


Original Article

Antimicrobial-resistant pathogens associated with adult healthcare-associated infections: Summary of data reported to the National Healthcare Safety Network, 2015–2017

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Abstract

Objective: Describe common pathogens and antimicrobial resistance patterns for healthcare-associated infections (HAIs) that occurred during 2015–2017 and were reported to the Centers for Disease Control and Prevention's (CDC's) National Healthcare Safety Network (NHSN).

Methods: Data from central line-associated bloodstream infections (CLABSIs), catheter-associated urinary tract infections (CAUTIs), ventilator-associated events (VAEs), and surgical site infections (SSIs) were reported from acute-care hospitals, long-term acute-care hospitals, and inpatient rehabilitation facilities. This analysis included device-associated HAIs reported from adult location types, and SSIs among patients ≥ 18 years old. Percentages of pathogens with nonsusceptibility (%NS) to selected antimicrobials were calculated for each HAI type, location type, surgical category, and surgical wound closure technique.

Results: Overall, 5,626 facilities performed adult HAI surveillance during this period, most of which were general acute-care hospitals with < 200 beds. *Escherichia coli* (18%), *Staphylococcus aureus* (12%), and *Klebsiella* spp (9%) were the 3 most frequently reported pathogens. Pathogens varied by HAI and location type, with oncology units having a distinct pathogen distribution compared to other settings. The %NS for most pathogens was significantly higher among device-associated HAIs than SSIs. In addition, pathogens from long-term acute-care hospitals had a significantly higher %NS than those from general hospital wards.

Conclusions: This report provides an updated national summary of pathogen distributions and antimicrobial resistance among select HAIs and pathogens, stratified by several factors. These data underscore the importance of tracking antimicrobial resistance, particularly in vulnerable populations such as long-term acute-care hospitals and intensive care units.

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The National Healthcare Safety Network (NHSN), managed by the Centers for Disease Control and Prevention (CDC), is the nation's largest and most widely used electronic surveillance system for tracking healthcare-associated infections (HAIs). More than 25,000 healthcare facilities use the NHSN to enter and analyze data on HAIs, adverse events, and healthcare personnel safety. As the NHSN continues to expand its capacity with additional reporting modules, facility types, and location types eligible for participation, national surveillance reports and targeted benchmarks become increasingly vital for healthcare facilities and public health agencies to monitor progress in infection prevention.

The pathogens implicated in HAIs, and their antimicrobial susceptibilities, provide important information about the spread

and extent of antimicrobial-resistant infections in the United States. These data can be used to identify emerging resistant pathogens, to provide direction for new drug development, to encourage review and comparison of local pathogen and susceptibility data, and to inform policies such as those designed to interrupt the transmission of antimicrobial-resistant pathogens. This is the fourth summary of the NHSN pathogen and antimicrobial susceptibility data, and it builds upon the methodology from earlier reports.^{1–3} Most of the central line-associated bloodstream infections (CLABSIs) and catheter-associated urinary tract infections (CAUTIs) analyzed in this report were reported to the 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, long-term acute-care hospitals (LTACHs), and inpatient rehabilitation facilities (IRFs).^{4–6} Surgical site infections (SSIs) following colon surgeries and abdominal hysterectomies are also required to be reported under CMS QRPs, and ventilator-associated events

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(VAEs) became a required LTACH reporting element in January 2016. This report provides expanded pathogen distribution and susceptibility data, stratified by infection type, facility type, location within a facility, and/or surgery type. Publishing data at this level of granularity were made possible by the expansion of CMS and state HAI reporting requirements, as well as the commitment of healthcare facility staff to HAI surveillance.

Methods

The CLABSIs,⁷ CAUTIs,⁸ select VAEs,⁹ and SSIs¹⁰ that occurred between 2015–2017 and had been reported to the NHSN's Patient Safety Component as of July 1, 2018, were included in this report. These HAIs were reported by acute-care hospitals, critical access hospitals, LTACHs, and IRFs from all US states and territories. Unless otherwise noted, CLABSI data included events classified as mucosal barrier injury laboratory-confirmed bloodstream infection (MBI-LCBI). VAE data were limited to events classified as possible ventilator-associated pneumonia (PVAP) because this is the only subtype of VAE for which a pathogen can be reported. Asymptomatic bacteremic urinary tract infections, CLABSIs reported from IRFs, and outpatient SSIs were excluded.

The NHSN protocols provide guidance for attributing device-associated (DA) HAIs (ie, CLABSIs, CAUTIs, and PVAPs) to a CDC-defined location type, and SSIs to a CDC operative procedure code. Due to known differences in pathogens and resistance patterns between adult and pediatric populations,^{11,12} this report was limited to DA HAIs attributed to adult location types, and to SSIs that occurred in patients ≥ 18 years old at the time of surgery. Comparable data from pediatric locations and patients are described in a companion report.¹³

Unless otherwise noted, DA HAIs were stratified into 5 mutually exclusive location categories: hospital wards (inclusive of step-down, mixed acuity, and specialty care areas), hospital intensive care units (ICUs), hospital oncology units (ie, oncology ICUs and wards), LTACHs (ie, LTACH ICUs and wards), and IRFs (ie, freestanding IRFs and CMS-certified IRF units located within a hospital). SSI data were stratified into mutually exclusive surgical categories based on the operative procedure code. Pathogen distributions were also analyzed separately for each operative procedure code and are available in the online supplement.¹⁴

Up to 3 pathogens and their antimicrobial susceptibility testing (AST) results can be reported to the NHSN for each HAI. The AST results for the drugs included in this analysis were reported using the interpretive categories of "susceptible" (S), "intermediate" (I), "resistant" (R), or "not tested." Instead of "intermediate," cefepime had the category interpretation of "intermediate/susceptible-dose dependent" (I/S-DD), which was treated as I for this analysis. Laboratories are expected to follow current guidelines from the Clinical and Laboratory Standards Institute (CLSI) for AST.¹⁵ Naming conventions for pathogens generally adhered to the Systematized Nomenclature of Medicine Clinical Terms (SNOMED CT) Preferred Term.¹⁶ In some cases, pathogens were grouped by genus or clinically recognized group (eg, viridans group streptococci) (Appendices A2–A4 online). Results for *Klebsiella* spp were limited to *K. pneumoniae* and *K. oxytoca*; *K. aerogenes* was considered part of *Enterobacter* spp due to the timing of the NHSN's adoption of its name change.¹⁷

Staphylococcus aureus was defined as methicillin-resistant (MRSA) if the isolate was reported as R to oxacillin, cefoxitin, or methicillin. *Enterococcus* spp isolates were defined as vancomycin-resistant (VRE) if they tested R to vancomycin. VRE data were

analyzed for all HAIs except PVAP because *Enterococcus* spp are excluded from the NHSN's PVAP surveillance definition under most scenarios. Carbapenem-resistant Enterobacteriaceae (CRE) were defined as *Klebsiella* spp, *Escherichia coli*, or *Enterobacter* spp that tested R to imipenem, meropenem, doripenem, or ertapenem. All other pathogen-antimicrobial combinations (phenotypes) were described using a metric for nonsusceptibility, which included pathogens that tested I or R to the applicable drugs. To be defined as nonsusceptible to extended-spectrum cephalosporins (ESCs), pathogens must have tested I or R to either ceftazidime or cefepime (*Pseudomonas aeruginosa*) or to ceftazidime, cefepime, ceftriaxone, or cefotaxime (*Klebsiella* spp and *E. coli*). For *Enterobacter* spp, evaluation of nonsusceptibility to ESCs was limited to cefepime due to *Enterobacter*'s inducible resistance to other ESCs. Fluoroquinolone nonsusceptibility was defined as a result of I or R to either ciprofloxacin or levofloxacin (*P. aeruginosa*) or to ciprofloxacin, levofloxacin, or moxifloxacin (*E. coli*). Carbapenem nonsusceptibility in *P. aeruginosa* and *Acinetobacter* spp was defined as a result of I or R to imipenem, meropenem, or doripenem. Nonsusceptibility to aminoglycosides was defined as a result of I or R to gentamicin, amikacin, or tobramycin. Finally, multi-drug-resistance (MDR) was approximated by adapting previously established definitions¹⁸ that require nonsusceptibility to at least 1 agent within 3 different drug classes. For Enterobacteriaceae and *P. aeruginosa*, 5 classes were considered in the criteria: ESCs (or cefepime for *Enterobacter* spp), fluoroquinolones, aminoglycosides, carbapenems, and piperacillin (PIP) or piperacillin/tazobactam (PIPTAZ). A sixth class, ampicillin/sulbactam, was included in the criteria for *Acinetobacter* spp.

Data were analyzed using SAS version 9.4 software (SAS Institute, Cary, NC). For all HAIs and pathogens, absolute frequencies and distributions were calculated by HAI, location, and surgical category. The 15 most commonly reported pathogens were identified, and their frequencies and ranks within each stratum were calculated. A pooled mean percentage nonsusceptible (%NS) was calculated for each phenotype as the sum of nonsusceptible (or resistant) pathogens, divided by the sum of pathogens tested for susceptibility, and multiplied by 100. Percentage NS was not calculated for any phenotype for which < 20 pathogens were tested. Differences in the %NS across location types or surgical categories were assessed for statistical significance using a mid-P exact test, and $P < .05$ was considered statistically significant. The percentage of pathogens with reported susceptibility results (referred to as "percentage tested") is defined elsewhere³ and was calculated for each bacterial phenotype, as well as for select *Candida* spp. Pathogens and susceptibility data for CLABSIs categorized as MBI-LCBI were analyzed separately and are presented in the online supplement.¹⁴

"Selective reporting" occurs when laboratories suppress AST results as part of antimicrobial stewardship efforts. This practice could contribute to a higher number of pathogens reported to the NHSN as "not tested" to certain drugs. To assess the impact of selective reporting on the national %NS, we applied an alternate calculation for CRE and ESC nonsusceptibility. If a pathogen was reported as "not tested" to carbapenems, susceptibility was inferred as S if the pathogen tested susceptible to at least 2 of the following: ampicillin, ampicillin/sulbactam, amoxicillin/clavulanic acid, PIPTAZ, cefazolin, cefoxitin, or cefotetan. If a pathogen was reported as "not tested" to ESCs, susceptibility was inferred as S if the pathogen tested susceptible to at least 2 of the following: ampicillin, aztreonam, or cefazolin. Therefore, the number of tested isolates increases under the alternate calculation. Percentage NS was calculated using both the traditional (ie, strictly as reported) and alternate approaches.

Table 1. Characteristics of Facilities Performing Adult Healthcare-Associated Infection (HAI) Surveillance in the National Healthcare Safety Network, 2015–2017

Characteristic	No. (%) Facilities (n = 5,626)
Facility type	
General acute-care	3,492 (62.1)
Critical access	940 (16.7)
Long-term acute-care	507 (9.0)
Free-standing inpatient rehabilitation ^a	332 (5.9)
Surgical	131 (2.3)
Children's	60 (1.1)
Military	51 (0.9)
Psychiatric	30 (0.5)
Orthopedic	27 (0.5)
Oncology	17 (0.3)
Veterans' Affairs	14 (0.2)
Women's and children's	13 (0.2)
Women's	12 (0.2)
Facility bed size	
≤50	2,278 (40.5)
51–200	1,999 (35.5)
201–500	1,111 (19.7)
≥501	238 (4.2)

^aDoes not include inpatient rehabilitation facilities reporting to the NHSN as locations within acute-care hospitals.

Statistical analyses were not performed to test for temporal changes in the %NS; thus, this report does not convey any conclusions regarding changes in resistance over time. Due to differences in the stratification levels, inclusion criteria, and patient populations, the %NS values in this report should not be compared to those published in previous iterations of this report.

Results

During 2015–2017, 5,626 healthcare facilities performed surveillance of adult HAIs, and a total of 311,897 HAIs and 356,633 pathogens were reported (Tables 1 and 2). Facilities varied by type and size; 41% had ≤50 beds. SSIs contributed the highest proportion of pathogens (43%) followed by CAUTIs (29%), CLABSIs (25%) and PVAPs (3%). *Escherichia coli* was the most common pathogen across all HAIs, constituting almost 18% of reported pathogens (Table 3). *Staphylococcus aureus* (12%) and *Klebsiella* spp (9%) were the second and third most commonly reported pathogens, respectively.

The highest proportion of CLABSI and CAUTI pathogens were reported from hospital wards, with 9,648 individual wards reporting at least 1 CLABSI pathogen and 11,850 wards reporting at least 1 CAUTI pathogen (Table 4). Most PVAP pathogens (92%) were reported from hospital ICUs.

Pathogen distributions

Staphylococcus aureus and coagulase-negative staphylococci were among the most frequently reported CLABSI pathogens

Table 2. Frequency of Adult Healthcare-Associated Infection (HAI) Events and Pathogens, by HAI Type, 2015–2017

HAI Type	No. (%) HAI Events (n = 311,897)	No. (%) Pathogens (n = 356,633) ^a
SSI ^b	132,258 (42.4)	154,133 (43.2)
CAUTI	92,715 (29.7)	103,260 (29.0)
CLABSI	78,896 (25.3)	89,203 (25.0)
PVAP ^{b,c}	8,028 (2.6)	10,037 (2.8)

Note. SSI, surgical site infection; CAUTI, catheter-associated urinary tract infection; CLABSI, central line-associated bloodstream infection; PVAP, possible ventilator-associated pneumonia.

^aUp to 3 pathogens can be reported for each HAI.

^bSSIs and PVAPs can be reported to the NHSN without an associated pathogen. In total, 27,237 (20.6%) SSIs and 43 (0.5%) PVAPs were reported to the NHSN in 2015–2017 without a pathogen.

^cPVAP is the only type of ventilator-associated event (VAE) for which a pathogen can be reported.

Table 3. Distribution and Rank Order of the 15 Most Frequently Reported Pathogens Across All Types of Adult Healthcare-Associated Infections (HAIs), 2015–2017

Pathogen ^a	No. (%) Pathogens	Rank
<i>Escherichia coli</i>	62,571 (17.5)	1
<i>Staphylococcus aureus</i>	42,132 (11.8)	2
Selected <i>Klebsiella</i> spp	31,530 (8.8)	3
<i>Pseudomonas aeruginosa</i>	28,513 (8.0)	4
<i>Enterococcus faecalis</i> ^b	28,236 (7.9)	5
Coagulase-negative staphylococci	24,199 (6.8)	6
<i>Enterobacter</i> spp	16,568 (4.6)	7
<i>Enterococcus faecium</i> ^b	13,687 (3.8)	8
<i>Proteus</i> spp	11,463 (3.2)	9
<i>Candida albicans</i> ^b	11,043 (3.1)	10
Other <i>Enterococcus</i> spp ^{b,c}	11,020 (3.1)	11
<i>Bacteroides</i> spp	8,251 (2.3)	12
Viridans group streptococci	6,575 (1.8)	13
Other <i>Candida</i> spp ^{b,c}	6,467 (1.8)	14
<i>Candida glabrata</i> ^b	5,152 (1.4)	15
Other ^d	49,226 (13.8)	
Total	356,633 (100.0)	

Note. Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*.

^aThe following species were frequently reported to the NHSN but are considered part of a larger pathogen group for this table: *Staphylococcus epidermidis* (11,482; 47.4% of coagulase-negative staphylococci); *Enterobacter cloacae* complex group (11,886; 71.7% of *Enterobacter* spp); *Proteus mirabilis* (10,662; 93.0% of *Proteus* spp).

^bWhen analyzed on the genus level, *Enterococcus* ranks #2, and *Candida* ranks #7.

^cThe group 'Other *Enterococcus* spp' combines enterococci identified to the species level, excluding *E. faecium* and *E. faecalis*, and enterococci for which the species was not reported. The group 'Other *Candida* spp' combines *Candida* identified to the species level, excluding *C. albicans* and *C. glabrata*, and *Candida* for which the species were not reported.

^dA complete distribution of all pathogens reported from adult HAIs can be found in the 2015–2017 Adult Antimicrobial Resistance Report Online Supplement (<https://www.cdc.gov/nhsn/datastat/index.html>).

from wards, ICUs, and LTACHs (Table 5). However, when grouped at the genus level, *Candida* spp became the most common CLABSI pathogen in hospital wards and ICUs, making up 25% of ICU pathogens. *Enterococcus faecalis* made up a higher proportion

Table 4. Frequency of Adult Device-Associated Healthcare-Associated Infection (HAI) Pathogens, by HAI and Location Type,^a 2015–2017

Location Type ^a	CLABSI		CAUTI		PVAP ^b	
	No. of Units ^c	No. (%) Pathogens (n = 89,203)	No. of Units ^c	No. (%) Pathogens (n = 103,260)	No. of Units ^c	No. (%) Pathogens (n = 10,037)
Hospital Wards ^a	9,648	34,788 (39.0)	11,850	44,790 (43.4)	101	289 (2.9)
Hospital ICUs	4,179	27,396 (30.7)	4,626	40,755 (39.5)	1,728	9,233 (92.0)
Hospital Oncology Units	698	16,191 (18.2)	554	2,274 (2.2)	9 ^d	33 (0.3)
LTACHs	687	10,828 (12.1)	699	11,366 (11.0)	194	482 (4.8)
IRFs ^e	1,025	4,075 (4.0)	0	0 (0.0)

Note. CLABSI, central line-associated bloodstream infection; CAUTI, catheter-associated urinary tract infection; PVAP, possible ventilator-associated pneumonia; ICUs, intensive care units; LTACHs, long-term acute-care hospitals; IRFs, inpatient rehabilitation facilities.

^aLocation types are mutually exclusive. "Hospital wards" includes step-down units, mixed acuity units, and specialty care areas.

^bPVAP is the only type of ventilator-associated event (VAE) for which a pathogen can be reported.

^cNumber of units that reported at least 1 pathogen.

^dReported from oncology ICUs only.

^eConsists of free-standing IRFs and rehabilitation wards located within hospitals and defined as IRFs per the Centers for Medicare and Medicaid Services (CMS). CLABSI data reported from IRFs were excluded from this report.

Table 5. Distribution and Rank Order^a of the 15 Most Frequently Reported Adult Central Line-Associated Bloodstream Infection^b (CLABSI) Pathogens, by Location Type^c, 2015–2017

Pathogen	Hospital Wards ^c		Hospital ICUs ^a		Hospital Oncology Units ^a		LTACHs ^a	
	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank
<i>Staphylococcus aureus</i>	5,386 (15.5)	1	2,497 (9.1)	3	1,163 (7.2)	6	1,217 (11.2)	3
Coagulase-negative staphylococci	3,792 (10.9)	2	3,789 (13.8)	1	1,681 (10.4)	2	1,277 (11.8)	2
Selected <i>Klebsiella</i> spp	3,344 (9.6)	3	1,708 (6.2)	8	1,441 (8.9)	4	1,158 (10.7)	4
<i>Enterococcus faecalis</i> ^d	2,636 (7.6)	4	2,117 (7.7)	5	664 (4.1)	8	1,314 (12.1)	1
<i>Candida albicans</i> ^d	2,469 (7.1)	5	2,844 (10.4)	2	216 (1.3)	15	642 (5.9)	7
<i>Escherichia coli</i>	2,279 (6.6)	6	1,129 (4.1)	9	2,667 (16.5)	1	394 (3.6)	10
Other <i>Candida</i> spp ^{d,e,f}	1,876 (5.4)	7	2,186 (8.0)	4	559 (3.5)	9	739 (6.8)	5
<i>Enterococcus faecium</i> ^d	1,673 (4.8)	8	1,981 (7.2)	6	1,670 (10.3)	3	691 (6.4)	6
<i>Candida glabrata</i> ^d	1,460 (4.2)	9	1,836 (6.7)	7	249 (1.5)	12	489 (4.5)	9
<i>Enterobacter</i> spp	1,453 (4.2)	10	1,078 (3.9)	10	532 (3.3)	10	383 (3.5)	11
<i>Pseudomonas aeruginosa</i>	1,407 (4.0)	11	1,061 (3.9)	11	701 (4.3)	7	495 (4.6)	8
<i>Serratia</i> spp	678 (1.9)	12	588 (2.1)	12	100 (0.6)	18	256 (2.4)	13
<i>Acinetobacter</i> spp	660 (1.9)	13	392 (1.4)	14	66 (0.4)	22	245 (2.3)	14
Other <i>Enterococcus</i> spp ^{d,e}	577 (1.7)	14	545 (2.0)	13	339 (2.1)	11	257 (2.4)	12
Viridans group streptococci	430 (1.2)	15	223 (0.8)	19	1,386 (8.6)	5	33 (0.3)	22
Other	4,668 (13.4)		3,422 (12.5)		2,757 (17.0)		1,238 (11.4)	
Total	34,788 (100.0)		27,396 (100.0)		16,191 (100.0)		10,828 (100.0)	

Note. ICUs, intensive care units; LTACHs, long-term acute-care hospitals; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*.

^aThe 15 most frequently reported pathogens from hospital wards are shown, along with their distribution and rank within the other location types. Some rankings within the other location types are not shown: hospital ICUs #15 (Yeast, not otherwise specified); hospital oncology units #13 (*Rothia mucilaginosa*), #14 (*Bacteroides* spp); LTACHs #15 (*Proteus* spp).

^bSupplemental tables are available in the 2015–2017 Adult Antimicrobial Resistance Report Online Supplement that show pathogen rankings separately for mucosal barrier injury laboratory-confirmed bloodstream infection (MBI-LCBI) and non-MBI-LCBIs (<https://www.cdc.gov/nhsn/datastat/index.html>).

^cLocation types are mutually exclusive. "Hospital wards" includes step-down units, mixed acuity units, and specialty care areas.

^dWhen analyzed on the genus level, *Candida* and *Enterococcus* resulted in the following rankings: *Candida*: hospital wards (#1), hospital ICUs (#1), hospital oncology units (#7), LTACHs (#2); *Enterococcus*: hospital wards (#3), hospital ICUs (#2), hospital oncology units (#1), LTACHs (#1).

^eThe group "Other *Enterococcus* spp" combines enterococci identified to the species level, excluding *E. faecium* and *E. faecalis*, and enterococci for which the species was not reported. The group "Other *Candida* spp" combines *Candida* identified to the species level, excluding *C. albicans* and *C. glabrata*, and *Candida* for which the species was not reported.

^f*Candida parapsilosis* was reported with the following frequencies: hospital wards (846); hospital ICUs (810); hospital oncology units (122); LTACHs (446).

of CLABSI pathogens in LTACHs (12%) compared to all other location types. In contrast, *E. coli* was the most common CLABSI pathogen in oncology units (17%) and was more likely

to be reported from those units than non-oncology units (eg, 4% from ICUs and LTACHs). Viridans group streptococci were also reported more frequently in oncology-unit CLABSI (9%)

Table 6. Distribution and Rank Order^a of the 15 Most Frequently Reported Adult Catheter-Associated Urinary Tract Infection (CAUTI) Pathogens, by Location Type,^b 2015–2017

Pathogen	Hospital Wards ^b and ICUs		Hospital Oncology Units ^a		LTACHs		IRFs ^a	
	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank
<i>Escherichia coli</i>	29,348 (34.3)	1	653 (28.7)	1	2,389 (21.0)	2	1,414 (34.7)	1
Selected <i>Klebsiella</i> spp	12,143 (14.2)	2	337 (14.8)	2	1,882 (16.6)	3	704 (17.3)	2
<i>Pseudomonas aeruginosa</i>	10,982 (12.8)	3	300 (13.2)	3	2,570 (22.6)	1	629 (15.4)	3
<i>Enterococcus faecalis</i> ^c	7,958 (9.3)	4	266 (11.7)	4	739 (6.5)	6	273 (6.7)	4
<i>Proteus</i> spp	4,756 (5.6)	5	79 (3.5)	9	933 (8.2)	4	244 (6.0)	5
<i>Enterobacter</i> spp	4,232 (4.9)	6	111 (4.9)	6	555 (4.9)	7	226 (5.5)	6
Other <i>Enterococcus</i> spp ^{c,d}	3,420 (4.0)	7	80 (3.5)	8	249 (2.2)	8	108 (2.7)	7
Coagulase-negative staphylococci	2,271 (2.7)	8	83 (3.6)	7	111 (1.0)	15	85 (2.1)	8
<i>Enterococcus faecium</i> ^c	2,242 (2.6)	9	115 (5.1)	5	765 (6.7)	5	33 (0.8)	12
<i>Citrobacter</i> spp	1,763 (2.1)	10	48 (2.1)	11	201 (1.8)	9	83 (2.0)	9
<i>Staphylococcus aureus</i>	1,757 (2.1)	11	60 (2.6)	10	166 (1.5)	11	83 (2.0)	9
<i>Serratia</i> spp	844 (1.0)	12	23 (1.0)	13	146 (1.3)	12	45 (1.1)	11
<i>Morganella</i> spp	777 (0.9)	13	24 (1.1)	12	116 (1.0)	14	29 (0.7)	13
<i>Acinetobacter</i> spp	455 (0.5)	14	15 (0.7)	14	174 (1.5)	10	13 (0.3)	14
<i>Providencia stuartii</i>	297 (0.3)	15	2 (0.1)	25	136 (1.2)	13	9 (0.2)	16
Other	2,300 (2.7)		78 (3.4)		234 (2.1)		97 (2.4)	
Total	85,545 (100.0)		2,274 (100.0)		11,366 (100.0)		4,075 (100.0)	

Note. ICUs, intensive care units; LTACHs, long-term acute-care hospitals; IRFs, inpatient rehabilitation facilities; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*.

^aThe 15 most frequently reported pathogens from hospital wards and ICUs are shown, along with their distribution and rank within the other location types. Some rankings within the other location types are not shown: hospital oncology units #14 (*Stenotrophomonas maltophilia*); IRFs #15 (*Pseudomonas*, not otherwise specified).

^bLocation types are mutually exclusive. "Hospital wards" includes step-down units, mixed acuity units, and specialty care areas.

^cWhen analyzed on the genus level, *Enterococcus* resulted in the following rankings: hospital wards and ICUs (#2), hospital oncology units (#2), LTACHs (#4), IRFs (#4).

^dThe group 'Other *Enterococcus* spp' combines enterococci identified to the species level, excluding *E. faecium* and *E. faecalis*, and enterococci for which the species was not reported.

than non-oncology-unit CLABSIs ($\leq 1\%$). Notably, half of all CLABSIs in oncology units met the definition of an MBI-LCBI (Supplementary Table S1).¹⁴

Escherichia coli, *Klebsiella* spp, and *P. aeruginosa* were the 3 most frequently reported CAUTI pathogens for all location types analyzed (Table 6). Frequencies of *E. faecium* and *E. faecalis* as CAUTI pathogens differed by location type, with *E. faecium* rarely identified in IRFs (1%) and *E. faecalis* commonly reported by oncology units (12%). Several pathogens appeared among the most frequently reported PVAP pathogens that were not frequently reported from other DA infections, such as *Haemophilus influenzae* and *Stenotrophomonas maltophilia*. *Staphylococcus aureus*, *P. aeruginosa*, and *Klebsiella* spp were the 3 most frequently reported PVAP pathogens across all location types (Table 7).

More than half of SSI pathogens (54%) were reported following abdominal surgeries, and 24% were reported following orthopedic surgeries (Table 8). The type of SSI varied by surgical category; for example, 58% of abdominal SSI pathogens were identified as organ/space infections, 43% of orthopedic SSI pathogens were deep incisional, and 53% of obstetrical/gynecological (ob/gyn) SSI pathogens were superficial incisional. *Staphylococcus aureus* was the most commonly reported pathogen for all SSIs overall (18%), and was the most common pathogen for orthopedic, ob/gyn, and cardiac SSIs (Table 9). As expected, *E. coli* was the most commonly identified pathogen in abdominal SSIs, accounting for almost 20% of reported

pathogens. Notably, coagulase-negative staphylococci were frequently identified as cardiac and orthopedic SSI pathogens (15% and 13%, respectively).

Most SSIs reported to the NHSN occurred after a procedure with a primarily closed incision; the surgical categories with the highest proportion of non-primarily closed incisions were amputation (12% non-primary closure), colon surgeries (8% non-primary closure), and exploratory laparotomy (8% non-primary closure). SSI pathogens varied by closure technique, with the non-primarily closed colon SSIs having a higher proportion of *Candida* spp (7%) compared to SSIs identified from primarily closed procedures (5%) (data not shown).

Percentage tested and percentage nonsusceptibility

Most facilities reported AST results across all strata for the following pathogen/drug combinations: *S. aureus* with oxacillin/cefoxitin/methicillin, *Enterococcus* spp with vancomycin, *E. coli* with fluoroquinolones, and *P. aeruginosa* with aminoglycosides, fluoroquinolones, and ESCs (Tables 10–15). Overall, facilities reported low testing frequencies (<85%) for *Klebsiella* spp, *E. coli*, and *Enterobacter* spp with carbapenems, ESCs, and/or cefepime. *Pseudomonas aeruginosa* and *Acinetobacter* spp also had low testing frequencies to carbapenems. Overall, fluconazole susceptibility testing for *Candida* spp was relatively rare, with *Candida parapsilosis* having the highest percentage tested at 39% in 2015–2017

Table 7. Distribution and Rank Order^a of the 15 Most Frequently Reported Adult Possible Ventilator-Associated Pneumonia^b (PVAP) Pathogens, by Location Type,^c 2015–2017

Pathogen	Hospital ICUs ^d		Hospital Wards ^{a,c}		LTACHs ^a	
	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank	No. (%) Pathogens	Rank
<i>Staphylococcus aureus</i>	2,673 (28.8)	1	58 (20.1)	2	102 (21.2)	2
<i>Pseudomonas aeruginosa</i>	1,192 (12.9)	2	63 (21.8)	1	157 (32.6)	1
Selected <i>Klebsiella</i> spp	936 (10.1)	3	38 (13.1)	3	50 (10.4)	3
<i>Enterobacter</i> spp	781 (8.4)	4	18 (6.2)	4	21 (4.4)	7
<i>Haemophilus influenzae</i>	550 (5.9)	5	10 (3.5)	8	1 (0.2)	16
All <i>Streptococcus</i> spp ^e	527 (5.7)	6	6 (2.1)	10	1 (0.2)	16
<i>Escherichia coli</i>	520 (5.6)	7	14 (4.8)	7	18 (3.7)	8
<i>Serratia</i> spp	428 (4.6)	8	6 (2.1)	10	24 (5.0)	6
<i>Stenotrophomonas maltophilia</i>	372 (4.0)	9	17 (5.9)	5	25 (5.2)	5
<i>Acinetobacter</i> spp	294 (3.2)	10	17 (5.9)	5	32 (6.6)	4
<i>Proteus</i> spp	134 (1.4)	11	7 (2.4)	9	14 (2.9)	9
<i>Citrobacter</i> spp	110 (1.2)	12	6 (2.1)	10	6 (1.2)	10
<i>Moraxella catarrhalis</i>	71 (0.8)	13	0 (0.0)	...	4 (0.8)	12
<i>Morganella</i> spp	32 (0.3)	14	0 (0.0)	...	0 (0.0)	...
<i>Burkholderia cepacia</i>	26 (0.3)	15	0 (0.0)	...	0 (0.0)	...
<i>Haemophilus</i> NOS	26 (0.3)	15	1 (0.3)	19	0 (0.0)	...
Other	594 (6.4)		28 (9.7)		27 (5.6)	
Total	9,266 (100.0)		289 (100.0)		482 (100.0)	

Note. ICUs, intensive care units; LTACHs, long-term acute-care hospitals; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*; NOS, not otherwise specified.

^aThe 15 most frequently reported pathogens from hospital ICUs are shown, along with their distribution and rank within the other location types. Some rankings within the other location types are not shown: hospital wards #13 (*Providencia stuartii*), #14 (*Achromobacter* NOS and *Corynebacterium* NOS); LTACHs 3 species tied for rank #13, each was reported twice.

^bPVAP is the only type of ventilator-associated event (VAE) for which a pathogen can be reported.

^cLocation types are mutually exclusive. "Hospital wards" includes step-down units, mixed acuity units, and specialty care areas.

^dIncludes oncology ICUs.

^eThe group 'All *Streptococcus* spp' includes all members of genus *Streptococcus*, including those not identified to the species level. *Streptococcus pneumoniae* was frequently reported in hospital ICUs (277, 52.6% of the *Streptococcus* group).

(Appendix A1 online). Given this low testing frequency, a national %NS was not calculated for any *Candida* spp.

For all phenotypes analyzed except CRE *E. coli*, the national %NS was statistically significantly higher in DA HAIs compared to SSIs, with the greatest difference appearing among *E. faecium* resistant to vancomycin (82% resistant in DA HAIs vs 56% resistant in SSIs) (Table 10). Among CLABSIs, the %NS for most phenotypes was significantly higher in LTACHs and ICUs compared to wards (Table 11). Several phenotypes had a substantially higher prevalence of nonsusceptibility in LTACHs than hospital wards: MRSA, *Klebsiella* spp nonsusceptibility to ESCs, CRE *Klebsiella* spp and *Enterobacter* spp, all MDR phenotypes, *P. aeruginosa* nonsusceptibility to aminoglycosides and PIP/PIPTAZ, and *Acinetobacter* spp nonsusceptibility to carbapenems. Significant differences in the CLABSI %NS were also observed between oncology units and hospital wards. *Klebsiella* spp, *Acinetobacter* spp, and some *P. aeruginosa* phenotypes identified in oncology units had a lower %NS than those in hospital wards, whereas *E. coli* nonsusceptibility to fluoroquinolones was significantly higher in oncology units (65% vs 47%). Within oncology units, MBI-LCBIs had a higher %NS for all pathogens analyzed compared to non-MBI-LCBIs, several of which were statistically significantly different. For example, the percentage of *E. coli* displaying

nonsusceptibility to fluoroquinolones was 71% among MBI-LCBIs, compared with 44% in non-MBI-LCBIs (Supplementary Table S5).¹⁴

Among CAUTIs, LTACHs had a significantly higher %NS than hospital wards for all pathogens (Table 12). For example, 23% of *Klebsiella* spp were CRE in LTACHs, compared with 7% in wards. Hospital ICUs had a lower %NS than hospital wards for all *Klebsiella* spp and *E. coli* phenotypes among CAUTIs. There was almost no difference in the %NS between CAUTIs in oncology units and those in hospital wards, but *E. coli* nonsusceptibility to fluoroquinolones was an exception. Among PVAPs, *Klebsiella* spp and *P. aeruginosa* pathogens had a lower %NS in hospital ICUs compared with hospital wards, most of which were statistically significantly different (Table 13). In addition, a lower proportion of *S. aureus* was identified as MRSA among PVAPs from ICUs (37%), compared with CLABSIs (50%) and CAUTIs (41%) from the same setting.

For SSIs following abdominal surgeries, the %NS varied by wound closure technique, with all pathogens showing a higher %NS among non-primarily closed procedures compared to primarily closed procedures (Table 14). The percentage of *P. aeruginosa* with nonsusceptibility to ESCs was 22% among non-primarily closed abdominal procedures, compared to 12%

Table 8. Frequency and Types of Adult Surgical Site Infection (SSI) Pathogens, by Surgical Category, 2015–2017

Surgical Category	Specific Type of SSI			All SSI Types, No. of Pathogens (Column %)
	No. of Pathogens (Row %)			
	Superficial Incisional	Deep Incisional	Organ/Space	
Abdominal ^a	25,120 (30.2)	9,637 (11.6)	48,540 (58.3)	83,297 (54.0)
Orthopedic ^b	9,798 (27.1)	15,362 (42.5)	10,987 (30.4)	36,147 (23.5)
Ob/Gyn ^c	10,851 (53.3)	2,616 (12.9)	6,878 (33.8)	20,345 (13.2)
Cardiac ^d	3,907 (45.2)	2,588 (29.9)	2,152 (24.9)	8,647 (5.6)
Vascular ^e	1,003 (48.7)	873 (42.4)	182 (8.8)	2,058 (1.3)
Neurosurgical ^f	245 (13.9)	398 (22.6)	1,118 (63.5)	1,761 (1.1)
Breast surgery	285 (29.9)	438 (46.0)	229 (24.1)	952 (0.6)
Kidney ^g	223 (43.2)	50 (9.7)	243 (47.1)	516 (0.3)
Neck ^h	104 (32.6)	198 (62.1)	17 (5.3)	319 (0.2)
Prostate surgery	25 (27.5)	5 (5.5)	61 (67.0)	91 (0.1)
Total	51,561 (33.5)	32,165 (20.9)	70,407 (45.7)	154,133 (100.0)

Note. Ob/Gyn, obstetrical and gynecological.

^aAppendix 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.

^bOpen reduction of fracture, hip prosthesis, knee prosthesis, limb amputation, spinal fusion/refusion, and laminectomy.

^cCesarean section, abdominal hysterectomy, ovarian surgery, and vaginal hysterectomy.

^dCardiac surgery, heart transplant, coronary artery bypass graft with chest incision with or without donor incision, pacemaker surgery, and thoracic surgery.

^eAbdominal aortic aneurysm repair, shunt for dialysis, carotid endarterectomy, and peripheral vascular bypass surgery.

^fCraniotomy and ventricular shunt.

^gKidney surgery and kidney transplant.

^hNeck surgery, and thyroid and/or parathyroid surgery.

among those primarily closed. In general, when compared to the abdominal surgical category, SSIs following ob/gyn surgeries had a significantly lower %NS for all phenotypes, particularly *E. coli* nonsusceptibility to fluoroquinolones (19% vs 35%), MRSA (39% vs 56%), and VRE *E. faecium* (36% vs 54%) (Table 15). SSIs following orthopedic surgeries also had a lower %NS than SSIs from abdominal surgeries for most phenotypes. However, the percentage of *E. faecium* resistant to vancomycin was significantly higher in SSIs following orthopedic surgeries (78%) and cardiac surgeries (79%) compared to abdominal surgeries (54%).

Less than 75% of *Klebsiella* spp, *E. coli*, and *Enterobacter* spp combined from DA HAIs were reported with AST results for carbapenems, and <85% were reported with results for ESCs (Table 16). Inferring susceptibilities for those pathogens reported as “not tested” increased the overall percentage tested to 90% for carbapenems and ESCs, which resulted in minimal decreases in the corresponding %NS.

Discussion

Due to HAI reporting requirements driven by state mandates and the CMS QRPs, the HAI data reported to the NHSN and included in this report provide a comprehensive national picture of the most common pathogens implicated in HAIs, as well as the percentage of pathogens displaying nonsusceptibility to selected antimicrobials. This report expands upon the NHSN’s prior reports by providing national %NS values stratified by facility type, location type, and surgical category, and is the first report to publish frequent pathogens and/or resistance profiles in MBI-LCBI, PVAPs, and SSIs following procedures with a non-primary closure technique.

This report provides an unprecedented level of detail about the national epidemiology of pathogens and important resistance phenotypes across the healthcare spectrum.

More than 5,000 healthcare facilities conducted surveillance of adult HAIs between 2015 and 2017; almost 80% had <200 beds. In 2015, the CMS QRP requirements for CLABSI and CAUTI surveillance in acute-care hospitals expanded to include infections from medical, surgical, and medical/surgical wards, in addition to the previously required ICU locations. This resulted in a substantial increase in the proportion of CLABSI and CAUTI pathogens reported from ward locations compared to the NHSN’s previous report.³ In addition, the 2016 expansion of CMS QRP requirements to include LTACH reporting of VAEs allowed us to assess differences in PVAP pathogens and resistance profiles across facility types.

In general, the pathogens associated with DA HAIs varied by location. Similar to previous studies, oncology units in particular had a different pathogen distribution than hospital ICUs and wards.¹⁹ *Escherichia coli* and viridans group streptococci were common CLABSI pathogens in oncology units. These pathogens are included in the MBI-LCBI definition, which is used to identify a subset of BSIs that are often the result of mucosal barrier injury from cytotoxic chemotherapy, rather than the result of a contaminated central line.

A lower %NS was seen for several CLABSI pathogens in oncology units compared to hospital ICUs and wards. Although the reason for this difference is not known, it may be related to differences in underlying illnesses and antimicrobial exposures between patients in oncology and non-oncology units. The high prevalence of *E. coli* nonsusceptibility to fluoroquinolones in oncology units,

Table 9. Distribution and Rank Order of the 15 Most Frequently Reported Adult Surgical Site Infection (SSI) Pathogens, by Surgical Category,^a 2015–2017

Pathogen	All Surgery Types ^b		Abdominal ^c	Orthopedic ^d	Ob/Gyn ^e	Cardiac ^f
	No. (%) Pathogens	Rank	No. (%) Pathogens	No. (%) Pathogens	No. (%) Pathogens	No. (%) Pathogens
<i>Staphylococcus aureus</i>	26,970 (17.5)	1	6,193 (7.4)	13,968 (38.6)	3,092 (15.2)	2,331 (27.0)
<i>Escherichia coli</i>	21,746 (14.1)	2	16,378 (19.7)	1,737 (4.8)	2,778 (13.7)	478 (5.5)
<i>Enterococcus faecalis</i> ^g	12,267 (8.0)	3	8,053 (9.7)	1,779 (4.9)	1,862 (9.2)	281 (3.2)
Coagulase-negative staphylococci	11,106 (7.2)	4	2,980 (3.6)	4,693 (13.0)	1,476 (7.3)	1,288 (14.9)
<i>Pseudomonas aeruginosa</i>	8,956 (5.8)	5	4,787 (5.7)	2,184 (6.0)	907 (4.5)	658 (7.6)
Selected <i>Klebsiella</i> spp	7,789 (5.1)	6	4,894 (5.9)	1,167 (3.2)	917 (4.5)	518 (6.0)
<i>Bacterioides</i> spp	7,321 (4.7)	7	5,968 (7.2)	150 (0.4)	1,100 (5.4)	38 (0.4)
<i>Enterobacter</i> spp	7,178 (4.7)	8	3,691 (4.4)	1,797 (5.0)	793 (3.9)	538 (6.2)
Other <i>Enterococcus</i> spp ^{g,h}	5,444 (3.5)	9	4,279 (5.1)	491 (1.4)	503 (2.5)	85 (1.0)
<i>Candida albicans</i> ^g	4,847 (3.1)	10	4,131 (5.0)	259 (0.7)	216 (1.1)	142 (1.6)
<i>Enterococcus faecium</i> ^g	4,515 (2.9)	11	3,942 (4.7)	324 (0.9)	139 (0.7)	53 (0.6)
<i>Proteus</i> spp	4,357 (2.8)	12	1,542 (1.9)	1,356 (3.8)	888 (4.4)	400 (4.6)
Viridans group streptococci	4,267 (2.8)	13	3,112 (3.7)	323 (0.9)	601 (3.0)	101 (1.2)
<i>Citrobacter</i> spp	2,099 (1.4)	14	1,395 (1.7)	249 (0.7)	275 (1.4)	105 (1.2)
<i>Serratia</i> spp	1,904 (1.2)	15	357 (0.4)	649 (1.8)	230 (1.1)	475 (5.5)
Other	23,367 (15.2)		11,595 (13.9)	5,021 (13.9)	4,568 (22.5)	1,156 (13.4)
Total	154,133 (100.0)		83,297 (100.0)	36,147 (100.0)	20,345 (100.0)	8,647 (100.0)

Note. Ob/Gyn, obstetrical and gynecological; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*.

^aThe 4 most frequently reported surgical categories by pathogen volume are shown. Supplemental tables are available in the 2015–2017 Adult Antimicrobial Resistance Report Online Supplement that show pathogen rankings separately for each NHSN operative procedure code (<https://www.cdc.gov/nhsn/datatool/index.html>).

^bConsists of all NHSN operative procedure codes and is not limited to the 4 surgical categories shown.

^cAppendix 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.

^dOpen reduction of fracture, hip prosthesis, knee prosthesis, limb amputation, spinal fusion/refusion, and laminectomy.

^eCesarean section, abdominal hysterectomy, ovarian surgery, and vaginal hysterectomy.

^fCardiac surgery, heart transplant, coronary artery bypass graft with chest incision with or without donor incision, pacemaker surgery, and thoracic surgery.

^gWhen analyzed on the genus level for all surgery types, *Enterococcus* ranks #2 and *Candida* ranks #9.

^hThe group 'Other *Enterococcus* spp' combines enterococci identified to the species level, excluding *E. faecium* and *E. faecalis*, and enterococci for which the species was not reported.

and particularly in MBI-LCBI within oncology units, is likely the result of widespread use of fluoroquinolone prophylaxis in this population.

Enterococcus spp have historically been reported as the most common resistant organism isolated from LTACH patients.^{20,21} The results of our analysis were consistent with those of earlier publications: *Enterococcus* spp represented the most common LTACH CLABSI pathogen. LTACHs consistently had a higher %NS for most phenotypes compared with other settings. This heightened antimicrobial resistance in LTACHs is well established and has been attributed to the longer patient length of stay, the acuity of patients, patient exposure to hospital ICUs and antimicrobials prior to their LTACH admission, and challenges in the implementation of infection control practices in LTACHs.^{22,23} Transmission of resistant organisms in these settings can contribute to an increase in the overall regional prevalence of these organisms due to frequent patient transfers. A coordinated approach across healthcare facilities connected by patient sharing has the greatest potential to reduce the spread of resistant infections in the region.²⁴

SSI pathogens varied by surgical category and procedure closure technique. The high frequency of *S. aureus* and coagulase-negative staphylococci reported from orthopedic and cardiac SSIs could be partially related to the use of implants, such as orthopedic

implants, during these procedures.²⁵ The differences between primarily closed and non-primarily closed abdominal procedures may reflect differences in the underlying pathophysiology that might lead a surgeon to choose one closure technique over another. In addition, patients with a non-primarily closed incision might be more likely to receive antimicrobial treatment for existing infections and/or prolonged prophylaxis prior to the procedure, both of which could contribute to an increase in yeast growth and a higher likelihood for the development of antimicrobial resistance. Pathogen susceptibility varied by surgical category, with ob/gyn procedures having a lower %NS for all phenotypes compared to general abdominal procedures. It is possible that more ob/gyn procedures are elective compared to other abdominal procedures, and patients undergoing ob/gyn procedures may be generally younger and healthier than those receiving non-elective abdominal surgeries.

Consistent with earlier reports, this analysis found a higher %NS in DA HAIs compared to SSIs. Patients with a CLABSI, CAUTI, or PVAP have often been admitted to an inpatient unit for several days prior to the infection, and therefore pathogens contributing to these infections are more likely to have been acquired during a patient's hospitalization, when patients are exposed to antimicrobials and where there is significant transmission pressure for resistant organisms. Alternatively, SSIs are often caused by bacterial

Table 10. Percentage of Pathogens Reported from Adult Healthcare-Associated Infections (HAIs) in Acute-Care Hospitals^a that Tested Nonsusceptible^b (NS) to Selected Antimicrobial Agents, by Infection Category, 2015–2017

Pathogen, Antimicrobial	Device-Associated HAIs ^c			Surgical Site Infections		
	No. Reported	% Tested	% NS ^b	No. Reported	% Tested	% NS ^b
<i>Staphylococcus aureus</i>	13,594			26,970		
OX/CEFOX/METH (MRSA)		92.3	48.4*		94.2	41.9
<i>Enterococcus faecium</i>	7,682			4,515		
Vancomycin (VRE)		95.1	82.1*		95.9	55.6
<i>Enterococcus faecalis</i>	13,643			12,267		
Vancomycin (VRE)		92.9	7.2*		92.7	3.4
Selected <i>Klebsiella</i> spp	19,947			7,789		
ESCs		84.7	21.1*		81.9	13.7
Carbapenems (CRE)		74.7	6.9*		72.6	3.1
MDR		93.2	13.2*		93.2	6.3
<i>Escherichia coli</i>	36,610			21,746		
ESCs		84.3	20.5*		81.8	18.2
Carbapenems (CRE)		73.8	0.7		73.4	0.6
FQs		95.8	37.8*		94.4	32.1
MDR		93.2	9.7*		92.7	7.4
<i>Enterobacter</i> spp	8,205			7,178		
Cefepime		74.6	11.4*		70.4	5.5
Carbapenems (CRE)		77.4	6.2*		74.7	3.7
MDR-2		92.2	6.5*		92.5	1.9
<i>Pseudomonas aeruginosa</i>	15,706			8,956		
AMINOs		96.9	14.4*		96.3	5.8
ESCs-2		95.8	20.3*		95.0	10.2
FQs-2		95.8	26.2*		95.5	11.0
Carbapenems-2		81.3	20.7*		77.8	9.1
PIP/PIPTAZ		89.6	15.0*		89.6	7.7
MDR-3		96.9	14.2*		96.3	4.5
<i>Acinetobacter</i> spp	1,899			625		
Carbapenems-2		79.1	43.2*		77.0	26.6
MDR-4		95.1	43.1*		94.1	26.5

Note. Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*; OX/CEFOX/METH, oxacillin, cefoxitin, or methicillin; MRSA, methicillin-resistant *Staphylococcus aureus*; VRE, vancomycin-resistant *Enterococcus*; ESCs, extended-spectrum cephalosporins (cefepime, cefotaxime, ceftazidime, or ceftriaxone); CRE, carbapenem-resistant Enterobacteriaceae (imipenem, meropenem, doripenem, or ertapenem); MDR, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs, FQs, AMINOs, carbapenems (R only), PIPTAZ); MDR-2, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: cefepime, FQs, AMINOs, carbapenems (R only), PIPTAZ); FQs, fluoroquinolones (ciprofloxacin, levofloxacin, or moxifloxacin); AMINOs, aminoglycosides (amikacin, gentamicin, or tobramycin); ESCs-2, extended-spectrum cephalosporins (cefepime or ceftazidime); FQs-2, fluoroquinolones (ciprofloxacin or levofloxacin); PIP, piperacillin; PIPTAZ, piperacillin/tazobactam; Carbapenems-2, imipenem, meropenem, or doripenem; MDR-3, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ); MDR-4, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ, ampicillin/sulbactam).

*Statistically significantly different than %NS in surgical site infections; $P < .05$.

^aLong-term acute-care hospitals (LTACHs) and inpatient rehabilitation facilities (IRFs) are excluded from this table.

^bMRSA, VRE, and CRE data are presented as %R (ie, includes only those pathogens that tested resistant). All other phenotypes are shown as %NS (ie, includes pathogens that tested intermediate or resistant).

^cConsists of central line-associated bloodstream infections (CLABSIs), catheter-associated urinary tract infections (CAUTIs), and possible ventilator-associated pneumonias (PVAPs).

contamination from the patient's endogenous skin flora,²⁶ and thus may be less likely to show nonsusceptibility to antimicrobials.

Statistically significant differences existed in the %NS between hospital wards and ICUs, with ICUs tending to have a higher %NS for CLABSI pathogens and a lower %NS for CAUTI pathogens. Previous studies reported higher resistance percentages in ICUs, noting several contributing factors such as the severity of patient illness and the common use of prophylactic antimicrobials in

ICUs.^{27–29} However, among CAUTIs, the %NS values were higher in wards than ICUs. This could reflect differences in the frequency and duration of urinary catheter use in these settings. In the past few years, reductions in device utilization have been greater on wards than ICUs³⁰; the remaining ward patients with catheters might represent patients who are more likely to have long-term catheters that are challenging to discontinue, and thus could be more likely to have infections with resistant organisms.

Table 11. Percentage of Pathogens Reported from Adult Central Line-Associated Bloodstream Infections^a (CLABSIs) that Tested Nonsusceptible^b (NS) to Selected Antimicrobial Agents, by Location Type,^c 2015–2017

Pathogen, Antimicrobial	Hospital Wards ^c			Hospital ICUs			Hospital Oncology Units			LTACHs		
	No. Reported	% Tested	% NS ^b	No. Reported	% Tested	% NS ^b	No. Reported	% Tested	% NS ^b	No. Reported	% Tested	% NS ^b
<i>Staphylococcus aureus</i>	5,386			2,497			1,163			1,217		
OX/CEFOX/METH (MRSA)		91.0	53.8		90.7	50.0*		91.2	45.8*		96.5	77.6*
<i>Enterococcus faecium</i>	1,673			1,981			1,670			691		
Vancomycin (VRE)		94.9	78.3		94.5	84.5*		94.5	81.6*		98.3	84.4*
<i>Enterococcus faecalis</i>	2,636			2,117			664			1,314		
Vancomycin (VRE)		93.6	10.7		93.0	8.5*		89.9	7.4*		95.4	18.0*
Selected <i>Klebsiella</i> spp	3,344			1,708			1,441			1,158		
ESCs		81.9	25.2		83.0	29.6*		85.5	19.7*		92.3	49.6*
Carbapenems (CRE)		74.9	8.4		76.9	11.0*		73.6	4.9*		88.3	24.7*
MDR		90.9	15.7		90.5	20.2*		91.8	12.5*		97.8	40.0*
<i>Escherichia coli</i>	2,279			1,129			2,667			394		
ESCs		81.7	27.4		82.2	29.8		84.7	28.3		89.3	40.3*
Carbapenems (CRE)		74.6	1.2		73.9	2.4*		76.6	1.4		87.6	2.3
FQs		91.8	47.1		90.4	43.2*		90.3	65.3*		96.2	60.2*
MDR		91.0	14.1		88.8	14.4		90.1	17.6*		94.7	26.3*
<i>Enterobacter</i> spp	1,453			1,078			532			383		
Cefepime		74.2	10.5		74.5	12.2		77.6	10.9		77.0	17.3*
Carbapenems (CRE)		80.2	4.7		76.2	7.2*		78.0	7.2		86.2	9.4*
MDR-2		91.5	6.2		89.6	7.7		90.0	7.1		95.6	13.7*
<i>Pseudomonas aeruginosa</i>	1,407			1,061			701			495		
AMINOs		93.3	12.8		90.9	14.9		92.6	8.9*		96.2	23.5*
ESCs-2		92.0	21.9		90.2	26.5*		91.2	15.2*		94.9	37.7*
FQs-2		92.0	23.5		89.8	27.1		91.9	22.5		96.4	41.9*
Carbapenems-2		80.0	19.8		77.5	26.3*		81.9	19.2		88.7	37.4*
PIP/PIPTAZ		86.9	15.5		85.6	20.2*		88.2	12.5		87.7	29.3*
MDR-3		93.2	13.6		91.2	18.6*		92.4	11.6		97.2	29.9*
<i>Acinetobacter</i> spp	660			392			66			245		
Carbapenems-2		78.8	33.1		80.6	47.2*		75.8	12.0*		86.1	75.4*
MDR-4		94.1	34.6		92.6	46.6*		93.9	12.9*		99.6	76.6*

Note. ICUs, intensive care units; LTACHs, long-term acute-care hospitals; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*; OX/CEFOX/METH, oxacillin, cefoxitin, or methicillin; MRSA, methicillin-resistant *Staphylococcus aureus*; VRE, vancomycin-resistant *Enterococcus*; ESCs, extended-spectrum cephalosporins (cefepime, cefotaxime, ceftazidime, or ceftriaxone); CRE, carbapenem-resistant Enterobacteriaceae (imipenem, meropenem, doripenem, or ertapenem); MDR, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs, FQs, AMINOs, carbapenems (R only), PIPTAZ); MDR-2, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: cefepime, FQs, AMINOs, carbapenems (R only), PIPTAZ); FQs, fluoroquinolones (ciprofloxacin, levofloxacin, or moxifloxacin); AMINOs, aminoglycosides (amikacin, gentamicin, or tobramycin); ESCs-2, extended-spectrum cephalosporins (cefepime or ceftazidime); FQs-2, fluoroquinolones (ciprofloxacin or levofloxacin); PIP, piperacillin; PIPTAZ, piperacillin/tazobactam; Carbapenems-2, imipenem, meropenem, or doripenem; MDR-3, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ); MDR-4, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ, ampicillin/sulbactam).

*Statistically significantly different than %NS in hospital wards; $P < .05$.

^aSupplemental tables are available in the 2015–2017 Adult Antimicrobial Resistance Report Online Supplement that show the %NS separately for mucosal barrier injury laboratory-confirmed bloodstream infection (MBI-LCBI) and non-MBI-LCBIs within hospital oncology locations (<https://www.cdc.gov/nhsn/datastat/index.html>).

^bMRSA, VRE, and CRE data are presented as %R (ie, includes only those pathogens that tested resistant). All other phenotypes are shown as %NS (ie, includes pathogens that tested intermediate or resistant).

^cLocation types are mutually exclusive. “Hospital wards” includes step-down units, mixed acuity units, and specialty care areas.

We continue to notice low reporting frequencies of AST results for *Klebsiella* spp, *E. coli*, and *Enterobacter* spp with carbapenems and/or ESCs. To account for this, we compared the %NS for these phenotypes to an alternate %NS in which susceptibility results were imputed for those pathogens without AST results. The slight decrease

in %NS that resulted from this method is evidence that the NHSN’s typical %NS calculations may be a small overestimation of the true nonsusceptibility in the population, which has been suggested in prior NHSN reports. Given that any overestimation appears to be minimal (0.5% decrease for CRE and 1.2% decrease for ESC

Table 12. Percentage of Pathogens Reported from Adult Catheter-Associated Urinary Tract Infections (CAUTIs) that Tested Nonsusceptible^a (NS) to Selected Antimicrobial Agents, by Location Type,^b 2015–2017

Pathogen, Antimicrobial	Hospital Wards ^b			Hospital ICUs			Hospital Oncology Units			LTACHs			IRFs		
	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a
<i>Staphylococcus aureus</i>	1,102			655			60			166			83		
OX/CEFOX/METH (MRSA)		94.2	55.2		94.7	40.5*		96.7	46.6*		96.4	79.4*		96.4	63.8
<i>Enterococcus faecium</i>	1,208			1,034			115			765			33		
Vancomycin (VRE)		95.8	83.1		97.1	82.8		94.8	88.1		98.3	93.2*		97.0	84.4
<i>Enterococcus faecalis</i>	4,077			3,881			266			739			273		
Vancomycin (VRE)		93.2	7.2		92.6	4.2*		94.0	7.2		93.0	30.0*		93.4	8.2
Selected <i>Klebsiella</i> spp	6,368			5,775			337			1,882			704		
ESCs		85.3	22.1		85.1	16.6*		89.3	23.6		91.9	48.2*		84.5	15.5*
Carbapenems (CRE)		75.8	7.2		73.0	5.1*		76.0	5.5		83.4	23.1*		75.3	4.2*
MDR		94.8	14.1		93.8	9.6*		95.3	13.4		96.9	38.0*		94.3	8.6*
<i>Escherichia coli</i>	14,958			14,390			653			2,389			1,414		
ESCs		84.2	21.5		84.7	16.0*		84.8	24.9		90.7	32.3*		85.6	13.3*
Carbapenems (CRE)		74.3	0.6		72.7	0.3*		74.7	1.2		78.8	2.0*		74.4	0.3
FQs		97.0	37.9		96.6	31.1*		96.5	44.1*		98.2	58.2*		97.2	31.9*
MDR		94.2	9.9		93.4	6.9*		94.0	11.9		96.2	19.6*		94.7	6.6*
<i>Enterobacter</i> spp	2,112			2,120			111			555			226		
Cefepime		73.8	12.3		74.1	12.6		76.6	12.9		76.2	22.9*		73.5	9.6
Carbapenems (CRE)		76.5	7.0		76.7	6.5		75.7	8.3		81.8	13.7*		74.3	3.6
MDR-2		92.8	7.4		92.4	6.2		91.9	9.8		93.9	16.5*		92.0	5.3
<i>Pseudomonas aeruginosa</i>	5,935			5,047			300			2,570			629		
AMINOs		98.0	14.7		98.1	15.3		98.0	13.3		98.7	28.5*		97.3	13.6
ESCs-2		96.8	19.9		97.1	18.6		97.0	16.5		97.0	35.6*		97.0	13.0*
FQs-2		97.1	27.5		96.8	24.9*		96.3	29.1		98.3	48.2*		96.0	23.3*
Carbapenems-2		81.3	19.4		81.5	19.7		84.0	21.8		85.5	35.9*		79.2	13.1*
PIP/PIPTAZ		90.3	14.0		90.3	13.8		91.3	12.0		88.4	25.2*		91.3	8.5*
MDR-3		98.0	13.9		98.1	13.6		98.0	12.2		98.8	28.8*		97.1	8.3*
<i>Acinetobacter</i> spp	258			197			15			174			13		
Carbapenems-2		79.1	60.8		81.7	52.8		80.0	...		84.5	76.9*		61.5	...
MDR-4		96.1	62.5		98.5	53.1*		86.7	...		99.4	81.5*		100.0	...

Note. ICUs, intensive care units; LTACHs, long-term acute-care hospitals; IRFs, inpatient rehabilitation facilities; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*; OX/CEFOX/METH, oxacillin, ceftazidime, or methicillin; MRSA, methicillin-resistant *Staphylococcus aureus*; VRE, vancomycin-resistant *Enterococcus*; ESCs, extended-spectrum cephalosporins (cefepime, cefotaxime, ceftazidime, or ceftriaxone); CRE, carbapenem-resistant Enterobacteriaceae (imipenem, meropenem, doripenem, or ertapenem); MDR, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs, FQs, AMINOs, carbapenems (R only), PIPTAZ); MDR-2, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: cefepime, FQs, AMINOs, carbapenems (R only), PIPTAZ); FQs, fluoroquinolones (ciprofloxacin, levofloxacin, or moxifloxacin); AMINOs, aminoglycosides (amikacin, gentamicin, or tobramycin); ESCs-2, extended-spectrum cephalosporins (cefepime or ceftazidime); FQs-2, fluoroquinolones (ciprofloxacin or levofloxacin); PIP, piperacillin; PIPTAZ, piperacillin/tazobactam; Carbapenems-2, imipenem, meropenem, or doripenem; MDR-3, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ); MDR-4, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ, ampicillin/sulbactam).

*Statistically significantly different than %NS in hospital wards; $P < .05$.

^aMRSA, VRE, and CRE data are presented as %R (ie, includes only those pathogens that tested resistant). All other phenotypes are shown as %NS (ie, includes pathogens that tested intermediate or resistant). This metric is only calculated when at least 20 isolates have been tested.

^bLocation types are mutually exclusive. "Hospital wards" includes step-down units, mixed acuity units, and specialty care areas.

Table 13. Percentage of Pathogens Reported from Adult Possible Ventilator-Associated Pneumonias^a (PVAPs) that Tested Nonsusceptible^b (NS) to Selected Antimicrobial Agents, by Location Type,^c 2015–2017

Pathogen, Antimicrobial	Hospital Wards ^c			Hospital ICUs ^c			LTACHs		
	No. Reported	% Tested	% NS ^b	No. Reported	% Tested	% NS ^b	No. Reported	% Tested	% NS ^b
<i>Staphylococcus aureus</i>	58			2,673			102		
OX/CEFOX/METH (MRSA)		93.1	40.7		95.0	36.9		90.2	53.3
Selected <i>Klebsiella</i> spp	38			936			50		
ESC		92.1	31.4		87.3	14.3*		82.0	34.1
Carbapenems (CRE)		78.9	23.3		73.6	5.4*		88.0	11.4
MDR		94.7	25.0		93.4	8.7*		98.0	20.4
<i>Escherichia coli</i>	14			520			18		
ESC		100.0	...		85.8	23.8		100.0	...
Carbapenems (CRE)		71.4	...		73.7	1.0		83.3	...
FQ		100.0	...		94.8	32.7		94.4	...
MDR		100.0	...		93.1	11.8		94.4	...
<i>Enterobacter</i> spp	18			781			21		
Cefepime		88.9	...		75.9	6.7		81.0	...
Carbapenems (CRE)		77.8	...		77.5	3.5		81.0	...
MDR-2		100.0	...		96.2	3.1		100.0	9.5
<i>Pseudomonas aeruginosa</i>	63			1,192			157		
Aminos		98.4	22.6		98.4	13.6		98.1	29.9
ESC-2		98.4	30.6		97.1	25.9		95.5	44.7
FQ-2		98.4	53.2		96.6	26.7*		97.5	45.8
Carbapenems-2		85.7	42.6		84.6	26.3*		89.2	61.4*
PIP/PIPTAZ		85.7	25.9		90.6	21.7		87.9	34.8
MDR-3		98.4	29.0		98.2	16.8*		98.1	39.0
<i>Acinetobacter</i> spp	17			294			32		
Carbapenems-2		94.1	...		75.9	41.3		90.6	75.9
MDR-4		100.0	...		98.0	37.5		100.0	75.0

Note. ICUs, intensive care units; LTACHs, long-term acute-care hospitals; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*; OX/CEFOX/METH, oxacillin, ceftazidime, or methicillin; MRSA, methicillin-resistant *Staphylococcus aureus*; ESCs, extended-spectrum cephalosporins (cefepime, cefotaxime, ceftazidime, or ceftriaxone); CRE, carbapenem-resistant Enterobacteriaceae (imipenem, meropenem, doripenem, or ertapenem); MDR, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs, FQs, AMINOs, carbapenems (R only), PIPTAZ); MDR-2, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: cefepime, FQs, AMINOs, carbapenems (R only), PIPTAZ); FQs, fluoroquinolones (ciprofloxacin, levofloxacin, or moxifloxacin); AMINOs, aminoglycosides (amikacin, gentamicin, or tobramycin); ESCs-2, extended-spectrum cephalosporins (cefepime or ceftazidime); FQs-2, fluoroquinolones (ciprofloxacin or levofloxacin); PIP, piperacillin; PIPTAZ, piperacillin/tazobactam; Carbapenems-2, imipenem, meropenem, or doripenem; MDR-3, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ); MDR-4, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, Carbapenems-2, PIP/PIPTAZ, ampicillin/sulbactam).

*Statistically significantly different than %NS in hospital wards; $P < .05$.

^aPVAP is the only type of ventilator-associated event (VAE) for which a pathogen can be reported.

^bMRSA and CRE data are presented as %R (ie, includes only those pathogens that tested resistant). All other phenotypes are shown as %NS (ie, includes pathogens that tested intermediate or resistant). This metric is only calculated when at least 20 isolates have been tested. In most cases, *Enterococcus* species are excluded organisms from VAE surveillance, and therefore VRE data are not displayed.

^cLocation types are mutually exclusive. "Hospital wards" includes step-down units, mixed acuity units, and specialty care areas. For this table, "hospital ICUs" includes oncology ICUs.

nonsusceptibility), the NHSN will continue to publish %NS under the traditional definitions that are based strictly on the data reported. Comprehensive reporting of AST results is important to public health surveillance efforts and can allow for the consistent identification and tracking of emerging phenotypes.

Increases over time in the proportion of *Candida* spp tested for fluconazole susceptibility are encouraging, particularly for *C. parapsilosis*. The 2016 national guidelines for management of *Candida* infections recommend that all bloodstream and clinically relevant *Candida* isolates are tested for azole susceptibility.³¹ As more hospitals and laboratories adopt these recommendations, and data entry for antifungal susceptibility increases in the NHSN, we will be able to track a national resistance metric for *Candida* spp.

Our results have some limitations. The HAI, pathogen, and AST results are self-reported to the NHSN and are not validated by the CDC. Only the final AST interpretations are reported to the NHSN; therefore, differences may have existed among laboratory testing practices, reporting methods, and breakpoint interpretations that could not be accounted for in this analysis. This report does not account for any community-acquired infections or antimicrobial resistance that occurs outside of an inpatient healthcare facility. In addition, DA HAIs were classified as "adult" based on the location in which the patient resided; data from pediatric patients housed in adult location types at the time of their infection are thus included in this analysis.

Table 14. Percentage of Pathogens Reported from Adult Abdominal^a Surgical Site Infections (SSIs) that Tested Nonsusceptible^b (NS) to Selected Antimicrobial Agents, by Procedure Closure Technique, 2015–2017

Pathogen, Antimicrobial	Primary Closure ^c			Non-primary Closure ^d		
	No. Reported	% Tested	% NS ^b	No. Reported	% Tested	% NS ^b
<i>Staphylococcus aureus</i>	5,909			284		
OX/CEFOX/METH (MRSA)		94.4	55.8		95.4	64.2*
<i>Enterococcus faecium</i>	3,584			358		
Vancomycin (VRE)		96.1	53.1		94.4	61.5*
<i>Enterococcus faecalis</i>	7,584			469		
Vancomycin (VRE)		92.9	3.4		92.5	4.1
Selected <i>Klebsiella</i> spp	4,591			303		
ESC		82.4	14.3		85.8	21.5*
Carbapenems (CRE)		72.7	3.5		74.3	8.0*
MDR		93.6	6.4		93.4	12.7*
<i>Escherichia coli</i>	15,302			1,076		
ESC		81.7	18.5		84.9	19.3
Carbapenems (CRE)		73.5	0.6		73.8	1.8*
FQ		94.7	34.7		94.1	36.0
MDR		92.8	7.8		92.6	9.4
<i>Enterobacter</i> spp	3,471			220		
Cefepime		71.7	7.3		75.0	13.9*
Carbapenems (CRE)		76.4	5.4		81.4	7.3
MDR-2		93.3	2.6		95.9	4.7
<i>Pseudomonas aeruginosa</i>	4,405			382		
Aminos		96.6	6.8		97.4	8.6
ESC-2		95.4	12.3		95.5	21.9*
FQ-2		96.0	12.3		96.6	16.8*
Carbapenems-2		78.2	11.2		79.3	19.5*
PIP/PIPTAZ		89.9	9.6		86.1	15.5*
MDR-3		96.6	5.5		96.6	9.8*
<i>Acinetobacter</i> spp	118			18		
Carbapenems-2		81.4	32.3		72.2	...
MDR-4		93.2	33.6		94.4	...

Note. Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*; OX/CEFOX/METH, oxacillin, ceftazidime, or methicillin; MRSA, methicillin-resistant *Staphylococcus aureus*; VRE, vancomycin-resistant *Enterococcus*; ESCs, extended-spectrum cephalosporins (cefepime, cefotaxime, ceftazidime, or ceftriaxone); CRE, carbapenem-resistant Enterobacteriaceae (imipenem, meropenem, doripenem, or ertapenem); MDR, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs, FQs, AMINOs, carbapenems (R only), PIPTAZ); MDR-2, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: cefepime, FQs, AMINOs, carbapenems (R only), PIPTAZ); FQs, fluoroquinolones (ciprofloxacin, levofloxacin, or moxifloxacin); AMINOs, aminoglycosides (amikacin, gentamicin, or tobramycin); ESCs-2, extended-spectrum cephalosporins (cefepime or ceftazidime); FQs-2, fluoroquinolones (ciprofloxacin or levofloxacin); PIP, piperacillin; PIPTAZ, piperacillin/tazobactam; Carbapenems-2, imipenem, meropenem, or doripenem; MDR-3, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ); MDR-4, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ, ampicillin/sulbactam).

*Statistically significantly different than %NS among SSIs following primarily closed procedures; $P < .05$.

^aConsists of 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.

^bMRSA, VRE, and CRE data are presented as %R (ie, includes only those pathogens that tested resistant). All other phenotypes are shown as %NS (ie, includes pathogens that tested intermediate or resistant). This metric is only calculated when at least 20 isolates have been tested.

^cPrimary closure technique is defined as the closure of a surgical wound in which the skin level has been closed, by any means, during the original surgery. In this table, 79% of primary closure abdominal SSI pathogens are from colon procedures.

^dNon-primary closure technique is defined as the closure of a surgical wound in which the skin level has been left completely open. In this table, 87% of non-primary closure abdominal SSI pathogens are from colon procedures.

This report provides updated information on pathogens and resistance phenotypes most commonly reported from HAIs in US healthcare facilities, and it facilitates a greater understanding of the national burden of HAIs and antimicrobial-resistant pathogens.

These data have the potential to inform infection prevention strategies and, when tracked over time, to provide feedback on the impact of these strategies. Healthcare facilities are encouraged to regularly review their facility-specific pathogen and antimicrobial resistance

Table 15. Percentage of Pathogens Reported from Adult Surgical Site Infections (SSIs) that Tested NonSusceptible^a (NS) to Selected Antimicrobial Agents, by Surgical Category,^b 2015–2017

Pathogen, Antimicrobial	All Surgery Types ^c			Abdominal ^d			Orthopedic ^e			Ob/Gyn ^f			Cardiac ^g		
	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a	No. Reported	% Tested	% NS ^a
<i>Staphylococcus aureus</i>	26,970			6,193			13,968			3,092			2,331		
OX/CEFOX/METH (MRSA)		94.2	41.9		94.4	56.2		94.2	38.0*		94.7	38.9*		94.3	36.6*
<i>Enterococcus faecium</i>	4,515			3,942			324			139			53		
Vancomycin (VRE)		95.9	55.6		96.0	53.8		94.4	77.8*		95.0	35.6*		98.1	78.8*
<i>Enterococcus faecalis</i>	12,267			8,053			1,779			1,862			281		
Vancomycin (VRE)		92.7	3.4		92.9	3.5		91.8	5.3*		92.2	1.0*		92.9	6.1*
Selected <i>Klebsiella</i> spp	7,789			4,894			1,167			917			518		
ESC		81.9	13.7		82.6	14.8		82.0	14.8		77.4	6.8*		82.4	11.2*
Carbapenems (CRE)		72.6	3.1		72.8	3.8		71.5	2.0*		72.1	0.8*		74.1	2.6
MDR		93.2	6.3		93.6	6.8		92.1	7.3		92.1	2.4*		93.6	5.6
<i>Escherichia coli</i>	21,746			16,378			1,737			2,778			478		
ESC		81.8	18.2		81.9	18.6		82.3	16.9		79.7	15.4*		85.6	21.0
Carbapenems (CRE)		73.4	0.6		73.5	0.7		71.9	0.2*		72.1	0.3*		78.9	0.3
FQ		94.4	32.1		94.7	34.8		93.1	26.9*		94.2	18.9*		93.7	32.4
MDR		92.7	7.4		92.7	7.9		91.9	6.4*		92.7	4.3*		94.1	9.3
<i>Enterobacter</i> spp	7,178			3,691			1,797			793			538		
Cefepime		70.4	5.5		71.9	7.7		68.1 ^h	4.0*		67.0 ^h	1.1*		71.0	3.4*
Carbapenems (CRE)		74.7	3.7		76.7	5.5		71.8	1.9*		72.9	0.7*		74.0	2.0*
MDR-2		92.5	1.9		93.5	2.8		91.8	1.5*		89.8	0.4*		92.9	0.6*
<i>Pseudomonas aeruginosa</i>	8,956			4,787			2,184			907			658		
Aminos		96.3	5.8		96.7	7.0		95.8	4.4*		96.0	3.8*		96.8	5.2
ESC-2		95.0	10.2		95.4	13.0		94.2	8.1*		95.3	2.9*		95.6	8.7*
FQ-2		95.5	11.0		96.1	12.7		95.0	9.5*		95.8	4.8*		95.9	11.3
Carbapenems-2		77.8	9.1		78.3	11.8		76.1	6.1*		80.2	3.6*		77.2	8.3*
PIP/PIPTAZ		89.6	7.7		89.6	10.1		89.9	6.0*		88.6	2.9*		91.3	5.2*
MDR-3		96.3	4.5		96.6	5.8		95.7	2.7*		96.3	1.3*		96.7	5.0
<i>Acinetobacter</i> spp	625			136			289			96			44		
Carbapenems-2		77.0	26.6		80.1	33.9		76.8	31.1		75.0	6.9*		70.5	32.3
MDR-4		94.1	26.5		93.4	35.4		94.1	32.4		96.9	4.3*		86.4	28.9

Note. Ob/Gyn, obstetrical and gynecological; Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*; OX/CEFOX/METH, oxacillin, cefoxitin, or methicillin; MRSA, methicillin-resistant *Staphylococcus aureus*; VRE, vancomycin-resistant *Enterococcus*; ESCs, extended-spectrum cephalosporins (cefepime, cefotaxime, ceftazidime, or ceftriaxone); CRE, carbapenem-resistant Enterobacteriaceae (imipenem, meropenem, doripenem, or ertapenem); MDR, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs, FQs, AMINOs, carbapenems (R only), PIPTAZ); MDR-2, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: cefepime, FQs, AMINOs, carbapenems (R only), PIPTAZ); FQs, fluoroquinolones (ciprofloxacin, levofloxacin, or moxifloxacin); AMINOs, aminoglycosides (amikacin, gentamicin, or tobramycin); ESCs-2, extended-spectrum cephalosporins (cefepime or ceftazidime); FQs-2, fluoroquinolones (ciprofloxacin or levofloxacin); PIP, piperacillin; PIPTAZ, piperacillin/tazobactam; Carbapenems-2, imipenem, meropenem, or doripenem; MDR-3, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ); MDR-4, multidrug-resistant (NS to 1 drug in at least 3 of the following classes: ESCs-2, FQs-2, AMINOs, carbapenems-2, PIP/PIPTAZ, ampicillin/sulbactam).

^hIf the percentage tested is <70%, caution should be used when interpreting the %NS.

*Statistically significantly different than %NS among abdominal SSIs; $P < .05$.

^aMRSA, VRE, and CRE data are presented as %R (ie, includes only those pathogens that tested resistant). All other phenotypes are shown as %NS (ie, includes pathogens that tested intermediate or resistant).

^bThe 4 most frequently reported surgical categories by pathogen volume are shown.

^cConsists of all NHSN operative procedure codes, and is not limited to the 4 surgical categories shown in this table.

^dAppendix 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.

^eOpen reduction of fracture, hip prosthesis, knee prosthesis, limb amputation, spinal fusion/refusion, and laminectomy.

^fCesarean section, abdominal hysterectomy, ovarian surgery, and vaginal hysterectomy.

^gCardiac surgery, heart transplant, coronary artery bypass graft with chest incision with or without donor incision, pacemaker surgery, and thoracic surgery.

Table 16. Estimated Effect of Incomplete Reporting of Carbapenem and Extended-Spectrum Cephalosporin Susceptibility Results on the National^a Percentage Nonsusceptible^b (%NS), by Pathogen and Phenotype, 2015–2017

Pathogen	No. Reported	CRE				ESC-NS			
		As Reported to NHSN		With Inferred Susceptibilities ^c		As Reported to NHSN		With Inferred Susceptibilities ^d	
		% Tested	% NS ^b	% Tested	% NS ^b	% Tested	% NS ^b	% Tested	% NS ^b
<i>Enterobacter</i> spp	8,205	77.4	6.2	78.1	6.1
<i>Escherichia coli</i>	36,610	73.8	0.7	91.5	0.5	84.3	20.5	91.4	18.9
Selected <i>Klebsiella</i> spp	19,947	74.7	6.9	91.6	5.6	84.7	21.1	86.9	20.6
Total	CRE: 64,762 ESC-NS: 56,557	74.5	3.3	89.8	2.8	84.4	20.7	89.8	19.5

Note. CRE, carbapenem-resistant Enterobacteriaceae (imipenem, meropenem, doripenem, or ertapenem); ESC-NS, extended-spectrum cephalosporin nonsusceptible (cefepime, cefotaxime, ceftazidime, or ceftriaxone); Selected *Klebsiella* spp, *K. oxytoca* and *K. pneumoniae*.

^aThis table consists of adult device-associated infections from acute-care hospitals: central line-associated bloodstream infections (CLABSIs), catheter-associated urinary tract infections (CAUTIs), and possible ventilator-associated pneumonias (PVAPs). Data from inpatient rehabilitation facilities (IRFs) and long-term acute-care hospitals (LTACHs) were excluded.

^bCRE data are presented as %R (ie, includes only those pathogens that tested resistant). ESC-NS data are presented as %NS (ie, includes pathogens that tested intermediate or resistant).

^cIf a pathogen was reported as “not tested” to carbapenems, susceptibility was inferred as susceptible (S) if the pathogen was susceptible to at least 2 of the following antimicrobials: ampicillin, ampicillin/sulbactam, amoxicillin/clavulanic acid, piperacillin/tazobactam, cefazolin, ceftiofur, or cefotetan. Inferring susceptibility effectively raises the number of tested isolates (ie, the denominator of %NS).

^dIf a pathogen was reported as “not tested” to ESCs, susceptibility was inferred as susceptible (S) if the pathogen tested susceptible to at least 2 of the following antimicrobials: ampicillin, aztreonam, or cefazolin. Inferring susceptibility effectively raises the number of tested isolates (ie, the denominator of %NS). Due to *Enterobacter* spp’s inducible resistance to some ESCs, the inferred susceptibility method for ESC-NS was not applied to *Enterobacter* spp.

data, particularly for high-risk units, to implement targeted prevention efforts. Aggressive support from public health is necessary to reduce the spread of resistant organisms in healthcare settings, particularly those with high acuity patients and longer lengths of stay, such as hospital ICUs and LTACHs.

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APPENDICES

A1. *Candida* Species Reported From Selected Adult Healthcare-Associated Infections¹ (HAIs) in Acute Care Hospitals and Tested for Susceptibility to Fluconazole, 2011-2017

	2011-2014		2015-2017	
	# Reported	% Tested	# Reported	% Tested
<i>Candida albicans</i>	7,994	21.8	10,376	24.3
<i>Candida glabrata</i>	3,454	32.9	4,649	34.8
<i>Candida parapsilosis</i>	1,627	34.2	1,995	38.9

1. This table is limited to central line-associated bloodstream infections (CLABSIs) and surgical site infections (SSIs). Data from inpatient rehabilitation facilities (IRFs) and long-term acute care hospitals (LTACHs) are excluded from this table. Due to NHSN definition changes over time and the low volume of *Candida* reported for certain HAIs, catheter-associated urinary tract infections (CAUTIs), possible ventilator-associated pneumonias (PVAPs), and ventilator-associated pneumonias (VAPs) are excluded from this table.

A2. Organisms Included in NHSN's 'Enterobacter spp' Group for this Report

<i>Enterobacter</i> , not otherwise specified
<i>Enterobacter aerogenes</i>
<i>Enterobacter amnigenus</i>
<i>Enterobacter asburiae</i> ¹
<i>Enterobacter cancerogenus</i>
<i>Enterobacter cloacae</i> ¹
<i>Enterobacter cloacae</i> complex ¹
<i>Enterobacter cowanii</i>
<i>Enterobacter dissolvens</i>
<i>Enterobacter gergoviae</i>
<i>Enterobacter hormaechei</i> ¹
<i>Enterobacter intermedius</i>
<i>Enterobacter kobei</i> ¹
<i>Enterobacter ludwigii</i> ¹
<i>Enterobacter nimipressuralis</i> ¹
<i>Enterobacter pyrinus</i>

1. These species are considered part of the "Enterobacter cloacae complex" group.

A3. Organisms Included in NHSN's 'Coagulase-Negative Staphylococci' Group for this Report

Coagulase-negative staphylococci, not otherwise specified
<i>Staphylococcus arlettae</i>
<i>Staphylococcus auricularis</i>
<i>Staphylococcus capitis</i>
<i>Staphylococcus capitis capitis</i>
<i>Staphylococcus capitis urealyticus</i>
<i>Staphylococcus caprae</i>
<i>Staphylococcus carnosus</i>
<i>Staphylococcus carnosus carnosus</i>
<i>Staphylococcus carnosus utilis</i>
<i>Staphylococcus chromogenes</i>
<i>Staphylococcus cohnii</i>
<i>Staphylococcus cohnii cohnii</i>
<i>Staphylococcus cohnii urealyticus</i>
<i>Staphylococcus condimenti</i>
<i>Staphylococcus epidermidis</i>
<i>Staphylococcus equorum</i>
<i>Staphylococcus equorum equorum</i>
<i>Staphylococcus equorum linens</i>
<i>Staphylococcus felis</i>
<i>Staphylococcus fleurettii</i>
<i>Staphylococcus gallinarum</i>
<i>Staphylococcus haemolyticus</i>
<i>Staphylococcus hominis</i>
<i>Staphylococcus hominis hominis</i>
<i>Staphylococcus hominis novobioceticus</i>
<i>Staphylococcus kloosii</i>
<i>Staphylococcus lentus</i>
<i>Staphylococcus lugdunensis</i>
<i>Staphylococcus muscae</i>
<i>Staphylococcus nepalensis</i>

(Continued)

A3. (Continued)

<i>Staphylococcus pasteurii</i>
<i>Staphylococcus pettenkoferi</i>
<i>Staphylococcus piscifermentans</i>
<i>Staphylococcus saccharolyticus</i>
<i>Staphylococcus saprophyticus</i>
<i>Staphylococcus saprophyticus bovis</i>
<i>Staphylococcus saprophyticus saprophyticus</i>
<i>Staphylococcus schleiferi</i>
<i>Staphylococcus schleiferi schleiferi</i>
<i>Staphylococcus sciuri</i>
<i>Staphylococcus sciuri carnaticus</i>
<i>Staphylococcus sciuri rodentium</i>
<i>Staphylococcus scuiroi scuiroi</i>
<i>Staphylococcus simulans</i>
<i>Staphylococcus succinus</i>
<i>Staphylococcus succinus casei</i>
<i>Staphylococcus succinus succinus</i>
<i>Staphylococcus vitulinus</i>
<i>Staphylococcus warneri</i>
<i>Staphylococcus xylosum</i>

A4. Organisms Included in NHSN's 'Viridans Group Streptococci' Group for this Report

Viridans group streptococci, not otherwise specified
Alpha-hemolytic <i>Streptococcus</i> species, not <i>Streptococcus pneumoniae</i>
Small-colony-forming beta-hemolytic group A streptococci
Small-colony-forming beta-hemolytic group C streptococci
Small-colony-forming beta-hemolytic group G streptococci
<i>Streptococcus anginosus</i> group
<i>Streptococcus anginosus</i>
<i>Streptococcus anginosus-constellatus</i>
<i>Streptococcus australis</i>
<i>Streptococcus bovis</i> group
<i>Streptococcus constellatus</i>
<i>Streptococcus constellatus constellatus</i>
<i>Streptococcus constellatus pharyngis</i>
<i>Streptococcus criceti</i>
<i>Streptococcus cristatus</i>
<i>Streptococcus dentisani</i>
<i>Streptococcus downei</i>
<i>Streptococcus entericus</i>
<i>Streptococcus equinus</i>
<i>Streptococcus ferus</i>
<i>Streptococcus gallolyticus</i>
<i>Streptococcus gallolyticus gallolyticus</i>

(Continued)

A4. (Continued)

<i>Streptococcus gallolyticus macedonicus</i>
<i>Streptococcus gallolyticus pasteurianus</i>
<i>Streptococcus gordonii</i>
<i>Streptococcus infantarius</i>
<i>Streptococcus infantarius infantarius</i>
<i>Streptococcus infantis</i>
<i>Streptococcus intermedius</i>
<i>Streptococcus lutetiensis</i>
<i>Streptococcus mitis</i>
<i>Streptococcus mitis</i> group
<i>Streptococcus mutans</i>
<i>Streptococcus mutans</i> group
<i>Streptococcus oralis</i>
<i>Streptococcus parasanguinis</i>
<i>Streptococcus peroris</i>
<i>Streptococcus rattii</i>
<i>Streptococcus salivarius</i>
<i>Streptococcus salivarius</i> group
<i>Streptococcus salivarius salivarius</i>
<i>Streptococcus salivarius thermophilus</i>
<i>Streptococcus sanguinis</i>
<i>Streptococcus sanguinis</i> group
<i>Streptococcus sobrinus</i>
<i>Streptococcus tigurinus</i>
<i>Streptococcus vestibularis</i>
<i>Streptococcus</i> , group F