

HAI Pathogens and Antimicrobial Resistance Report

2018–2021



**Centers for Disease
Control and Prevention**
National Center for Emerging and
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Executive Summary

Introduction

Antimicrobial resistance (AR) in U.S. healthcare facilities poses a substantial threat to patient safety and is an urgent public health concern. Pathogens with resistance pose an increasing challenge to clinicians, as fewer antibiotics and antifungals are available to effectively treat these infections, leading to increases in patient morbidity and mortality. Surveillance of pathogens and antimicrobial resistance is crucial to understanding the national burden of drug-resistant infections and can help identify concerning changes or trends in resistance.

This report is the next iteration of the Healthcare-Associated Infection (HAI) Pathogen and AR Report and is based on data reported to the Centers for Disease Control and Prevention's (CDC's) National Healthcare Safety Network (NHSN). The data tables accompanying this report provide a national snapshot of the common HAI pathogens in U.S. inpatient healthcare facilities from 2018-2021 and include national benchmark values for antimicrobial resistance across 8 drug-resistant phenotypes. Like the previous reports, this report provides detailed information about the national epidemiology of pathogens causing selected types of HAIs in the United States.¹ Results are presented for multiple infection types, healthcare facility types, location types, and surgical procedure categories. Prior iterations of this report were published as manuscripts and are available on the [NHSN HAI Pathogens and Antimicrobial Resistance \(AR\) Reports](#) webpage.

Many of the HAIs analyzed in this report were reported to NHSN under federal requirements for participation in the Centers for Medicare and Medicaid Services (CMS) [Quality Reporting Programs](#) (QRPs), which apply to acute care hospitals (ACH), long-term acute care hospitals (LTACHs), and inpatient rehabilitation facilities (IRFs).² Thus, the results presented in this report represent almost all hospitals, LTACHs, and IRFs in the United States.

[Previous reports](#) using NHSN data have shown that the pathogens implicated in HAIs, as well as their antimicrobial resistance patterns, vary greatly between adult and pediatric patients.¹ Thus, all results were generated separately for adult and pediatric patient populations. This report is the third summary of NHSN data specific to pathogens and antimicrobial resistance in pediatric HAIs.

Methodology

Pathogens and their antimicrobial susceptibility test (AST) results reported from central line-associated bloodstream infections (CLABSIs), catheter-associated urinary tract infections (CAUTIs), surgical site infections (SSIs), and possible ventilator-associated pneumonias (PVAPs) that occurred between 2018-2021 were included in the analysis for this report. The distribution of the top 15 most frequently reported pathogens for each HAI type, facility type and/or location type, and surgical category are presented for the pooled time period (2018-2021); complete lists of pathogen distributions, by year, are available in the [Supplemental Files](#). Resistance is measured as a percentage (%R) of the total number of isolates that tested resistant, and/or in some cases intermediate, to specified antimicrobials. National values of %R are calculated for 8 AR phenotypes of public health importance; results are stratified by HAI type, facility and/or location type, and procedure category. For selected phenotypes, national resistance values in this report were compared to those published in earlier time periods.

Highlights of Findings

Adults

- *Escherichia coli* (16%), *Staphylococcus aureus* (11%), and *Enterococcus faecalis* (9%) were the 3 most commonly reported HAI pathogens among the adult population
 - o The top pathogens reported by ACHs:
 - CLABSI: coagulase-negative staphylococci (17% of ICU pathogens)
 - CAUTI: *E. coli* (30-34% in each ACH location type)
 - PVAP: *S. aureus* (30% across all ACH locations)
 - SSI: *S. aureus* (35% across all surgical categories)
 - o The top pathogens reported by LTACHs, when different from ACHs:
 - CLABSI: *E. faecalis* (13%)
 - PVAP: *Pseudomonas aeruginosa* (30%)
- LTACHs reported the highest %R on all phenotypes included in this report, compared to other settings
- Resistance values were statistically significantly lower in 2018-2021 compared to those published in the 2015-2017 report for the following phenotypes:
 - o Vancomycin-resistant enterococci (VRE)
 - o Multidrug-resistant (MDR) *P. aeruginosa*
 - o Methicillin, oxacillin, or ceftiofloxacin-resistant *S. aureus* (MRSA)

Pediatrics

- *S. aureus* (15%), *E. coli* (13%), and coagulase-negative staphylococci (11%) were the 3 most commonly reported pediatric HAI pathogens
 - o CLABSI: *S. aureus* (27% of NICU pathogens); *E. faecalis* (14.8% of ICU pathogens)
 - o CAUTI: *E. coli* (32% across all facility and location types)
 - o SSI: *S. aureus* (17% across all surgical categories)
- Vancomycin resistance among *E. faecium* reported from pediatric ICU and oncology CLABSIs was significantly lower in 2018-2021 than in 2015-2017
- Methicillin resistance among *S. aureus* reported from pediatric oncology locations was significantly higher in 2018-2021 (34%) than during 2015-2017 (24%)

Conclusions

This report provides a current assessment of the common pathogens associated with HAIs and the prevalence of selected types of antimicrobial resistance among HAIs identified in inpatient healthcare settings. Pathogens and antimicrobial resistance percentages varied by facility type, infection type, patient age, location type, and/or surgical category. Our results demonstrate that antimicrobial resistance remains a significant problem in hospitals, especially among high-risk patient populations such as pediatrics, oncology patients, and LTACHs. Further research is needed to confirm the changes in resistance observed between this report and the previous report.

The data shown in this report, used in conjunction with other available data, highlight the need for targeted infection prevention and stewardship activities to address the challenges posed by antimicrobial-resistant pathogens.³⁻⁹ CDC remains committed to supporting state and local infection control and public health communities by providing necessary surveillance data and prevention strategies to help identify and reduce the spread of antimicrobial-resistant pathogens in healthcare settings.

Considerations for COVID-19, CDC’s AR Threats Report, and CDC’s Antibiotic Resistance & Patient Safety Portal

The COVID-19 pandemic occurred during the surveillance period for this report. The pandemic impacted healthcare facilities nationwide, and national increases in healthcare-associated infections (HAIs) and antimicrobial resistance have been observed. As assessment of COVID-19 and its impact on HAI pathogens and/or antimicrobial resistance is not the purpose of this report; an exploration of these topics, including the impact of COVID-19 on HAI incidence, device utilization, participation in NHSN surveillance modules, reported pathogens, and antimicrobial resistance can be found in [separate NHSN publications](#), as well as in the [2022 COVID-19 U.S. Impact on Antimicrobial Resistance Report](#).³⁻⁷

[CDC’s 2019 AR Threats Report](#) highlighted antimicrobial resistance phenotypes that pose a significant threat to human health in the United States.⁸ While the NHSN *HAI Pathogens and Antimicrobial Resistance Report* covers many of the same pathogens and phenotypes, our report contains data solely on pathogens identified in patients with a CDC-defined HAI, thus complementing the AR Threats Report (which is not limited to hospitalized patients with an HAI).

HAI antimicrobial resistance data from NHSN are also available on CDC’s [Antibiotic Resistance & Patient Safety Portal](#) (AR&PSP).⁹ The AR&PSP allows users to explore annual antimicrobial resistance data for 29 AR phenotypes and generate customized visualizations. State and regional-level values for resistance are available on the portal, as well as stratifications for specific populations based on patient and facility characteristics (e.g., facility size and medical school affiliation, patient type, acuity level, sex, and age). More information about the data available on the AR&PSP is available [here](#) and in the table below.

	HAI Pathogens and Antimicrobial Resistance Report	CDC’s AR&PSP
Purpose	National surveillance report inclusive of benchmarks for common HAI pathogens and important resistance phenotypes. Includes discussion and commentary.	Interactive web portal that provides access to NHSN HAI AR data through customized queries and data visualizations.
Time period	2018-2021; historical reports available here containing data from 2006 and forward	2011 – 2020, at time of publication
Common pathogen species identified in HAIs	Yes	No
National resistance data	Yes, for 8 ‘Urgent’ and ‘Serious’ AR phenotypes. Historical reports contain additional phenotypes.	Yes, for 29 AR phenotypes
State & regional-level resistance data	No	Yes, for 29 AR phenotypes

Background

The National Healthcare Safety Network (NHSN), maintained and operated by the U.S. Centers for Disease Control and Prevention (CDC), is the nation's most extensive and widely used electronic surveillance system for tracking HAIs, and its capacity continues to expand with additional reporting modules, facility types, and location types eligible for participation. More than 40,000 healthcare facilities use the NHSN to enter and analyze data on HAIs, antimicrobial use and resistance, COVID-19, hospital capacity and supplies, adverse events, and healthcare process measures. National surveillance reports and targeted benchmarks are essential for healthcare facilities and public health agencies to monitor improvements in infection prevention.

HAIs and antimicrobial-resistant (AR) pathogens threaten patient safety and cause severe consequences for hospitalized patients, including extended hospital stay and increased healthcare costs. Data on the pathogens implicated in HAIs provide essential information about the extent of AR infections in the United States. These data can alert us to new resistant pathogens, provide insight for new drug development, encourage evaluation of local pathogen and susceptibility data, and guide strategies intended to interrupt the transmission of antimicrobial-resistant pathogens. CDC's [2019 AR Threats Report](#) highlighted 18 drug-resistant pathogens that pose a threat to human health, noting that nationwide prevention efforts had led to a decrease in the number of deaths from AR infections between 2012 and 2017.⁸ However, more recent publications such as the [2022 COVID-19 U.S. Impact on Antimicrobial Resistance Report](#) and several [analyses of NHSN's HAI data](#) concluded that HAIs and antimicrobial resistance increased with the onset of the COVID-19 pandemic.³⁻⁷

This report provides a national snapshot of the common HAI pathogens in U.S. inpatient healthcare facilities from 2018-2021 and includes national benchmark values for select types of antimicrobial resistance.

Methods

The methodology used for this report is similar to that published in [previous iterations](#) of this report.¹ Pathogens and their AST results reported from central line-associated bloodstream infections (CLABSIs), catheter-associated urinary tract infections (CAUTIs), surgical site infections (SSIs), and selected types of ventilator-associated events (VAEs) that occurred between 2018-2021 and were reported to NHSN's Patient Safety Component as of June 1, 2022, were included in this report. ACHs, critical access hospitals, LTACHs, and IRFs from all U.S. states and territories reported these HAIs. [NHSN protocols](#) provide standard definitions and reporting elements for each type of HAI.¹⁰ Data must have been listed on a facility's NHSN monthly reporting plan to be included in CDC's national analyses for this report.

HAI inclusion criteria for this report

- CLABSIs classified as mucosal barrier injury laboratory-confirmed bloodstream infection (MBI-LCBI) were included in the analysis. CLABSIs reported from IRFs were excluded.
- CAUTI data were limited to symptomatic urinary tract infections (SUTIs).
- VAE data were limited to events classified as possible ventilator-associated pneumonia (PVAP), as this is the only sub-type of VAE for which a pathogen can be reported.
 - o Pediatric VAE (pedVAE) and pediatric VAP (pedVAP) were excluded from this report due to the low volume of pathogen data reported for these event types.
- SSI data included all types of SSIs following an inpatient surgery, regardless of the closure technique used on the incision.

Age stratification

Due to known differences in pathogens and resistance patterns between adult and pediatric populations, pathogen and AST data were analyzed separately for adults and pediatrics. The [NHSN protocols](#) provide guidance for attributing device-associated (DA) HAIs (i.e., CLABSIs, CAUTIs, PVAPs) to a NHSN-defined age-specific patient care area (i.e., location type) and SSIs to a NHSN surgical procedure code.¹⁰

- Adult data were classified as DA HAIs attributed to adult location types, and SSIs that occurred in patients who were ≥ 18 years old on the date of surgery.
- Pediatric data were classified as DA HAIs attributed to pediatric location types, and SSIs that occurred in patients who were < 18 years old on the date of surgery.

Note: NHSN uses standard definitions for HAIs, applicable to all age groups. Both pediatric and adult patients are assessed for an HAI using the same definition and criteria.

Stratification by Location and Surgery Type

When sufficient data existed, DA HAIs were stratified into mutually-exclusive categories based on the attributed location type:

- Adult data: hospital intensive care units (ICUs), hospital wards (inclusive of all non-ICU, non-oncology locations), hospital oncology units (consisting of oncology ICUs and wards), LTACH ICUs and wards, and IRF units and facilities (CAUTI only). Note: The majority of PVAP data were

reported from ICUs, and PVAP pathogen distributions were therefore stratified by facility type rather than location type.

- Pediatric data: neonatal intensive care units (NICUs; Level II/III, Level III, and Level IV per [NHSN protocol](#)¹¹), pediatric ICUs, pediatric oncology units (consisting of oncology ICUs and wards), and general pediatric wards (inclusive of newborn nurseries, special care nurseries, step-down units, mixed acuity units, specialty care areas, and pediatric inpatient rehabilitation units). Due to low volume of data, CAUTI pathogen and AST results for pediatrics were not stratified.

SSI data for adult and pediatric patients were stratified into mutually-exclusive [surgical categories](#) based on body site.

Pathogens and Antimicrobial Susceptibility Results

Up to 3 pathogens and their AST results can be reported to NHSN for each HAI. Due to differences in NHSN definitions and reporting requirements across infection types, some HAIs can be reported to NHSN without a pathogen¹⁰; all CLABSIs and CAUTIs, 97% of VAEs, and 76% of SSIs reported to NHSN from 2018-2021 contained pathogen data and were included in this analysis. AST results for the drugs included in this analysis were reported using the interpretive categories of “susceptible” (S), “intermediate” (I), “intermediate or susceptible-dose dependent” (I/S-DD), “resistant” (R), or “not tested”. Pathogen naming conventions used in this report generally adhered to the Systematized Nomenclature of Medicine Clinical Terms ([SNOMED CT](#)) Preferred Term.¹² In some cases, pathogens were grouped by genus or clinically recognized group (for example, viridans group streptococci). Results from 2018-2019 for *Klebsiella* spp. were limited to *K. pneumoniae* and *K. oxytoca*; unless otherwise noted, *K. aerogenes* was incorporated into this pathogen group for 2020-2021 data, aligning with NHSN’s adoption of the pathogen taxonomy change.¹³ Refer to the [Technical Resources](#) for information on *Candida* and *Enterococcus* pathogen groupings.

For all HAIs and pathogens, absolute frequencies and distributions were calculated by HAI, location, and surgical category when appropriate. The top 15 reported pathogens were identified, and their frequencies and ranks within each stratum were calculated.

Antimicrobial Resistance Calculations

Eight pathogen-antimicrobial combinations (phenotypes) were defined for this analysis. The selection of these phenotypes was informed by CDC’s [2022 COVID-19 U.S. Impact on Antimicrobial Resistance Report](#)⁷; we identified phenotypes that closely paralleled those identified by CDC as ‘Urgent’ or ‘Serious’ threats to human health and for which NHSN’s AST data collection allows (example: [CLABSI data entry form](#)¹⁴). Refer to the [Technical Resources](#) for the definition of each phenotype calculated in this report.

Methicillin, oxacillin, or ceftiofex-resistant *S. aureus* (MRSA), vancomycin-resistant *E. faecalis* and *E. faecium* (VRE), multidrug-resistant (MDR) *P. aeruginosa*, and carbapenem-non-susceptible *Acinetobacter* were calculated in this report using definitions consistent with those published in previous NHSN reports.¹ Compared to the last report, carbapenem-resistant Enterobacterales (CRE) and extended-spectrum cephalosporin (ESC) non-susceptibility were defined in this report using updated criteria that included modified pathogen groupings and/or antimicrobials, based on recent changes to SNOMED CT pathogen terminology and NHSN data collection. ESC non-susceptibility served as a proxy

for ESBL-production. For *Enterobacter*, evaluation of ESC non-susceptibility was limited to cefepime due to *Enterobacter*'s inducible resistance to other ESCs. Multidrug-resistant (MDR) *P. aeruginosa* was defined using adapted definitions for multidrug-resistance.¹⁵

For each HAI and location/surgical category, a pooled mean percent resistance (%R) was calculated for each phenotype as the sum of resistant (or in some cases, resistant and intermediate, collectively referred to as "non-susceptible" in this report) pathogens, divided by the sum of pathogens tested for susceptibility, and multiplied by 100. Percent resistance was not calculated for any phenotype for which less than 20 pathogens were tested. The percent of pathogens with reported susceptibility results (referred to as "percent tested") was also calculated for each phenotype and is defined as the sum of tested pathogens divided by the sum of pathogens reported to NHSN (i.e., "number reported").

Resistance percentages among certain phenotypes in this report (phenotypes with a static definition and pathogen grouping over time) were compared to those published in the prior (2015-2017) reports. Percentages were compared using a mid-P Exact test; $p < 0.05$ was considered statistically significant. While these comparisons may point to changes in resistance between two distinct time periods, this report does not convey any conclusions regarding changes or trends in resistance over time, which require in-depth statistical analyses not conducted as part of this report.

Data were analyzed in SAS 9.4 (SAS Institute).

Results: HAIs in Adult Patients

Pathogens

During 2018–2021, 4,836 healthcare facilities performed surveillance of HAIs in adult patients, and a total of 401,323 HAIs and 452,940 pathogens were reported (Tables 1 and 2). Facilities varied by type and size; 34% had ≤50 beds. SSIs contributed the highest proportion of pathogens (48%), followed by CLABSI (25%), CAUTIs (24%), and PVAPs (4%). *Escherichia coli* (16%) was the most commonly reported pathogen for all HAIs analyzed (Table 3), followed by *S. aureus* (11%) and *E. faecalis* (9%). Annual pathogen distributions containing data for each year are available in the [Supplemental Files](#).

There were 113,604 CLABSI pathogens reported from 2,988 ACHs and 420 LTACHs (Table 4). Across all location and facility types, the greatest proportion of CLABSI pathogens (39%) were reported from ACH ICUs. The most common CLABSI pathogen varied by location type; coagulase-negative staphylococci (CNS) were the most common pathogens (17%) reported in ICUs, whereas *S. aureus* (15%), *E. coli* (18%), and *E. faecalis* (13%) were the top CLABSI pathogens reported from ACH wards, oncology units, and LTACHs respectively. While *Candida* species were commonly reported from ICUs, wards, and LTACHs, they were rarely identified (5%) in oncology locations.

A total of 107,934 CAUTI pathogens were reported to NHSN from 3,550 ACHs, 428 LTACHs, and 924 IRFs (Table 5). Compared to other location types, the largest proportion of CAUTI pathogens were reported from wards (45%). The top 3 most frequently reported CAUTI pathogens were the same across all location/facility types: *E. coli*, *Klebsiella*, and *P. aeruginosa*.

More than 15,000 PVAP pathogens were reported from 1,155 ACHs (Table 6). *S. aureus* and *P. aeruginosa* combined made up almost 50% of the PVAP pathogens reported from both ACH and LTACHs. There were 169 (1%) PVAP pathogens reported from ACHs as either human coronavirus or SARS-CoV-2; zero were reported from LTACHs.

Across all surgical categories, a total of 215,669 SSI pathogens were reported, of which 54% were reported as an organ/space infection (Table 7). SSI pathogens varied by type of infection and surgical category. While *S. aureus* and CNS were commonly identified in superficial and deep incisional SSIs, *E. coli* and *Bacteroides* were more commonly reported from organ/space infections (Table 8). *S. aureus* was the most commonly reported SSI pathogen among several surgical categories: orthopedic (34%), cardiac (25%), neurosurgical (22%), vascular (22%), and breast (33%). *E. coli* was the most frequently reported pathogen in abdominal (20%) and Ob/Gyn surgeries (14%) (Tables 9-10).

Antimicrobial Resistance

In general, AST results were reported to NHSN for the majority of pathogens and drugs included in this report (Table 11). Across DA infections and SSIs, drug results were reported for a majority of pathogens (around 90%) used in the VRE, MDR *P. aeruginosa*, and MRSA phenotypes. Consistent with [previous iterations](#) of this report, drug results were reported less frequently for Enterobacterales pathogens; 74-76% of Enterobacterales were reported with a carbapenem test result.¹

The resistance percentages among the two ‘Urgent’ phenotypes were higher in DA infections than in SSIs. For DA infections, 3% of tested Enterobacterales were resistant to carbapenems (CRE), compared to 2% resistance among SSIs. DA infections reported 45% of tested *Acinetobacter* as non-susceptible to carbapenems, compared to 28% in SSIs. Among the phenotypes classified as ‘Serious’ threats, the

highest resistance percentages were recorded for vancomycin-resistant *E. faecium* (77% for DA infections and 49% for SSIs) and MRSA (46% for DA infections and 39% for SSIs).

Tables 12 - 14 summarize the testing and resistance percentages for CLABSI and CAUTI pathogens. Across all phenotypes, resistance percentages were highest for vancomycin-resistant *E. faecium* (in CLABSIs, between 70 – 80%). Of the *E. faecium* CLABSI isolates reported from oncology units, 1,535 (78%) were identified as mucosal barrier injury laboratory-confirmed bloodstream infection (MBI-LCBI), and 72% of those tested were resistant to vancomycin (Table 13). Additionally, ESC and cefepime non-susceptibility in Enterobacterales appeared especially higher in MBI-LCBIs than non-MBI-LCBIs.

Compared to ACH locations, LTACHs reported the highest resistance percentage for every phenotype included in this report for CLABSIs and CAUTIs (Tables 12, 14). Notably, among CLABSIs in LTACHs, 70% of tested *Acinetobacter* were non-susceptible to carbapenems, 17% of tested Enterobacterales were classified as CRE, 70% of tested *S. aureus* were classified as MRSA, and almost 50% of tested Enterobacterales were non-susceptible to ESCs. Comparatively, CLABSI resistance percentages were ≤ 6% for CRE and 43-48% for MRSA across all ACH locations.

For PVAP pathogens from ACHs, carbapenem-non-susceptible *Acinetobacter* and MRSA had the highest resistance percentages (both at 36%) compared to the other phenotypes. Similarly, these two phenotypes had high resistance percentages in LTACHs, although the volume of tested isolates was relatively low (Table 15).

Resistance among SSI pathogens varied by surgical category. For example, MRSA had a high %R for SSIs following abdominal surgeries (53%) and a lower %R following cardiac surgeries (34%) (Table 16). The percentage of tested *E. faecium* isolates with vancomycin resistance was high for SSIs following cardiac and orthopedic surgeries (78% and 76% resistance, respectively), but resistance was reported less frequently following Ob/Gyn surgeries (33%). National resistance data for each NHSN procedure code can be found in CDC's [Antibiotic Resistance & Patient Safety Portal](#)⁹.

Antimicrobial Resistance Compared to Prior Report (Adult Data)

National resistance percentages among some phenotypes in this report were compared to those published in the 2015-2017 [report](#), and some noteworthy changes were identified.¹⁶ While further studies and statistical trend analyses are needed to confirm any changes in resistance over time, our comparisons highlight potential significant changes in resistance.

National Values for Resistance Percentages, 2015-2017 vs 2018-2021:

HAI, setting	MRSA		
	2015-2017	2018-2021	p-value
CLABSIs, ICUs	50.0%	44.9%	0.0003
CLABSIs, LTACHs	77.6%	69.6%	0.0001
CLABSIs, oncology locations	45.8%	43.4%	0.2640
CLABSIs, wards	53.8%	48.3%	<0.0001
CAUTIs, ICUs	40.5%	39.8%	0.8172
SSIs	41.9%	39.2%	<0.0001

	VRE, <i>E. faecalis</i>		
HAI, setting	2015-2017	2018-2021	p-value
CLABSIs, ICUs	8.5%	3.8%	<0.0001
CLABSIs, LTACHs	18.0%	12.9%	0.0008
CLABSIs, oncology locations	7.4%	4.6%	0.0267
CLABSIs, wards	10.7%	6.7%	<0.0001
CAUTIs, ICUs	4.2%	2.8%	0.0011
SSIs	3.4%	2.4%	<0.0001

	MDR <i>P. aeruginosa</i>		
HAI, setting	2015-2017	2018-2021	p-value
CLABSIs, ICUs	18.6%	14.2%	0.0064
CLABSIs, LTACHs	29.9%	25.3%	0.1256
CLABSIs, oncology locations	11.6%	8.5%	0.0492
CLABSIs, wards	13.6%	11.9%	0.1937
CAUTIs, ICUs	13.6%	8.7%	<0.0001
SSIs	4.5%	3.9%	0.0325

Percent resistance values for VRE, MDR *P. aeruginosa*, and MRSA were all statistically significantly lower in this report than in our previous report for ICU CLABSIs and SSIs. Among CLABSIs in oncology locations and CAUTIs in ICUs, resistance percentages were significantly lower in 2018-2021 for VRE and MDR *P. aeruginosa*. No significant changes were detected in the resistance percentages for carbapenem-non-susceptible *Acinetobacter*.

Despite generally high resistance percentages, some evidence of decreases in resistance over time within LTACHs can be seen. MRSA resistance among CLABSIs in LTACHs was significantly lower in 2018-2021 than in 2015-2017 (70% vs 78%, $p=0.0001$), and VRE *E. faecalis* resistance dropped from 18% to 13% ($p=0.0008$) during the same time frame.

Results: HAIs in Pediatric Patients

Pathogens

Throughout 2018-2021, 925 healthcare facilities reported 20,677 pediatric HAIs and 22,690 associated pathogens (Tables P1 and P2). Facilities varied by type and size; 30% had between 201-350 beds, and 24% had more than 500 beds. CLABSIs contributed the highest proportion of pathogens (69%) followed by SSIs (23%) and CAUTI (7%). Across all pediatric HAIs, *S. aureus* (15%) was the most reported pathogen, followed by *E. coli* (13%) and CNS (11%) (Table P3).

The most common pathogens associated with pediatric CLABSIs varied by location type (Table P4). *S. aureus* (27%) and CNS (19%) were the most common CLABSI pathogens in NICU locations, viridans group streptococci (15%) and CNS (12%) ranked first and second among oncology locations, and *E. faecalis* (15%) and selected *Klebsiella* (14%) were the top pathogens in pediatric ICUs and wards, respectively.

There were 268 facilities that reported a total of 1,653 pediatric CAUTI pathogens (Table P5). Almost one-third of these pathogens were identified as *E. coli* (32%). *P. aeruginosa* (20%) was also commonly reported for pediatric CAUTIs.

A total of 5,282 pediatric SSI pathogens were reported by 479 facilities; 59% of pathogens were reported from organ/space infections, 27% reported from superficial incisional SSIs, and 14% from deep incisional SSIs (Table P6). Across all surgical categories, facilities most frequently reported *S. aureus* (17%), followed by *E. coli* (17%) and *P. aeruginosa* (9%) (Table P7). Common pathogen species varied by surgical category; *S. aureus* was the most commonly reported pathogen for orthopedic (31%), neurosurgical (26%), and cardiac surgeries (40%), while *E. coli* was the most common pathogen identified in SSIs following abdominal surgeries (24%). Additional surgical categories are not shown in Table P7 due to the low volume of SSIs.

Antimicrobial Resistance

Some variation existed in CLABSI resistance percentages across pediatric location types (Table P8). MRSA had a higher percent resistance in pediatric oncology units (34%) and wards (32%) compared with pediatric ICUs (27%) and NICUs (29%). For many CLABSI phenotypes, a relatively high percent resistance was reported in pediatric oncology units, and a relatively lower percent resistance was found in NICUs, such as CRE (4% in oncology vs. 1% in NICUs), ESC non-susceptibility in Enterobacterales (35% in oncology vs. 10% in NICUs), cefepime non-susceptibility in *Enterobacter* (16% in oncology vs. 1% in NICUs) and VRE *E. faecium* (38% in oncology vs. 5% in NICUs).

Across all SSI phenotypes and surgical categories, MRSA (25%) and ESC non-susceptible Enterobacterales (17%) had the first and second highest values for percent resistance (Table P10). For some phenotypes, percent resistance varied by surgical category; MRSA ranged from 17% resistance (cardiac SSIs) to 33% resistance (abdominal SSIs), and ESC non-susceptible Enterobacterales ranged from 8% resistance (neurosurgical SSIs) to 18% (orthopedic SSIs). Additional surgical categories are not shown in Table P10 due to the low volume of SSIs; however, national resistance data for each NHSN procedure code can be found in CDC's [Antibiotic Resistance & Patient Safety Portal](#)⁹.

Antimicrobial Resistance Compared to Prior Report (Pediatric Data)

National resistance percentages among some phenotypes in this report (those defined using criteria consistent with the prior report) were compared to those published in the 2015-2017 [pediatric report](#), and some noteworthy changes were identified.¹⁷ While further studies and statistical trend analyses are needed to confirm any changes in resistance over time, our comparisons highlight potential significant changes in resistance. Among CLABSIs that occurred in pediatric ICUs and oncology locations, the percentage of tested *E. faecium* that were resistant to vancomycin (VRE) was significantly lower in 2018-2021 (22%, 38%) than in 2015-2017 (43%, 55%), respectively ($p=0.0023$, $p=0.0091$). However, MRSA resistance in pediatric oncology locations was significantly higher in 2018-2021 (34%) than during 2015-2017 (24%) ($p=0.017$). Although not statistically significant, an increase in the MRSA resistance percentage was also noted in pediatric wards (from 26% in 2015-2017 to 32% in 2018-2021).

Discussion & Conclusion

This report provides national pathogen frequencies and resistance profiles (%R) stratified by facility type, infection type, location type, and surgical category, with supplemental materials providing additional detail.

Overall, this report continued to show differences in common HAI pathogens based on facility type, infection type, and patient population. Consistent with previous analyses, *E.coli* and *S. aureus* remain the top two pathogen species associated with HAIs in both the adult and pediatric populations. The third most common pathogen varied by patient age. CNS was the 3rd ranked pathogen (11%) among pediatrics and was especially common in NICU CLABSIs (2nd ranked pathogen; 19%). Among adults, *E. faecalis* rose to the 3rd ranked pathogen (9%) from its ranking of #5 (8%) in the prior report.¹⁶ While this modest increase in *E. faecalis* can be seen in the national pathogen distribution from all HAIs, a drastic increase in *E. faecalis* was observed in ICU CLABSIs, increasing from 7.7% of pathogens in 2015-2017 (rank 5) to 12.5% of pathogens in 2018-2021 (rank 2).¹⁶ This increase in *E. faecalis* is not surprising and may be reflective, in some part, of secondary infections in patients with COVID-19; a previous [analysis](#) of NHSN pathogen data found an increase in *E. faecalis* CLABSIs during the COVID-19 pandemic, and numerous other studies have documented increases in *Enterococcus* infections among patients with COVID-19.^{6, 18-20}

All phenotypes analyzed in this report had a higher resistance percentage for DA infections compared with SSIs. This finding has been consistently seen throughout these NHSN reports, and a discussion of this was included in the prior report. In addition, for some phenotypes, we continued to observe higher resistance percentages among selected high-risk patient populations, such as those housed in LTACHs and pediatric oncology locations; this is likely the result of widespread use of antimicrobials in these patients and extended exposures to healthcare settings and medical devices. Alternatively, CLABSI resistance percentages were lower in NICUs than in other pediatric locations, possibly reflecting less lifetime antimicrobial and hospital exposures for NICU patients. Additional discussion on these topics can be found in the 2015-2017 adult and pediatric [reports](#).¹

Significant changes in %R values were observed in this report compared to the 2015-2017 time period. The %R for VRE was significantly lower in 2018-2021, for both adults and pediatrics and across multiple HAI and location types. While this is encouraging and consistent with a previous [analysis](#)⁶, additional research is needed to fully understand the trends in VRE over time. On the other- hand, the significant increase in MRSA %R among the pediatric oncology population is concerning, especially given that there was no significant change in the MRSA resistance percentage in the adult oncology population. Further studies are needed to explore the reasons behind these changes, as well as to investigate potential changes over time for the other phenotypes included in this report.

Limitations

Our results have limitations. The types of infections included in this report were based on those required by the CMS QRPs and/or in which a high volume of national data exists in NHSN. HAI data reported to NHSN and included in this report are influenced by the infection types, location types, facility types, and surgical procedure types that are included in federal and/or local HAI reporting requirements; thus, this report does not represent all types of HAIs.² Facilities only report the final AST interpretations to NHSN; therefore, differences may have existed among laboratory testing practices, reporting methods, and breakpoint interpretations that could not be accounted for in this analysis. Minimal misclassification

may have occurred for DA infections identified in pediatric patients who were housed in adult locations (or vis a versa) at the time of their infection. Furthermore, “[selective reporting](#)” could have contributed to a higher number of pathogens reported to NHSN as “not tested” to certain drugs in scenarios when laboratories suppressed AST results as part of antimicrobial stewardship efforts²¹; this is reflected in the “% tested” columns in our data tables, and may have had some impact on Enterobacterales phenotypes. However, as roughly 90% of the other pathogens were tested for susceptibility to the drugs included in this report, selective reporting is assumed to have a minimal impact on %R results. An analysis of the impact of selective reporting on CRE resistance can be found in the [prior report](#).¹⁶

Conclusion

Differences in common HAI pathogens and resistance patterns across patient populations and facility types suggest that targeted prevention strategies may be needed for distinct populations. Healthcare staff and public health agencies should closely monitor data from their facilities or jurisdictions to understand the common pathogens and resistance patterns, particularly for high-risk populations, and use those data to inform prevention practices. The national data in this report can be used as a benchmark for comparisons to local data. This report can also inform national prevention strategies and provide a greater awareness of the national burden of antimicrobial-resistant infections in healthcare settings.

CDC remains committed to the analysis and dissemination of antimicrobial resistance data. CDC’s Antibiotic Resistance & Patient Safety Portal includes a [Data Explorer](#) feature allowing researchers, pharmacists, clinicians, and other public health practitioners to query NHSN’s HAI AR data and create customized maps and other visualizations.⁹ Continual analyses of NHSN’s surveillance data will allow CDC to track resistance pathogens across U.S. healthcare settings and identify new or emerging trends in resistance phenotypes.

Judicious use of antibiotics and antifungals and adherence to recommended infection control practices are important strategies for combating antimicrobial resistance. CDC has identified the Core Elements of hospital antimicrobial stewardship programs, which outline a set of guiding principles that can improve antibiotic use. More information about CDC’s Core Elements of Antibiotic Stewardship²² can be found here: <https://www.cdc.gov/antibiotic-use/healthcare/index.html>.

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Questions or suggestions for this report can be sent to NHSN@cdc.gov, subject line: HAI-AR Report.

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<https://www.cdc.gov/nhsn/hai-report/index.html>

Glossary

Term	Description
Hospital Wards	Includes non-ICU, non-oncology adult patient locations within acute care hospitals including step-down units, mixed acuity units, and specialty care areas.
Inpatient Rehabilitation Facility (IRF)	Unless otherwise noted, this term includes free-standing IRFs and CMS-certified inpatient rehabilitation units located within hospitals.
<i>Klebsiella aerogenes</i> (formerly <i>Enterobacter aerogenes</i>)	<i>Klebsiella aerogenes</i> (formerly <i>Enterobacter aerogenes</i>) is classed in the <i>Enterobacter</i> group in 2018-2019 and the <i>Klebsiella</i> group in 2020-2021.
Other <i>Candida</i>	Combines <i>Candida</i> identified to the species level (excluding <i>C. albicans</i> and <i>C. glabrata</i>), and <i>Candida</i> for which the species was not reported.
Other <i>Enterococcus</i>	Combines enterococci identifies to the species level (excluding <i>E. faecalis</i> and <i>E. faecium</i>) and enterococci for which the species was not reported.
Pediatric Wards	Includes non-ICU, non-oncology pediatric patient locations within acute care hospitals such as step-down units, mixed acuity units, and specialty care areas.
Selected <i>Klebsiella</i> spp.	Includes <i>K. oxytoca</i> and <i>K. pneumoniae</i> ; for 2020-2021 data, this group also includes <i>K. aerogenes</i> .
Surgical Category	<u>Abdominal</u>—Appendix surgery, bile duct, liver, or pancreatic surgery, liver transplant, gallbladder surgery, colon surgery, gastric surgery, herniorrhaphy, small bowel surgery, spleen surgery, exploratory laparotomy, and rectal surgery. <u>Breast</u>—Breast surgery. <u>Cardiac</u>—Cardiac surgery, heart transplant, coronary artery bypass graft with chest incision with or without donor incision, pacemaker surgery, and thoracic surgery. <u>Kidney</u>—Kidney surgery and kidney transplant. <u>Neck</u>—Neck surgery, and thyroid and/or parathyroid surgery. <u>Neurosurgical</u>—Craniotomy and ventricular shunt. <u>Ob/Gyn</u>—Cesarean section, abdominal hysterectomy, ovarian surgery, and vaginal hysterectomy. <u>Orthopedic</u>—Open reduction of fracture, hip prosthesis, knee prosthesis, limb amputation, spinal fusion/refusion, and laminectomy. <u>Prostate</u>—Prostate surgery. <u>Vascular</u>—Abdominal aortic aneurysm repair, shunt for dialysis, carotid endarterectomy, and peripheral vascular bypass surgery.
SSI Type	<u>Deep Incisional</u>—Involves deep soft tissues of the incision (for example, fascial and muscle layers). <u>Organ/Space</u>—Involves any part of the body deeper than the fascial/muscle layers that is opened or manipulated during the operative procedure. <u>Superficial Incisional</u>—Involves only the skin and subcutaneous tissue of the incision. Full definitions of these terms are available in the NHSN Protocol

Acronyms

Acronym	Description
ACH	Acute care hospital
AR	Antimicrobial resistance
AST	Antimicrobial susceptibility test
CAUTI	Catheter-associated urinary tract infection
CDC	Centers for Disease Control and Prevention
CLABSI	Central line-associated bloodstream infection
CMS	Centers for Medicare and Medicaid Services
CNS	Coagulase-negative staphylococci
DA	Device-associated
ESC	Extended-spectrum cephalosporin
HAI	Healthcare-associated infection
ICU	Intensive care unit
IRF	Inpatient rehabilitation facility
LCBI	Laboratory-confirmed bloodstream infection
LTACH	Long-term acute care hospital
MBI	Mucosal barrier injury
NHSN	National Healthcare Safety Network
NICU	Neonatal intensive care unit. Includes locations identified in NHSN as Level II/III, Level III, and Level IV NICUs ¹¹
PVAP	Possible ventilator-associated pneumonia
SSI	Surgical site infection
VAE	Ventilator-associated event

Phenotype Definitions

Phenotype Name	Phenotype Definition
Carbapenem-non-susceptible (NS) <i>Acinetobacter</i> spp.	<i>Acinetobacter</i> species (spp.) with a result of intermediate (I) or resistant (R) to imipenem, meropenem, or doripenem
Carbapenem-resistant Enterobacterales (CRE)	<i>E.coli</i> , selected <i>Klebsiella</i> spp.*, and <i>Enterobacter</i> species with a result of resistant (R) to at least one of the following drugs: imipenem, meropenem, doripenem, ertapenem, imipenem/relebactam, or meropenem/vaborbactam
Cefepime-non-susceptible (NS) <i>Enterobacter</i> spp.	<i>Enterobacter</i> ⁺ spp. with a result of intermediate/susceptible-dose dependent (I/S-DD) or resistant (R) to cefepime
Extended-spectrum cephalosporin-NS Enterobacterales	<i>E.coli</i> , <i>Klebsiella pneumoniae</i> , and <i>Klebsiella oxytoca</i> with a result of intermediate (I), intermediate/susceptible-dose dependent (I/S-DD, cefepime only), or resistant (R) to at least one of the following drugs: cefepime, cefotaxime, ceftazidime, ceftriaxone, ceftazidime/avibactam, or ceftolozane/tazobactam
Meth/ox/cefox-resistant <i>Staphylococcus aureus</i> (MRSA)	<i>Staphylococcus aureus</i> with a result of resistant (R) to methicillin, oxacillin, or cefoxitin
Multidrug-resistant (MDR) <i>Pseudomonas aeruginosa</i>	<i>Pseudomonas aeruginosa</i> with a result of intermediate (I) or resistant (R) to at least one drug in at least three antimicrobial classes: a. Extended-spectrum cephalosporins (cefepime, ceftazidime, ceftazidime/avibactam, or ceftolozane/tazobactam) b. Fluoroquinolones (ciprofloxacin or levofloxacin) c. Carbapenems (imipenem, meropenem, or doripenem) d. Aminoglycosides (amikacin, gentamicin, or tobramycin) e. Piperacillin/tazobactam
Vancomycin-resistant <i>Enterococcus faecalis</i> (VRE)	<i>Enterococcus faecalis</i> with a result of resistant (R) to vancomycin
Vancomycin-resistant <i>Enterococcus faecium</i> (VRE)	<i>Enterococcus faecium</i> with a result of resistant (R) to vancomycin

* Included *K. oxytoca* and *K. pneumoniae*; for 2020-2021 data, this group also included *K. aerogenes*, formerly known as *Enterobacter aerogenes*.

⁺ Included all species of *Enterobacter*. Data from 2018-2019 included *E. aerogenes*.