



## Emerging Infections Program Healthcare-Associated Infections Community Interface Report Invasive *Staphylococcus aureus*, 2019

Last Updated: December 10, 2024

*Erratum: The rates among people on dialysis were corrected. The previous version of this report used an incorrect denominator for calculating these rates. Laboratory data have also been added in this update.*

### Surveillance Catchment Areas

**Methicillin-resistant *Staphylococcus aureus* (MRSA):** California (3 county San Francisco Bay area); Connecticut; 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 16,105,493 persons. The MSSA surveillance areas represent 10,298,036 persons.

Source: National Center for Health Statistics bridged-race vintage 2019 postcensal file.

### Case Definition

Invasive *Staphylococcus aureus* (SA) infection: isolation of SA from a normally sterile site in a resident of the surveillance area in 2019. 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<sup>1</sup>;
- healthcare-associated community-onset (HACO) if the culture was obtained in an outpatient setting or before the third<sup>1</sup> 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.

<sup>1</sup> This case definition represents an update in nomenclature from previous years (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 *SCCmec* 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<sup>1</sup>. 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<sup>2</sup>. 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: *SCCmec* type, presence of Panton-Valentine leukocidin and Toxic Shock Syndrome Toxin genes, and antimicrobial susceptibility results<sup>3</sup>. 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<sup>1</sup>, with 2016 isolates identified as USA300 confirmed using a SNP assay<sup>2</sup>. In 2019, MRSA isolates were collected in five sites (California, Georgia, Minnesota, New York, and Tennessee) and MSSA isolates in two (Georgia and New York).

Rates of invasive SA infection among all patients were calculated using population estimates for 2019. 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, 2018, 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) (<https://www.niddk.nih.gov/about-niddk/strategic-plans-reports/usrds>). The figures depicting the overall invasive MRSA incidence by epidemiologic class and incidence of invasive HACO MRSA among persons on dialysis, 2009–2019 are restricted to the continuous catchment area (California [3 county San Francisco Bay area]; Connecticut; 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 December 5, 2021, 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.

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<sup>1</sup> [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)

(<https://archive.cdc.gov/#/details?url=https://www.cdc.gov/hai/settings/lab/ccalgorithm.html>)

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

(<https://msphere.asm.org/content/msph/3/3/e00464-17.full.pdf>)

<sup>3</sup> [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)

(<https://archive.cdc.gov/#/details?url=https://www.cdc.gov/hai/settings/lab/inferred-pfge-algorithm.html>)

## Results

**Table 1. MSSA (N=3800) and MRSA (N=3437) Cases by Race, Emerging Infections Program, 2019**

Race	MSSA No. (Rate <sup>a</sup> )	MRSA No. (Rate <sup>a</sup> )
White	2396 (36.9)	2134 (21.2)
Black	984 (44.1)	1148 (29.5)
Other	420 (24.8)	155 (7.3)
TOTAL	3800 (36.9)	3437 (21.3)

Unknown race (n= 450 MSSA, n= 345 MRSA) distributed amongst known

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<sup>a</sup> Cases per 100,000 population for EIP areas (crude rates)

**Table 2. MSSA (N=3800) and MRSA (N=3437) Case and Death Rate by Epidemiological Classification, Emerging Infections Program, 2019**

Class	MSSA Cases No. (Rate <sup>a</sup> )	MSSA Deaths No. (Rate <sup>a</sup> )	MRSA Cases No. (Rate <sup>a</sup> )	MRSA Deaths No. (Rate <sup>a</sup> )
CA	1410 (13.7)	119 (1.2)	838 (5.2)	54 (0.3)
HCA <sup>b</sup>	2361 (22.9)	293 (2.8)	2576 (16.0)	406 (2.5)
HCA - HO	454 (4.4)	97 (0.9)	446 (2.8)	117 (0.7)
HCA - HACO	1907 (18.5)	196 (1.9)	2130 (13.2)	289 (1.8)
Unknown	29 (0.3)	0 (0.0)	23 (0.1)	1 (<0.01)

<sup>a</sup> Cases per 100,000 population for EIP areas (crude rates) calculated using 2019 U.S. Census Data

<sup>b</sup> HCA: Healthcare-associated invasive SA infection; sum of patients that are classified as either the HO or HACO classes

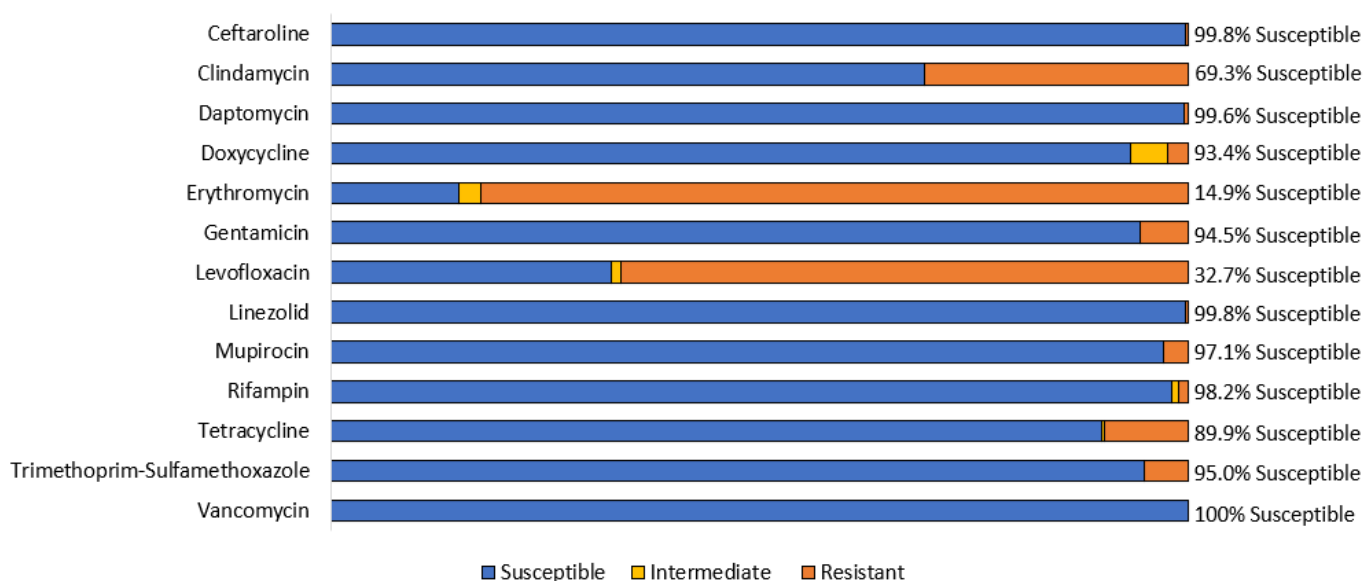
**Table 3. MRSA Inferred PFGE Type by Epidemiologic Classification, Isolates Tested at CDC (N=456), Emerging Infections Program, 2019**

Class	Total	CC5 USA100 No. (%)	Other CC5 No. (%)	CC8 USA300 No. (%)	Other CC8 No. (%)	Other (not CC5 or CC8) No. (%)
CA	110	13 (11.8)	9 (8.2)	74 (67.3)	5 (4.5)	9 (8.2)
HCA <sup>a</sup>	342	80 (23.4)	30 (8.8)	167 (48.8)	29 (8.5)	36 (10.5)
HCA - HO	54	12 (22.2)	5 (9.3)	26 (48.1)	2 (3.7)	9 (16.7)
HCA - HACO	288	68 (23.6)	25 (8.7)	141 (49.0)	27 (9.4)	27 (9.4)
Total <sup>b</sup>	456	93 (20.4)	40 (8.8)	244 (53.5)	34 (7.5)	45 (9.9)

<sup>a</sup> HCA: Healthcare-associated invasive SA infection; sum of patients that are classified as either the HO or HACO classes

<sup>b</sup> Results for all isolates, including those with an unknown epidemiologic category (n=4), are included in the total

**Figure 1. MRSA Antimicrobial Susceptibility Testing Results by Agent<sup>a,b,c,d</sup> (N=456 Isolates Tested at CDC), Emerging Infections Program, 2019**



- <sup>a</sup> High level mupirocin resistance depicted in the figure as resistant; non-high level mupirocin resistance shown as susceptible.
- <sup>b</sup> Ceftaroline Susceptible Dose Dependent is reported as resistant
- <sup>c</sup> Daptomycin non-susceptible isolates are depicted in the figure as resistant
- <sup>d</sup> Isolates with inducible resistance to clindamycin are considered resistant

**Table 4. MSSA Clonal Complex<sup>a</sup> by Epidemiologic Classification, Isolates Tested at CDC (N=325), Emerging Infections Program, 2019**

Class	Total	CC5 No. (%)	CC8 No. (%)	CC30 No. (%)	CC72 No. (%)	Other clonal complex <sup>d</sup> No. (%)
CA	88	16 (18.2)	12 (13.9)	9 (10.2)	7 (8.0)	44 (50.0)
HCA <sup>b</sup>	224	50 (22.3)	33 (14.7)	29 (12.9)	28 (12.5)	84 (37.5)
HCA - HO	48	8 (16.7)	6 (12.5)	9 (18.8)	4 (8.3)	21 (43.8)
HCA - HACO	176	42 (23.9)	27 (15.3)	20 (11.4)	24 (13.6)	63 (35.8)
Total <sup>c</sup>	325	69 (21.2)	47 (14.5)	40 (12.3)	36 (11.1)	133 (40.9)

<sup>a</sup> The four most common clonal complexes are displayed

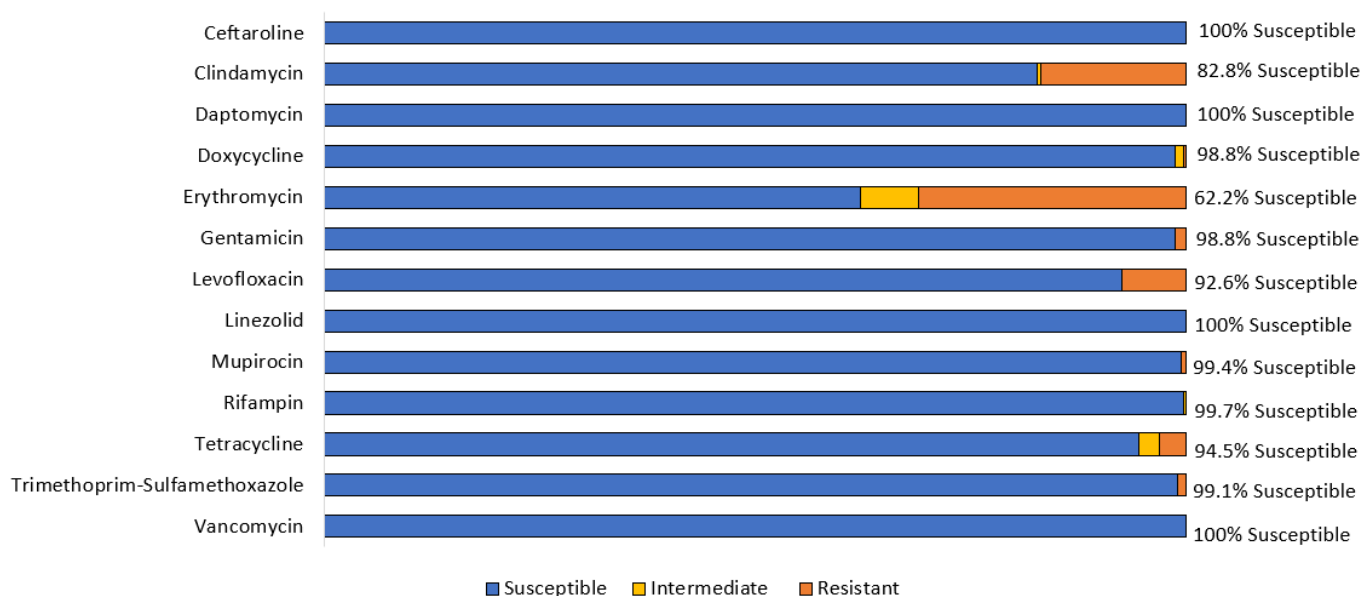
<sup>b</sup> HCA: Healthcare-associated invasive SA infection; sum of patients that are classified as either the HO or HACO classes

<sup>c</sup> Results for all isolates, including those with an unknown epidemiologic category (n=13), are included in the total

<sup>d</sup> 'Other clonal complex' includes CC15 (n=26), CC45 (n=24), CC398 (n=22), CC59 (n=15), CC97 (n=14), CC1 (n=14), unknown CC (n=11), CC22 (n=2), CC1/CC97 (n=1), CC12 (n=1), CC20 (n=1), CC25 (n=1), CC8/CC72 (n=1)



**Figure 2. MSSA Antimicrobial Susceptibility Testing Results by Agent<sup>a,b</sup> (N=325 Isolates Tested at CDC), Emerging Infections Program, 2019**



<sup>a</sup> High level mupirocin resistance depicted in the figure as resistant; non-high level mupirocin resistance shown as susceptible.

<sup>b</sup> Ceftaroline Susceptible Dose Dependent is reported as resistant

**Table 5. MSSA (N=3800) and MRSA (N=3437) Cases by Race and Ethnicity, Emerging Infections Program, 2019**

<b>Race/Ethnicity</b>	<b>MSSA No. (%)</b>	<b>MRSA No. (%)</b>
Hispanic, any race	360 (9.5)	231 (6.7)
Not known to be Hispanic <sup>a</sup> - White <sup>b</sup>	2027 (53.3)	1844 (53.7)
Not known to be Hispanic <sup>a</sup> - Black or African American <sup>c</sup>	880 (23.2)	1045 (30.4)
Not known to be Hispanic <sup>a</sup> - Asian <sup>d</sup>	266 (7.0)	84 (2.4)
Not known to be Hispanic <sup>a</sup> - Other or multiple races <sup>e</sup>	75 (2.0)	58 (1.7)
Not known to be Hispanic <sup>a,f</sup> - Unknown race	192 (5.1)	175 (5.1)

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

<sup>b</sup> 217 MSSA cases and 172 MRSA cases with unknown ethnicity

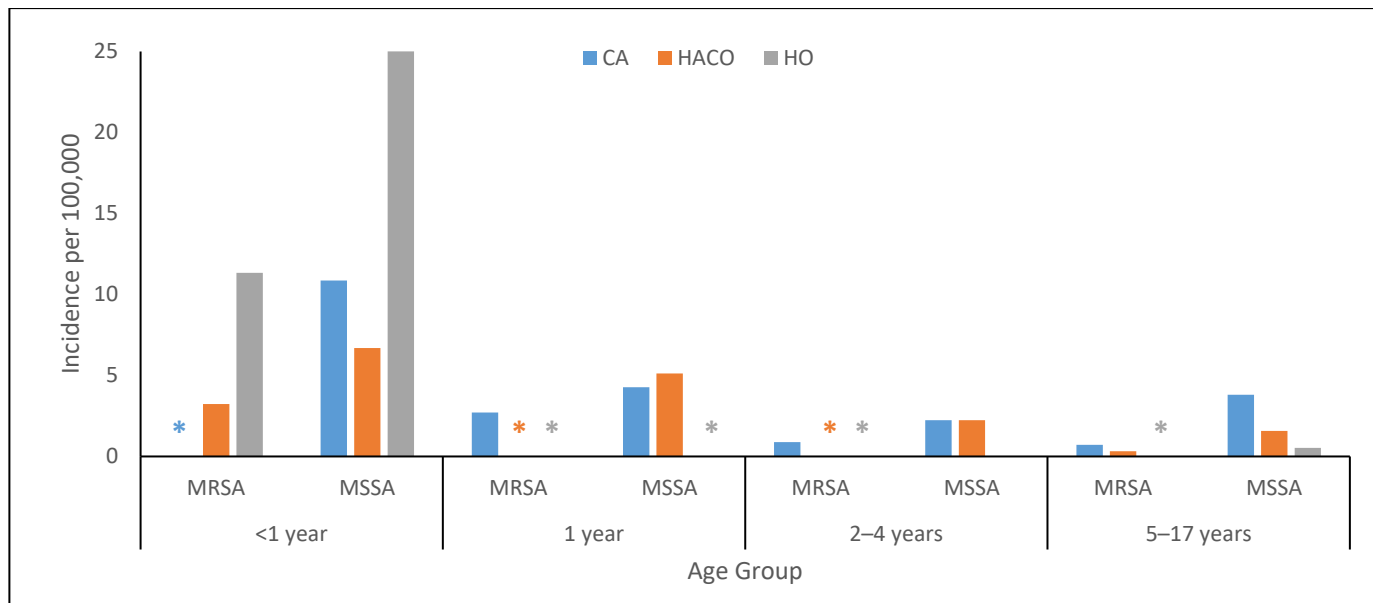
<sup>c</sup> 78 MSSA cases and 78 MRSA cases with unknown ethnicity

<sup>d</sup> 59 MSSA cases and 10 MRSA cases with unknown ethnicity

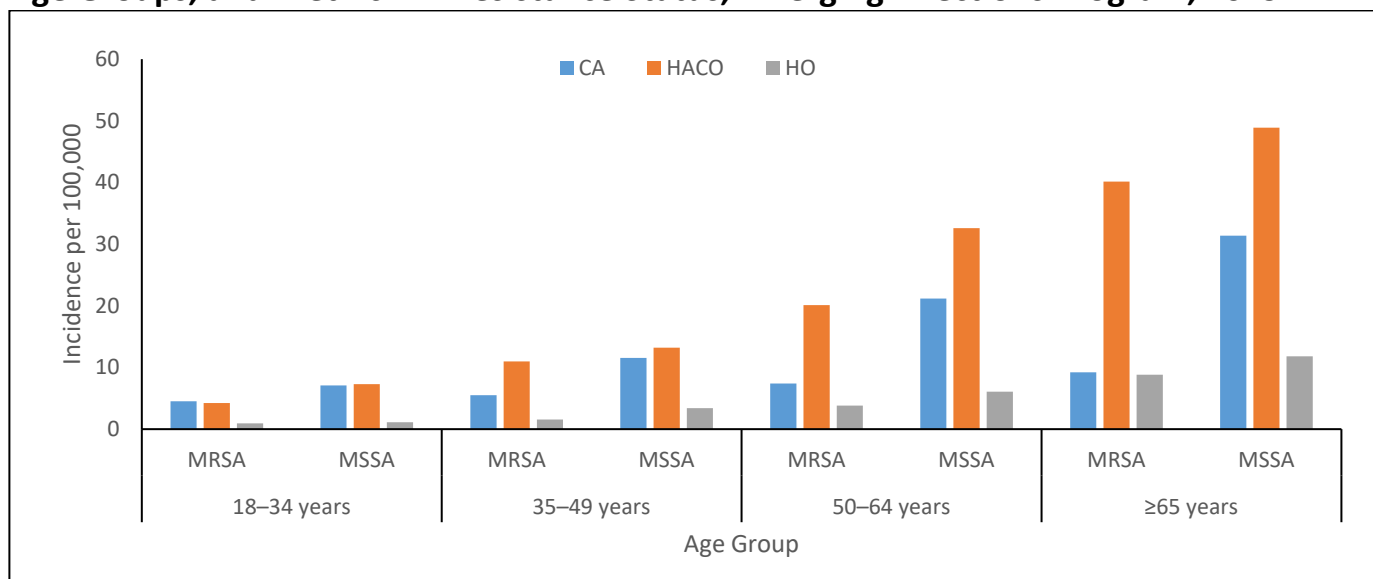
<sup>e</sup> American Indian or Alaska Native, Native Hawaiian or Other Pacific Islander, or ≥2 races reported; 17 MSSA cases and 33 MRSA cases with unknown ethnicity

<sup>f</sup> Of cases with unknown race, 113 MSSA and 135 MRSA cases had unknown ethnicity

**Figure 3. Incidence<sup>a,b</sup> of Invasive *Staphylococcus aureus*, by Epidemiologic Class, Pediatric Age Groups, and Methicillin-Resistance Status, Emerging Infections Program, 2019**



**Figure 4. Incidence<sup>a</sup> of Invasive *Staphylococcus aureus*, by Epidemiologic Class, Adult Age Groups, and Methicillin-Resistance Status, Emerging Infections Program, 2019**



<sup>a</sup> Incidence (no. per 100,000 population per year) calculated using 2019 U.S. Census Data

<sup>b</sup> An asterisk represents a case count of <5; rates for these groups have been suppressed

**Table 6. Location of Invasive MSSA (N=3800) and MRSA (N=3437) Cases Before Incident Specimen Collection, Emerging Infections Program, 2019**

Location of patient before incident specimen collection <sup>a</sup>	MSSA No. (%)	MRSA No. (%)
Private residence	2930 (77.1)	2270 (66.0)
Long-term care facility	219 (5.8)	502 (14.6)
Acute-care hospital (inpatient)	442 (11.6)	415 (12.1)
Long-term acute care hospital	8 (0.2)	12 (0.3)
Homeless	157 (4.1)	177 (5.2)
Incarcerated	8 (0.2)	22 (0.6)
Other	8 (0.2)	5 (0.1)
Unknown	28 (0.7)	34 (0.99)

<sup>a</sup> Represents location of the patient three days before incident specimen collection, where initial culture is day 0

**Table 7. Location of Invasive MSSA (N=3800) and MRSA (N=3437) Cases at Time of Incident Specimen Collection, Emerging Infections Program, 2019**

Location of incident specimen collection	MSSA No. (%)	MRSA No. (%)
Outpatient setting or emergency department	2671 (70.3)	2426 (70.6)
Acute care hospital	1075 (28.3)	944 (27.5)
Long-term care facility	15 (0.4)	28 (0.8)
Long-term acute care hospital	3 (0.1)	5 (0.1)
Other	16 (0.4)	11 (0.3)
Unknown	20 (0.5)	23 (0.7)

**Table 8. Selected Clinical Characteristics of Invasive MSSA (N=3800<sup>a</sup>) and MRSA (N=3437<sup>a</sup>) Cases by Epidemiological Class, Emerging Infections Program, 2019**

<b>Characteristics</b>	<b>MSSA CA (n=1410) No. (%)</b>	<b>MRSA CA (n=838) No. (%)</b>	<b>MSSA HACO (n=1907) No. (%)</b>	<b>MRSA HACO (n=2130) No. (%)</b>	<b>MSSA HO (n=454) No. (%)</b>	<b>MRSA HO (n=446) No. (%)</b>
Charlson comorbidity index <sup>b</sup> - 0	551 (39.3)	304 (36.6)	295 (15.6)	226 (10.7)	119 (26.2)	87 (19.5)
Charlson comorbidity index <sup>b</sup> - 1	407 (29.0)	281 (33.9)	347 (18.3)	372 (17.6)	78 (17.2)	64 (14.4)
Charlson comorbidity index <sup>b</sup> - ≥2	444 (31.7)	245 (29.5)	1255 (66.2)	1518 (71.7)	257 (56.6)	295 (66.1)
Underlying conditions <sup>b</sup> – Burn/surgical wound	5 (0.4)	4 (0.5)	27 (1.4)	51 (2.4)	3 (0.7)	9 (2.0)
Underlying conditions <sup>b</sup> - Chronic pulmonary disease	203 (14.4)	146 (17.4)	382 (20.0)	557 (26.2)	79 (17.4)	116 (26.0)
Underlying conditions <sup>b</sup> - Chronic kidney disease	154 (10.9)	77 (9.2)	729 (38.2)	873 (41.0)	135 (29.7)	150 (33.6)
Underlying conditions <sup>b</sup> - Decubitus/pressure ulcer	36 (2.6)	41 (4.9)	97 (5.1)	215 (10.1)	14 (3.1)	39 (8.7)
Underlying conditions <sup>b</sup> - Diabetes mellitus	410 (29.1)	227 (27.1)	788 (41.3)	997 (46.8)	155 (34.1)	164 (36.8)
Underlying conditions <sup>b</sup> - Hemiplegia	5 (0.4)	4 (0.5)	14 (0.7)	28 (1.3)	3 (0.7)	5 (1.1)
Underlying conditions <sup>b</sup> - Injection drug use	191 (13.5)	221 (26.4)	143 (7.5)	217 (10.2)	19 (4.2)	28 (6.3)
Underlying conditions <sup>b</sup> - Obesity or morbid obesity	200 (14.2)	93 (11.1)	360 (18.9)	336 (15.8)	62 (13.7)	72 (16.1)
Underlying conditions <sup>b</sup> - Other chronic ulcer or chronic wound	149 (10.6)	102 (12.2)	231 (12.1)	387 (18.2)	30 (6.6)	47 (10.5)
Underlying conditions <sup>b</sup> - Paraplegia	8 (0.6)	9 (1.1)	26 (1.4)	55 (2.6)	3 (0.7)	9 (2.0)
Underlying conditions <sup>b</sup> - Pregnancy	3 (0.2)	4 (0.5)	3 (0.2)	0 (0.0)	1 (0.2)	2 (0.4)
Syndrome <sup>c</sup> - Bloodstream infection <sup>d</sup> with other syndrome	712 (50.5)	548 (65.4)	935 (49.0)	1255 (58.9)	140 (30.8)	184 (41.3)

Characteristics	MSSA CA (n=1410) No. (%)	MRSA CA (n=838) No. (%)	MSSA HACO (n=1907) No. (%)	MRSA HACO (n=2130) No. (%)	MSSA HO (n=454) No. (%)	MRSA HO (n=446) No. (%)
Syndrome <sup>c</sup> - Bloodstream infection with no other syndrome	370 (26.2)	158 (18.9)	676 (35.4)	657 (30.8)	234 (51.5)	166 (37.2)
Syndrome <sup>c</sup> - Pneumonia	116 (8.2)	106 (12.6)	161 (8.4)	239 (11.2)	47 (10.4)	72 (16.1)
Syndrome <sup>c</sup> - Osteomyelitis	185 (13.1)	125 (14.9)	214 (11.2)	322 (15.1)	33 (7.3)	40 (9.0)
Syndrome <sup>c</sup> - Endocarditis	122 (8.7)	97 (11.6)	141 (7.4)	219 (10.3)	22 (4.8)	34 (7.6)
Syndrome <sup>c</sup> - Cellulitis	221 (15.7)	185 (22.1)	191 (10.0)	249 (11.7)	29 (6.4)	43 (9.6)
Syndrome <sup>c</sup> - Surgical wound <sup>e</sup>	26 (1.8)	2 (0.2)	110 (5.8)	137 (6.4)	9 (2.0)	13 (2.9)
Syndrome <sup>c</sup> - Decubitus/pressure ulcer	10 (0.7)	7 (0.8)	27 (1.4)	50 (2.3)	4 (0.9)	3 (0.7)
Syndrome <sup>c</sup> - Skin abscess <sup>f</sup>	64 (4.5)	82 (9.8)	63 (3.3)	81 (3.8)	14 (3.1)	12 (2.7)
Syndrome <sup>c</sup> - Other wound <sup>g</sup>	44 (3.1)	21 (2.5)	64 (3.4)	93 (4.4)	6 (1.3)	7 (1.6)
Syndrome <sup>c</sup> - Traumatic wound	6 (0.4)	5 (0.6)	2 (0.1)	10 (0.5)	4 (0.9)	3 (0.7)

<sup>a</sup> Excludes 29 MSSA and 23 MRSA cases with unknown epidemiological class

<sup>b</sup> Some case patients had more than one underlying condition. Excludes 8 CA MSSA, 8 CA MRSA, 10 HACO MSSA, and 14 HACO MRSA cases with unknown underlying conditions

<sup>c</sup> Some case patients had more than one syndrome

<sup>d</sup> Catheter site infection or AV fistula infection only are included in BSI with other syndrome

<sup>e</sup> Combines deep tissue/organ infection and infection of a surgical wound, post-operatively

<sup>f</sup> Category includes skin abscess, necrotizing fasciitis, gangrene

<sup>g</sup> Category includes non-traumatic and other chronic wound infections

**Table 9. Selected Healthcare Exposures and Risk Factors for Invasive MSSA (N=3800) and MRSA (N=3437), Emerging Infections Program, 2019**

Exposures	MSSA No. (%)	MRSA No. (%)
Healthcare facility stay in the year before incident specimen collection – any	1863 (49.0)	2242 (65.2)
Healthcare facility stay in the year before incident specimen collection – Acute care hospitalization	1784 (46.9)	2131 (62.0)
Healthcare facility stay in the year before incident specimen collection – Long-term care facility residence	392 (10.3)	880 (25.6)
Healthcare facility stay in the year before incident specimen collection – Long-term acute care hospitalization	18 (0.5)	41 (1.2)
Surgery in the year before the date of incident specimen collection	778 (20.5)	1028 (29.9)
Chronic dialysis – Any Modality	475 (6.6)	589 (8.1)
Chronic dialysis – Modality-Peritoneal <sup>a</sup>	31 (6.5)	19 (3.2)
Chronic dialysis – Modality-Hemodialysis	440 (92.6)	570 (96.8)
Chronic dialysis – Modality-Hemodialysis -AV Fistula/Graft <sup>b</sup>	245 (55.7)	256 (44.9)
Chronic dialysis - – Modality-Hemodialysis-CVC <sup>b</sup>	191 (43.4)	315 (55.3)
Chronic dialysis - – Modality-Hemodialysis-Unknown	8 (1.8)	5 (0.9)
Chronic dialysis - Modality - Unknown	4 (0.8)	1 (0.2)
Central vascular catheter in place at any time in the 2 calendar days before incident specimen collection	462 (12.2)	617 (18.0)
Unknown healthcare exposure or risk factor	29 (0.8)	25 (0.7)

<sup>a</sup> 1 MRSA case was reported to receive both peritoneal dialysis and hemodialysis

<sup>b</sup> 4 MSSA and 6 MRSA cases had both AV Fistula/Graft and CVC

**Table 10. Number and Incidence Rates of Invasive MRSA and MSSA Infections by Dialysis Status and Epidemiologic Class, Emerging Infections Program, 2019**

<b>Epidemiologic Class</b>	<b>MSSA Dialysis Patients No. (Rate<sup>a</sup>)</b>	<b>MRSA Dialysis Patients No. (Rate<sup>a</sup>)</b>	<b>MSSA Non-Dialysis Patients No. (Rate<sup>b</sup>)</b>	<b>MRSA Non-Dialysis Patients No. (Rate<sup>b</sup>)</b>	<b>MSSA Total<sup>c</sup> No. (Rate)</b>	<b>MRSA Total<sup>c</sup> No. (Rate)</b>
CA	NA	NA	1410 (13.7)	838 (5.2)	1410 (13.7)	838 (5.2)
HCA <sup>d</sup>	475 (2552.7)	589 (2064.7)	1884 (18.3)	1979 (12.3)	2361 (22.9)	2576 (16.0)
HCA - HO	35 (188.1)	69 (241.9)	419 (4.1)	375 (2.3)	454 (4.4)	446 (2.8)
HCA - HACO	440 (2364.6)	520 (1822.8)	1465 (14.3)	1604 (10.0)	1907 (18.5)	2130 (13.2)
Overall <sup>e</sup>	475 (2552.7)	589 (2064.7)	3294 (32.0)	2817 (17.5)	3800 (36.9)	3437 (21.3)

<sup>a</sup> Incidence (no. per 100,000 dialysis patients per year) for dialysis patients calculated using 2018 USRDS point prevalence data

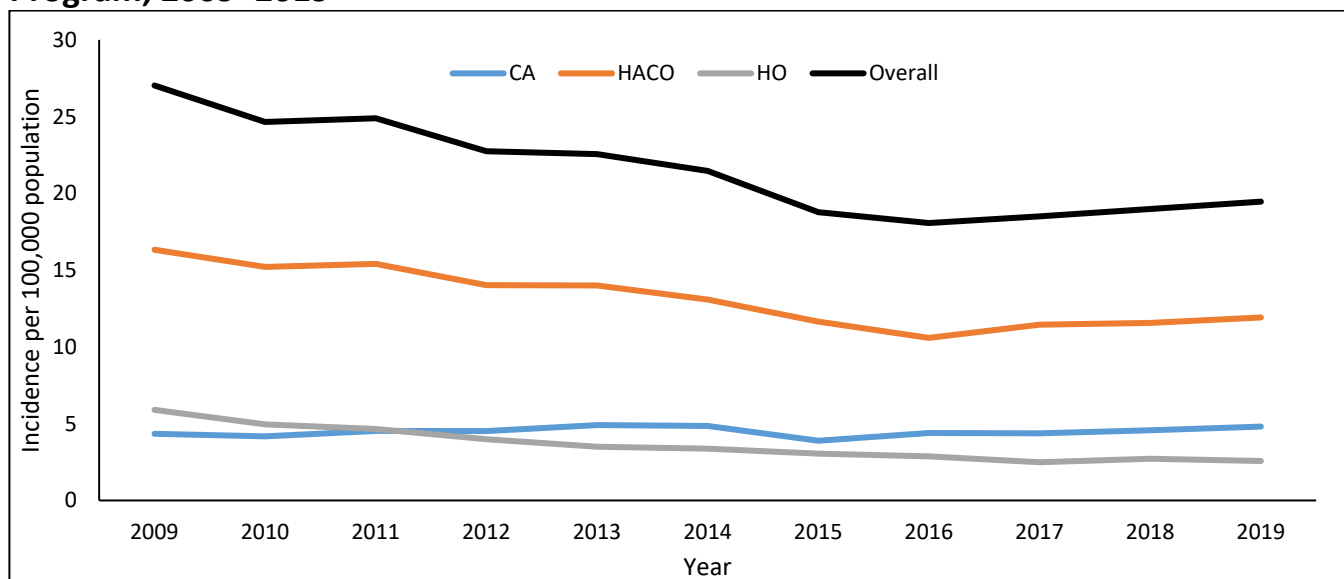
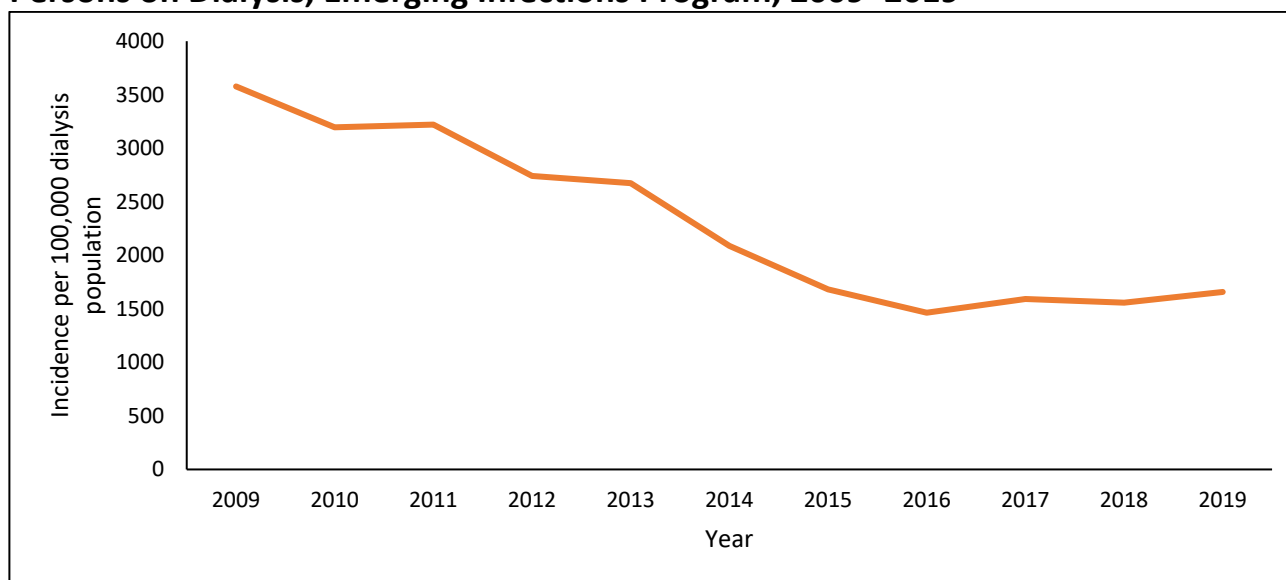
<sup>b</sup> Incidence (no. per 100,000 population per year) calculated using 2019 U.S. Census Data

<sup>c</sup> The total counts and rates include 2 HACO MSSA, 6 HACO MRSA, and 2 HO MRSA cases with unknown dialysis status

<sup>d</sup> HCA: Healthcare-associated invasive MRSA infection; sum of patients that are classified as either the HO or HACO classes

<sup>e</sup> The overall counts and rates include 29 MSSA and 23 MRSA cases with unknown epidemiological class



**Figure 5. Incidence of Invasive MRSA by Epidemiologic Class, Emerging Infections Program, 2009–2019<sup>a</sup>****Figure 6. Incidence of Invasive Healthcare-Associated Community-Onset MRSA among Persons on Dialysis, Emerging Infections Program, 2009–2019<sup>a</sup>**

<sup>a</sup> Restricted to the continuous catchment area (California [3 county San Francisco Bay area]; Connecticut; 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.

**Table 11. Outcomes of Invasive MSSA (N=3800<sup>a</sup>) and MRSA (N=3437<sup>a</sup>) Cases by Epidemiologic Class, Emerging Infections Program, 2019**

Outcomes	MSSA CA (n=1410) No. (%)	MRSA CA (n=838) No. (%)	MSSA HACO (n=1907) No. (%)	MRSA HACO (n=2130) No. (%)	MSSA HO (n=454) No. (%)	MRSA HO (n=446) No. (%)
Died	119 (8.4)	54 (6.4)	196 (10.3)	289 (13.6)	97 (21.4)	117 (26.2)
Survived	1278 (90.6)	781 (93.2)	1705 (89.4)	1823 (85.6)	356 (78.4)	329 (73.8)
Survived - discharged to long-term care facility after acute-care hospitalization <sup>b</sup>	363 (28.4)	234 (30.0)	572 (33.5)	809 (44.4)	136 (38.2)	136 (41.3)
Survived - discharged to long-term acute care hospital after acute-care hospitalization <sup>b</sup>	27 (2.1)	13 (1.7)	29 (1.7)	23 (1.3)	14 (3.9)	17 (5.2)
Survived - discharged to other <sup>c</sup> type of facility after acute-care hospitalization <sup>b</sup>	852 (66.7)	503 (64.4)	1079 (63.3)	937 (51.4)	205 (57.6)	171 (52.0)
Survived – discharged to unknown type of facility after acute-care hospitalization <sup>b</sup>	11 (0.9)	24 (3.1)	13 (0.8)	37 (2.0)	1 (0.3)	5 (1.5)
Unknown	13 (0.9)	3 (0.4)	6 (0.3)	18 (0.8)	1 (0.2)	0 (0.0)

<sup>a</sup> Excludes 29 MSSA and 23 MRSA cases with unknown epidemiological class

<sup>b</sup> Excludes 37 MSSA and 25 MRSA cases not admitted to acute care hospital

<sup>c</sup> Examples include private residence, correctional facility, homeless shelter, and drug rehabilitation program

## Summary

Surveillance data from 2019 represent the fifteenth full year of population-based surveillance for invasive MRSA infections through the Emerging Infections Program, and the fourth for MSSA. Incidence of invasive HO and HACO MRSA has decreased since 2009 but has increased for CA and HACO MRSA since 2017. The rate of HACO MRSA among persons on dialysis has increased since 2016. CA MSSA incidence and total MSSA incidence increased for the second consecutive year. Since 2017, USA300 continued to be the most common strain type among MRSA isolates tested for every epidemiologic classification, and in 2019, USA300 (which is part of CC8) comprised the majority of MRSA isolates received. This is the first annual surveillance summary with MSSA isolate data. Unlike for MRSA where >90% 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 25%.

## Citation

Centers for Disease Control and Prevention. 2021. 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>

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

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