increased from 8.4 per 100,000 to 10.4 per 100,000 (6.7% per year; $P < .01$) (Fig. 1). Significant increases in MSSA BSI rates were also observed for nondialysis HACO cases (9.3 per 100,000 to 11.1 per 100,000; 7.8% per year; $P < .01$) but not dialysis HACO cases (1,823.2 per 100,000 to 1,857.4 per 100,000; 1.4% per year; $P = .59$). Healthcare risk factors for HACO cases were hospitalization in the previous year (82%), surgery (31%), dialysis (27%), and long-term care facility residence (19%). **Conclusions:** MSSA BSI rates increased from 2016–2019 overall, among all epidemiologic classes, and among nondialysis HACO cases. Efforts to prevent MSSA BSIs among individuals with healthcare risk factors, particularly those related to hospitalization, might have an impact on MSSA BSI rates.

Funding: None
Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2022;2(Suppl. S1):s63–s64
doi:10.1017/ash.2022.179

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Surveillance/Public Health
Reduction in outpatient antibiotic utilization: An unintended benefit of the COVID-19 pandemic?
Satoshi Kakiuchi; Eli Perencevich; Daniel Livorsi and Michihiko Goto

Background: The COVID-19 pandemic heavily affected healthcare delivery systems in the United States. However, little is known about its impact on overall antimicrobial consumption, especially in outpatient settings. We assessed the impact of the COVID-19 pandemic on antimicrobial consumption in both outpatient and inpatient (acute-care, long-term care, and mental health) settings in the Veterans' Health Administration (VHA) during the 2 years before and after the start of the pandemic. **Methods:** We conducted a retrospective study for all patients who received care within the VHA from January 2018 to December 2021. We used antibiotic days as the primary outcome measure (days of therapy for inpatient settings and dispensed days supply for outpatient settings), and we obtained data for antimicrobial consumption from the VHA Corporate Data Warehouse. Antibiotics were categorized into classes by the NHSN protocol and included only systemic agents (oral and parenteral). We defined 2018–2019 as the prepandemic period and 2020–2021 as the pandemic period. We compared the relative and absolute difference in antibiotic consumption between the 2 periods. **Results:** Across all periods, 8.3 million patients received care in the VHA, and an average of 28,709,680 antibiotic days were prescribed per year. Overall, 92.9% of all antibiotic days were outpatient and 7.1% were inpatient. Total antibiotic days during the pandemic period decreased by 12.4% compared to the prepandemic period (pandemic period: 53,613,840 and prepandemic period: 61,224,878). This reduction was primarily driven by reductions in outpatient settings (relative reduction: 12.7% and absolute reduction: 7,254,880 antibiotic days over 2 years), but antibiotic days in inpatient settings decreased more modestly (relative reduction: 8.4% and absolute reduction: 356,158 antibiotic days over 2 years) (Fig. 1). When frequently prescribed antimicrobials were categorized by classes, fluoroquinolones and lincosamides showed the largest decreases (fluoroquinolones: 29.2% reduction and lincosamides: 27.2% reduction). Tetracyclines and sulfamethoxazole–trimethoprim had the smallest reductions (5.2% and 11.2%, respectively). **Conclusions:** Compared to the prepandemic period, the pandemic was associated with a substantial reduction in overall antibiotic consumption, especially in outpatient settings, which accounted for 95% of the overall reduction despite being outside the domain of most traditional antibiotic stewardship programs. The impact of the pandemic was most modest in the use of tetracyclines and trimethoprim–sulfamethoxazole and was most prominent in the use of fluoroquinolones and lincosamides. Further studies are required to improve the causal inference between the COVID-19 pandemic and this reduction in antibiotic consumption, as well as its impact on patient outcomes.

Funding: None
Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2022;2(Suppl. S1):s64
doi:10.1017/ash.2022.180

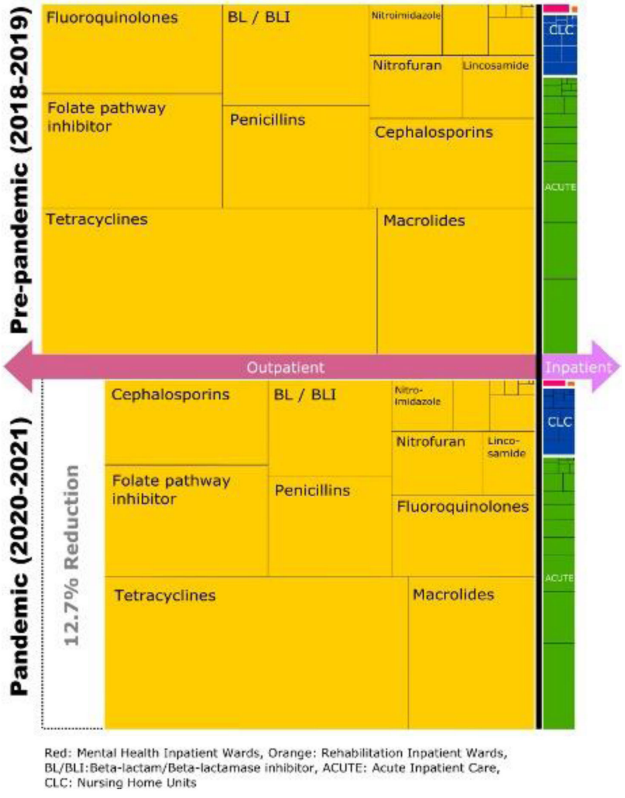

Fig. 1.

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Surveillance/Public Health
Mortality rates among non-Hispanic Black and White persons in carbapenemase-producing Enterobacterales, Tennessee, 2015–2019
Erika Kirtz; Rany Octaria; Carolyn Stover; Christopher Wilson and Allison Chan

Background: Carbapenem-resistant Enterobacterales (CRE) are an urgent public health threat, particularly those that produce carbapenemase (CP-CRE). Certain risk factors associated with CRE acquisition have been well described, such as older age, indwelling devices, prior hospitalizations, and underlying conditions. However, data are limited regarding the association of CRE and health disparities, such as race and ethnicity. Published literature has consistently shown that minority groups, including but not limited to Non-Hispanic Black persons, have higher risks of developing adverse health outcomes. To better understand the impact of race and ethnicity in CP-CRE cases, we compared 1-year mortality rates among Non-Hispanic Blacks and Non-Hispanic Whites. **Methods:** CRE are reportable in Tennessee; isolates must be sent to the State Public Health Laboratory for carbapenemase detection and resistance mechanism testing. We linked 2015–2019 CP-CRE surveillance cases and laboratory data from our statewide surveillance system, the National Disease Surveillance System (NEDDS)-Base System, with the Tennessee Hospital Discharge Data System (HDDS) and vital records databases. Database linkage and data analyses were performed using SAS version 9.4 software. **Results:** Among 615 CP-CRE cases, the mean age was lower among non-Hispanic Blacks (59 years; SD, 16.6) compared to non-Hispanic Whites (mean, 65 years; SD, 15.7). Among 156 non-Hispanic Blacks with CP-CRE, 101 (64.7%) were nursing home residents, whereas 281 (71.1%) among the 395 non-Hispanic Whites were nursing home residents.

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.

Funding: None
Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2022;2(Suppl. S1):s64–s65

doi:10.1017/ash.2022.181

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Surveillance/Public Health

Developing national benchmarks for antimicrobial resistance—NHSN, 2019

Hsiu Wu; Erin O'Leary; Minn Soe and Jonathan Edwards

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

Funding: None
Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2022;2(Suppl. S1):s65

doi:10.1017/ash.2022.182

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Surveillance/Public Health

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

Nadia Barahmani; Andrea Parriott; Erin Epson; Genie Tang and N. Neely Kazerouni

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