Also, 64 Non-Hispanic Blacks (41%) died within 1 year of their first specimen collection date compared to 92 Non-Hispanic Whites (23.3%). Non-Hispanic Blacks with CP-CRE who died within 1 year had a mortality rate of 5.6 per 100,000 (95% CI, 4.21–6.94) Black population, which was 1.6 times higher than Non-Hispanic White persons at 3.5 per 100,000 (95% CI, 2.94–3.95; χ^2 $P < .001$) White population. **Conclusions:** Despite a lower mean age, non-Hispanic Black CP-CRE cases had a higher 1-year mortality rate than non-Hispanic Whites. Racial and ethnicity data often are missing or incomplete from surveillance data. Data linkages can be a valuable tool to gather additional clinical and demographic data that may be missing from public health surveillance data to improve our understanding of health disparities. Recognition of these health disparities among CRE can provide an opportunity for public health to create more targeted interventions and educational outreach.

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Developing national benchmarks for antimicrobial resistance—NHSN, 2019

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Background: The emergence and spread of drug-resistant pathogens continues to significantly impact patient safety and healthcare systems. Although antimicrobial susceptibility test (AST) results of clinical specimens are used by individual facilities for antimicrobial resistance surveillance, accurate tracking and benchmark comparison of a facility's antimicrobial resistance using national data requires risk-adjusted methods to be more meaningful. The CDC NHSN Antimicrobial Resistance (AR) Option collects patient-level, deduplicated, isolate information, including AST results, for >20 organisms from cerebrospinal fluid, lower respiratory tract (LRT), blood, and urinary specimens. To provide risk-adjusted national benchmarks, we developed prediction models for incidence of hospital-onset isolates with antimicrobial resistance. **Methods:** We analyzed AST results of isolates reported through the NHSN AR Option for January through December 2019. Isolates from facilities that had >10% missing AST results for the organism-drug combinations or from hospitals that used outdated breakpoints were excluded. We assessed associations between facility-level factors and incidence rates of hospital-onset (specimen collected 3 days or more after hospital admission) isolates of specific drug-resistant phenotypes from blood, LRT, and urinary specimens. Factors included number of beds, length of stay, and prevalence of community onset isolates of the same phenotype. Drug-resistant phenotypes assessed included methicillin-resistant *Staphylococcus aureus* (MRSA), multidrug-resistant (MDR) *Pseudomonas aeruginosa*, carbapenem-resistant Enterobacterales (CRE), fluoroquinolone-resistant *Pseudomonas aeruginosa*, fluoroquinolone-resistant Enterobacterales, and extended-spectrum cephalosporin-resistant Enterobacterales. Isolates of different phenotypes and from different specimen sources were modeled separately. Negative binomial regression was used to evaluate the factors associated with antimicrobial resistance incidence. Variable entry into the models is based on significance level P Among the models, 1 for each drug-resistant phenotype-specimen type combination, the number of isolates with AST results ranged from 718 (*Pseudomonas aeruginosa*—fluoroquinolones, blood) to 16,412 (Enterobacterales—fluoroquinolones, urine). The pooled incidence rate was highest for fluoroquinolone-resistant Enterobacterales in urinary specimens (0.2179 isolates per 1,000 patient days) among all phenotype-specimen combinations evaluated (Table 1). The incidence of drug-resistant isolates was consistently associated with community-onset prevalence across models evaluated. Other associated factors varied across phenotype-specimen combinations (Table 2). **Conclusions:** We developed statistical models to predict facility-level incidence rates of hospital-onset antimicrobial resistant isolates based on community-onset drug-resistant prevalence and facility characteristics. These models will enable facilities to compare antimicrobial resistance rates to the national benchmarks and therefore to inform their antimicrobial stewardship and infection prevention efforts.

Table 1: Incidence of hospital-onset resistant isolates, by specimen type

Drug-resistant phenotype	Specimen type	Number of facilities in analysis dataset	Number of drug resistant isolates	Number of tested isolates	Pooled resistant isolate rate, per 1000 patient-days	Resistant isolate rate per 1000 patient-days, Median(Q1-Q3)
Pseudomonas aeruginosa-Fluoroquinolones	Blood	184	114	718	0.0074	0(0-0.012)
	LRT	296	1307	5640	0.0688	0.039(0-0.083)
	Urine	294	535	3092	0.0281	0.016(0-0.044)
Pseudomonas aeruginosa - Multidrug	Blood	191	96	783	0.0059	0(0-0.007)
	LRT	306	1084	6109	0.0534	0.027(0-0.067)
	Urine	316	329	3383	0.0158	0(0-0.022)
Enterobacterales[a]-Fluoroquinolones	Blood	274	907	3130	0.0488	0.0240(0-0.050)
	LRT	289	1255	7089	0.0677	0.043(0.015-0.088)
	Urine	344	4176	16412	0.2179	0.166(0.0845-0.0264)
Staphylococcus aureus-Methicillin	Blood	285	971	2330	0.0501	0.04(0.018-0.067)
	LRT	308	3865	7856	0.1910	0.16(0.085-0.242)
	Urine	207	312	599	0.0193	0.018(0-0.033)
Enterobacterales[a]-Carbapenem	Blood	181	91	2370	0.0070	0(0-0)
	LRT	203	190	5641	0.0136	0(0-0.015)
	Urine	241	168	12596	0.0117	0(0-0.009)
Enterobacterales[a]-Extended-spectrum cephalosporin	Blood	237	873	3036	0.0451	0.027(0-0.052)
	LRT	242	1837	7017	0.1091	0.077(0.031-0.127)
	Urine	291	3165	15246	0.1814	0.125(0.057-0.207)

a. Enterobacterales defined as E. coli, Klebsiella pneumoniae, K. oxytoca, and Enterobacter isolates
b. LRT: lower respiratory tract, Number of ICU beds: Number of beds in intensive care units (ICU), Number of beds: Number of hospital beds, ICU percent: Percentage of hospital beds in ICU among all hospital beds, Antibiotic test: Indicator of whether susceptibility testing is done onsite or offsite, Community-onset prevalence: Prevalence of community onset isolates of the same phenotype (per 10,000 admissions), this variable is relevant for hospital onset resistance infection model

Table 2: Risk-adjustment summary for hospital-onset antimicrobial resistant isolates

Drug-resistant phenotype	Specimen type	Community-onset prevalence	Hospital length of stay	Number of beds	Number of ICU beds	ICU percent	Facility type	Medical affiliation	Medical type
Pseudomonas aeruginosa-Fluoroquinolones	Blood	✓							
	LRT	✓		✓					
	Urine	✓							
Pseudomonas aeruginosa - Multidrug	Blood	✓							
	LRT	✓			✓				
	Urine	✓	✓						
Enterobacterales[a]-Fluoroquinolones	Blood	✓	✓	✓					
	LRT	✓		✓					
	Urine	✓	✓						
Staphylococcus aureus-Methicillin	Blood	✓	✓		✓				
	LRT	✓	✓						
	Urine	✓				✓			
Enterobacterales[a]-Carbapenem	Blood	✓							
	LRT	✓	✓						
	Urine	✓	✓						
Enterobacterales[a]-Extended-spectrum cephalosporin	Blood	✓	✓						
	LRT	✓		✓					
	Urine	✓	✓						

a. Enterobacterales defined as E. coli, Klebsiella pneumoniae, K. oxytoca, and Enterobacter isolates
b. LRT: lower respiratory tract, Number of ICU beds: Number of beds in intensive care units (ICU), Number of beds: Number of hospital beds, ICU percent: Percentage of hospital beds in ICU among all hospital beds, Antibiotic test: Indicator of whether susceptibility testing is done onsite or offsite, Community-onset prevalence: Prevalence of community onset isolates of the same phenotype (per 10,000 admissions), this variable is relevant for hospital onset resistance infection model

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Poster Presentation - Poster Presentation
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Findings from healthcare-associated infections data validation attestation in California general acute-care hospitals

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Background: Accurate and complete hospital healthcare-associated infection (HAI) data are essential to inform facility-level HAI prevention efforts and to ensure the validity and reliability of annual public reports. We implemented a validation attestation survey to assess and improve the HAI data reported by California hospitals via NHSN. **Methods:** The California Department of Public Health (CDPH) HAI Program invited all 401 general acute-care hospitals in California to participate in an annual HAI validation attestation survey in 2021. The survey was designed to be completed by the person with primary responsibility for HAI surveillance and reporting consistent with NHSN protocols and California laws. Survey questions addressed HAI reporting knowledge and practices and surgical procedures performed, and they included 3 hypothetical scenarios evaluating hospital application of HAI surveillance, decision making, and reporting methods. **Results:** We received responses from 345 hospitals (86%). For the 3 hypothetical scenarios, 171 hospitals (49.6%) correctly answered all 3 questions, 110 hospitals (31.9%) answered 2 questions correctly, 52 (15.1%) hospitals answered 1 question correctly, and 12 hospitals (3.5%) answered zero questions correctly. We did not detect a statistically

significant association between facility type (ie, acute-care hospital, critical access hospital, long-term acute-care hospital, or rehabilitation hospital or unit) and the probability of getting all questions correct (Fisher exact P = .42). Of the 303 hospitals (88.0%) that perform at least 1 of the 28 surgical procedures reportable in California, 269 (88.8%) apply CDPH-recommended postoperative ICD-10 diagnosis flag codes to identify records that might indicate a possible surgical site infection (SSI). Moreover, ~289 (84.0%) hospitals confirmed that someone at their facility reviews CDPH quality assurance–quality control reports to verify the accuracy and completeness of their hospital's reported HAI data. In 321 hospitals (93.0%) decisions about which infections are reported to NHSN are made solely by the infection preventionists or hospital epidemiologists, who are thoroughly familiar and follow NHSN protocol, definitions, and criteria. **Conclusions:** Most hospitals reported following best practices for evaluating records for SSIs; however, only half responded correctly to all 3 hypothetical scenarios. Our results highlight the need for ongoing education on HAI surveillance, decision making and reporting methods, and external HAI data validation in hospitals. This survey could serve as a model for other states that work with hospitals to improve HAI surveillance data and to ensure the integrity of public reports. Future research will link the results of this survey to NHSN validation audits.

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Lessons learned: Characteristics of first-year COVID-19 hospital outbreaks

Sophie Solar; Emily Blake; Sithembile Chithenga; Mefruz Haque; Anitra Denson; Renee Zell; Jennifer Steppe; Anil Mangla and Preetha Iyengar

Background: At the start of the COVID-19 pandemic, the DC Department of Health (DC Health) mandated new case reporting for early outbreak detection: (1) weekly healthcare personnel (HCP) absenteeism line lists indicating staff absent for confirmed or suspected SARS-CoV-2, (2) daily line lists of all SARS-CoV-2–positive inpatients, and (3) hospital contact tracing. Between March 27, 2020, and December 31, 2020, DC Health detected 36 confirmed and 14 suspected hospital outbreaks, of which only 18% (8 confirmed and 1 suspect) were known to the affected hospital. DC Health learned which outbreaks warranted early or aggressive intervention by tracking outbreak characteristics across its jurisdiction. This allowed prioritization of during surges when it was difficult for DC Health and hospital staff to investigate every outbreak. **Methods:** Potential outbreaks in short-stay and inpatient rehabilitation hospitals were flagged after identifying SARS-CoV-2 hospital-onset (HO) inpatients or staff clusters on line lists. Variables of interest in line lists included specimen collection and hospital admission dates, units or departments, and patient contact. Facility contact tracing by infection preventionists further verified epidemiological links among cases. Outbreak details were systematically tracked in a locally developed REDCap database and were analyzed if they had an initial case, outbreak start date, or an investigation start date in 2020. Frequency procedures, SQL statements, and date calculations were computed using SAS Enterprise Guide version 8.3 software. **Results:** Confirmed outbreaks had an average of 6.92 (range, 0–32) HCP and 2.58 (range, 0–22) patient cases, with 69% being confirmed-HO cases and 31% probable HO. Moreover, 53% of confirmed outbreaks occurred in the following departments: cardiac, behavioral health, intensive care, and environmental services (EVS)/facilities. All of these departments had recurrent outbreaks. Behavioral health, medical and cardiac units had the highest number of patient cases. On average, confirmed outbreak investigations lasted 24.6 days, with outbreaks prolonged in the ICU (40.25 days) and the medical unit (37.67 days). Top triggers for investigations ultimately classified as confirmed outbreaks were (1) positive symptomatic HCP, (2) confirmed-HO cases, and (3) exposures from positive HCP. **Conclusions:** The dynamic nature of COVID-19 created challenges in detecting and responding to hospital outbreaks. Developing a low-resource outbreak tracking system helped identify outbreak types and triggers that warranted early or aggressive interventions. Understanding the characteristics of hospital outbreaks was critical for maximizing infection control resources during surges of infectious disease outbreaks, such as COVID-19. Hospitals or local health departments could adapt this system to meet their needs.

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Susceptibility results discrepancy analysis between NHSN Antibiotic Resistance (AR) Option and laboratory instrument data

Youssoufou Ouedraogo; Christopher Evans; Daniel Muleta and Christopher Wilson

Background: The NHSN Antibiotic Resistance (AR) Option can serve as a useful tool for tracking antibiotic-resistant infections and can aid in the development of inpatient antibiograms. We recently described the frequency of antibiotic suppression in NHSN AR Option data. In this analysis, we describe the effects of suppression on practical uses of the NHSN AR Option, specifically selected agent antibiogram development, and detection of reportable conditions. **Methods:** Antibiotic susceptibility data were collected from the NHSN AR Option and commercial automated antimicrobial susceptibility testing instruments (cASTI) from 3 hospital networks. Data were obtained from January 1, 2017, to December 31, 2018. The clinical susceptibility data for third-generation cephalosporins and carbapenems against carbapenem-resistant Enterobacterales (CRE), *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* were included. Susceptibility results were defined as suppressed when susceptibility results were observed from the laboratory instrument but not from NHSN data. For the overall percentage susceptibility estimation, isolates with <30 susceptibility results were excluded. Percentage susceptibility of NHSN results were compared to their counterparts from cASTI. **Results:** Of the 852 matched isolates in the primary analysis, 804 had at least 1 suppressed result. Of the 804 isolates, 16.9% were *P. aeruginosa*, 67.3% by *E. coli*, and 11.1% by *Klebsiella* spp. The following pathogen–drug combinations had no difference observed in the percentage susceptible between the 2 systems: ceftazidime tested against *P. aeruginosa*, ceftriaxone tested against *Klebsiella* spp, ertapenem tested against *Klebsiella* spp, imipenem tested against *E. coli* and *P. aeruginosa*, and meropenem tested against *P. aeruginosa*. Significant differences were observed for the following drugs tested against *E. coli*: ceftazidime (11.1%), cefotaxime (8.6%), and ceftriaxone (8.3%). In the NHSN AR Option, the following isolates showed suppressed results related to their phenotypic case definition: 17 (3%) CRE isolates, 7 (28%) carbapenem-resistant *Acinetobacter baumannii* (CRAB) isolates, 511 (93.2%) extended spectrum β-lactamase (ESBL) isolates, and 94 (66.7%) carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) isolates. **Conclusions:** For select isolates, notably *E. coli*, we observed a large difference in the percentage of susceptible isolates reported into the NHSN AR Option compared to the cASTI data. This difference significantly limits the ability of the AR Option to create valid antibiograms for select pathogen–drug combinations. Moreover, significant numbers of CRAB, ESBL, and CRPA isolates would not be identified from NHSN AR Option because of suppression. This finding warrants the need for antimicrobial stewardship teams to regularly assess the impact of selective reporting in identifying pathogens of public health importance.

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