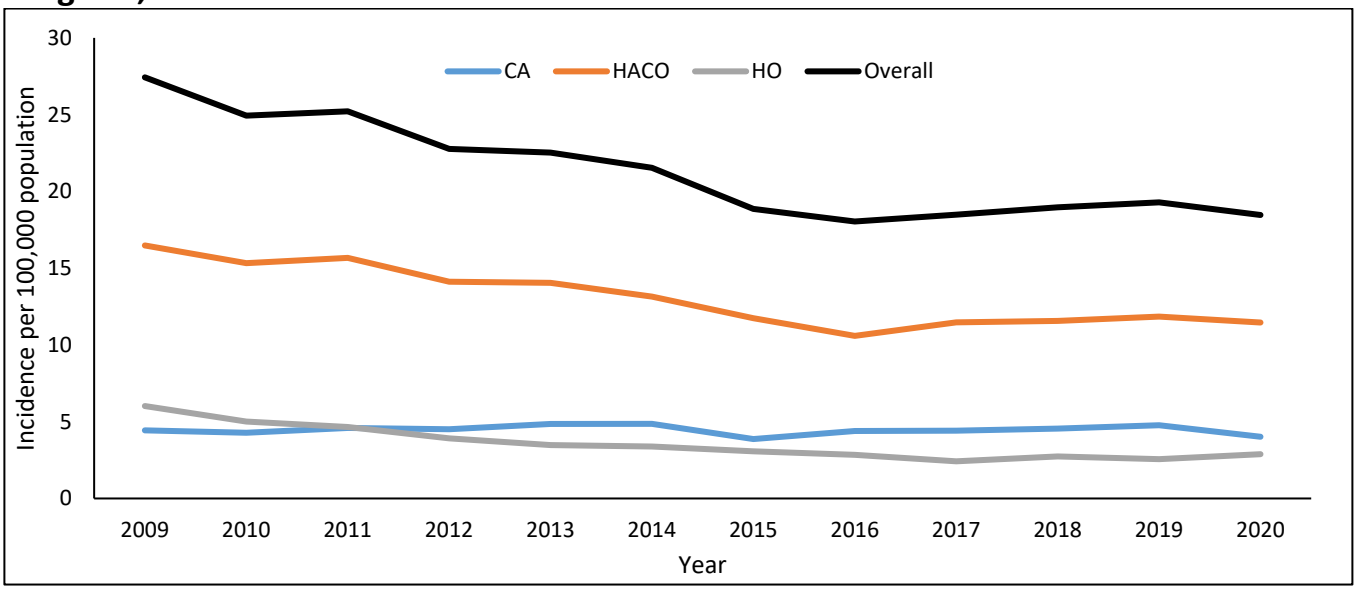
[b] Incidence (no. per 100,000 population per year) calculated using 2020 U.S. Census Data

[c] The total counts and rates include 2 HACO MSSA, 2 HACO MRSA, and 1 HO MRSA cases with unknown dialysis status

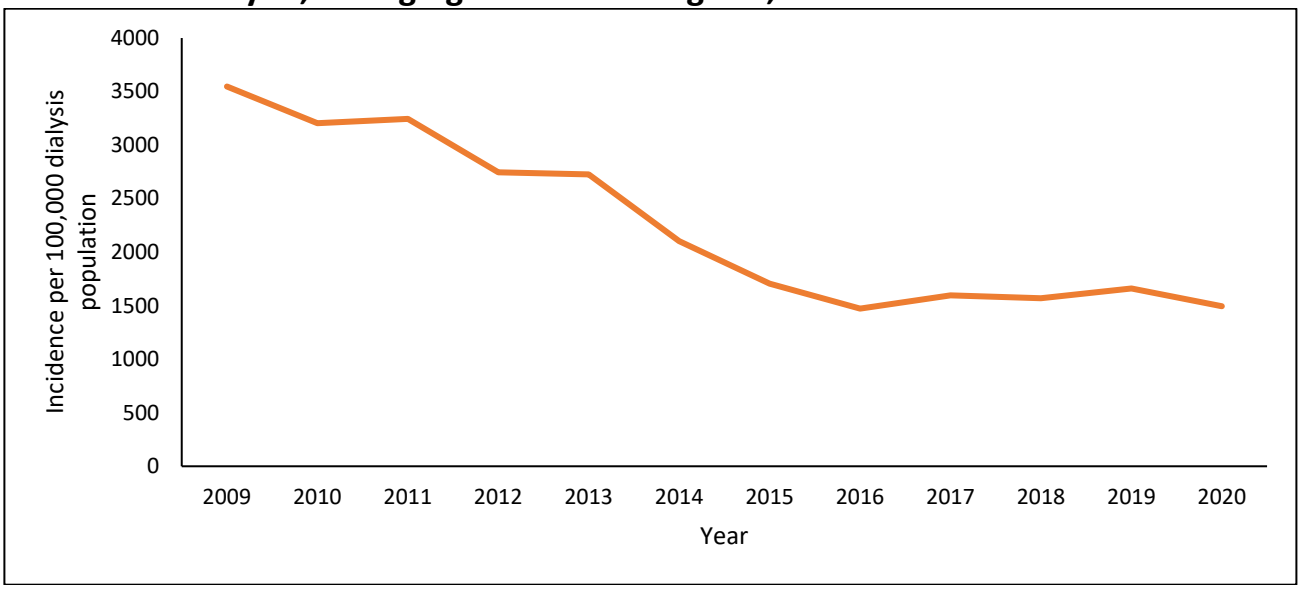
[d] HCA: Healthcare-associated invasive MRSA infection; sum of patients that are classified as either the HO or HACO classes

[e] The overall counts and rates include 45 MSSA and 25 MRSA cases with unknown epidemiological class

## Figure 5. Incidence of Invasive MRSA by Epidemiologic Class, Emerging Infections Program, 2009–2020[a]

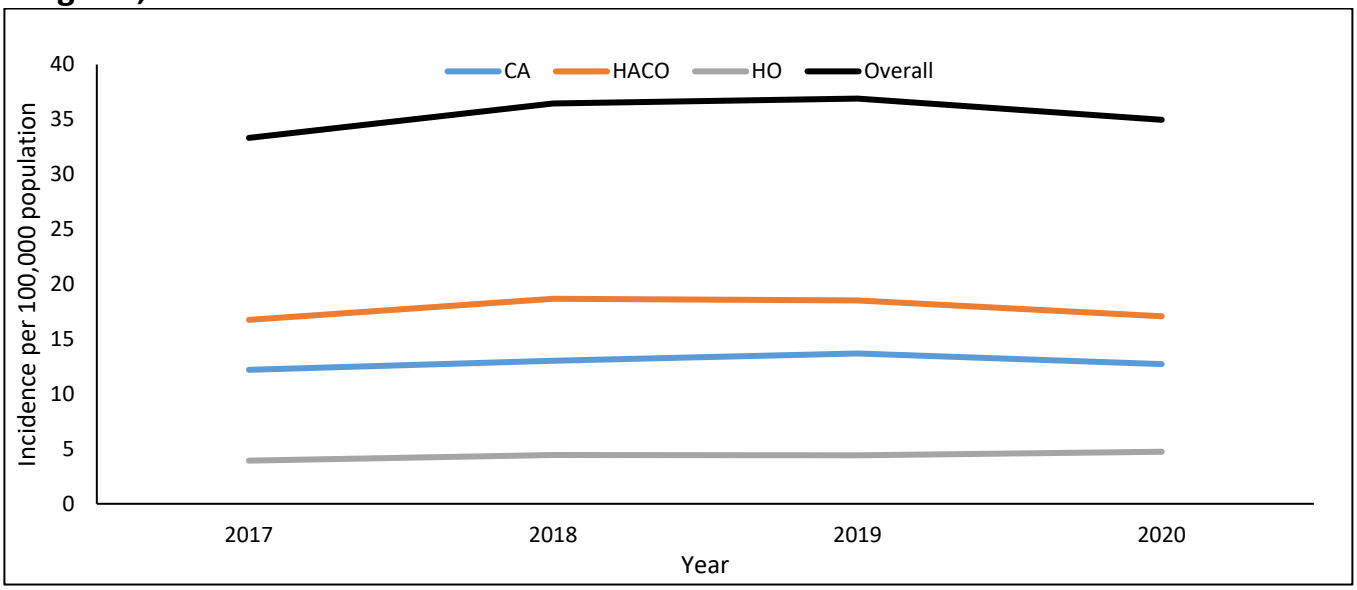



## Figure 6. Incidence of Invasive Healthcare-Associated Community Onset MRSA among Persons on Dialysis, Emerging Infections Program, 2009–2020[a]

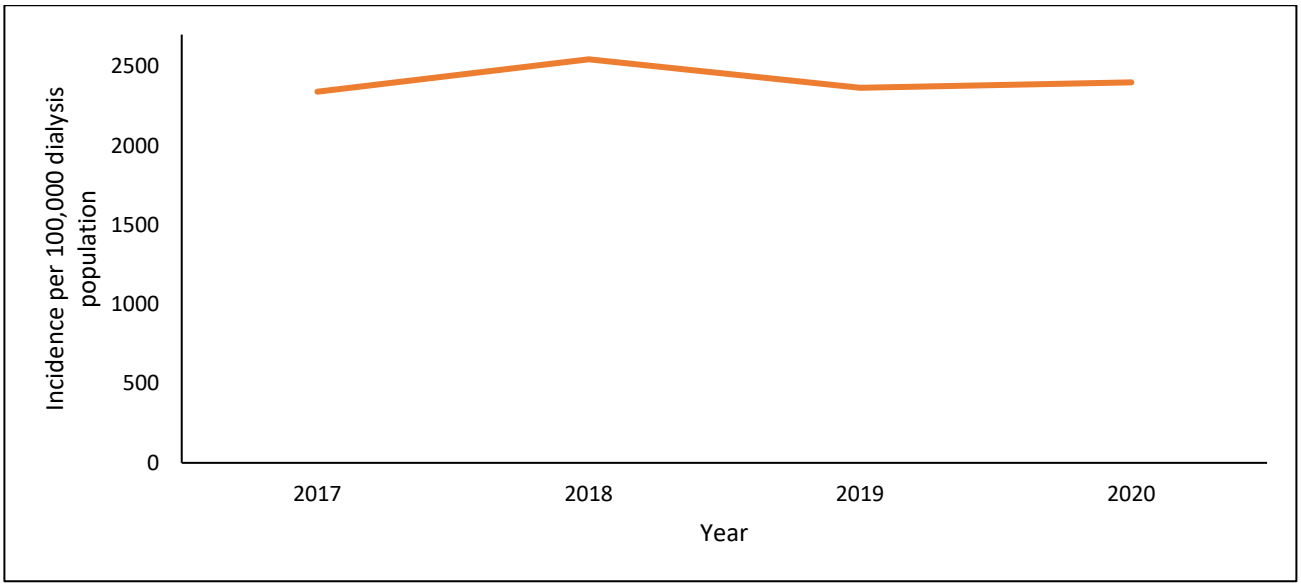



[a] Restricted to the continuous catchment area (California [3 county San Francisco Bay area]; Connecticut [Fairfield, Hartford, and New Haven counties]; Georgia [8 county Atlanta area]; Minnesota [2 county Minneapolis - Saint Paul area]; New York [1 Rochester county]; and Tennessee [1 Nashville county]) for comparison of trends over time.

## Figure 7. Incidence of Invasive MSSA by Epidemiologic Class, Emerging Infections Program, 2017–2020[a]




## Figure 8. Incidence of Invasive Healthcare-Associated Community-Onset MSSA among Persons on Dialysis, Emerging Infections Program, 2017–2020[a]




[a] Restricted to the continuous catchment area (California [3 county San Francisco Bay area]; Connecticut [New Haven county]; Georgia [1 Atlanta area county]; Minnesota [2 county Minneapolis–Saint Paul area]; New York [1 Rochester county]; and Tennessee [1 Nashville county]) for comparison of trends over time.

## Table 11. Outcomes of Invasive MSSA (N=3593[a]) and MRSA (N=3051[a]) Cases by Epidemiologic Class, Emerging Infections Program, 2020

| Outcomes | CA, No. (%) MSSA (n=1307) | CA, No. (%) MRSA (n=665) | HACO, No. (%) MSSA (n=1754) | HACO, No. (%) MRSA (n=1903) | HO, No. (%) MSSA (n=487) | HO, No. (%) MRSA (n=458) |
|---|---|---|---|---|---|---|
| Died | 131 (10.0) | 78 (11.7) | 200 (11.4) | 276 (14.5) | 112 (23.0) | 138 (30.1) |
| Survived | 1174 (89.8) | 582 (87.5) | 1547 (88.2) | 1618 (85.0) | 373 (76.6) | 319 (69.7) |
| Discharge location after acute-care hospitalization among patients who survived[b] - Long-term care facility | 325 (31.3) | 148 (28.2) | 479 (32.3) | 666 (42.7) | 131 (35.1) | 122 (38.2) |
| Discharge location after acute-care hospitalization among patients who survived[b] - Long-term acute care hospital | 15 (1.4) | 14 (2.7) | 20 (1.4) | 29 (1.9) | 17 (4.6) | 14 (4.4) |
| Discharge location after acute-care hospitalization among patients who survived[b] - Other[c] | 675 (64.9) | 335 (64.5) | 948 (63.9) | 813 (52.1) | 220 (59.0) | 173 (54.2) |
| Discharge location after acute-care hospitalization among patients who survived[b] – Unknown | 25 (2.4) | 22 (4.2) | 37 (2.5) | 51 (3.3) | 5 (1.3) | 10 (3.1) |
| Unknown | 2 (0.2) | 5 (0.8) | 7 (0.4) | 9 (0.5) | 2 (0.4) | 1 (0.2) |

[a] Excludes 45 MSSA and 25 MRSA cases with unknown epidemiological class

[b] Excludes 197 MSSA and 121 MRSA cases not admitted to acute care hospital

[c] Examples include private residence, correctional facility, homeless shelter, and drug rehabilitation program

# Summary

Surveillance data from 2020 represent the sixteenth full year of population-based surveillance for invasive MRSA infections through the Emerging Infections Program, and the fifth for MSSA.

Incidence of HO MRSA increased in 2020 compared to 2017-2019. Conversely, incidence of HACO and CA MRSA, including HACO MRSA among dialysis patients, decreased in 2020, interrupting the previous increases that had been noted since 2017. HACO and CA MSSA incidence decreased compared to 2018 and 2019, but HO MSSA incidence increased slightly and is the highest observed since 2017.

CC8 isolates with the USA300 inferred PFGE type continue to be the most common strain type among MRSA isolates tested for every epidemiologic classification (invasive *S. aureus* 2017–2019 annual reports)[1-3]. This is the second annual surveillance summary with MSSA isolate data. Unlike for MRSA where >85% of isolates are either CC5 or CC8, for MSSA there was substantially more diversity, and no single clonal complex comprised a majority of isolates; CC5 was the most common clonal complex but represented less than 20%.

# References

[1] Centers for Disease Control and Prevention. 2024. Emerging Infections Program, Healthcare-Associated Infections – Community Interface Surveillance Report, Invasive *Staphylococcus aureus*, 2017. Available at: https://www.cdc.gov/healthcare-associated-infections/media/pdfs/2017-MRSA-Report-508.pdf.

[2] Centers for Disease Control and Prevention. 2024. Emerging Infections Program, Healthcare-Associated Infections – Community Interface Surveillance Report, Invasive *Staphylococcus aureus*, 2018. Available at: https://www.cdc.gov/healthcare-associated-infections/media/pdfs/2018-MRSA-Report-508.pdf.

[3] Centers for Disease Control and Prevention. 2024. Emerging Infections Program, Healthcare-Associated Infections – Community Interface Surveillance Report, Invasive *Staphylococcus aureus*, 2019. Available at: https://www.cdc.gov/healthcare-associated-infections/media/pdfs/2019-MRSA-Report-508.pdf.

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- Invasive *Staphylococcus aureus* (MRSA/MSSA) Infection Tracking (https://www.cdc.gov/healthcare-associated-infections/php/haic-eip/invasive-staphylococcus.html)
- Methicillin-resistant *Staphylococcus aureus* (MRSA) (http://www.cdc.gov/mrsa/about/index.html)