

nonprescription use was reported by 246 (43%) of 564 individuals, with 91 (16%) reporting nonprescription use within the previous 12 months. Intention to use nonprescription antibiotics was reported by 140 participants (25%). The sensitivity and specificity of prior nonprescription use in the past 12 months to predict the intention to use nonprescription antibiotics in the future were 75.9% (95% CI, 65.3–84.6) and 91.4% (95% CI, 87.8–94.2), respectively. After the Bayes’ adjustment, the PPV and NPV of prior use to predict future intention were 74.5% (95% CI, 66.7–80.9) and 92.0% (95% CI, 88.7–94.4) (Table 1). **Conclusions:** These results show that prior nonprescription antibiotic use in the past 12 months predicted the intention to use nonprescription antibiotics in the future (PPV of 75%). As a stewardship effort, we suggest clinicians use a simple question about prior nonprescription antibiotic use in primary-care settings as a screening question for patients at high risk for future nonprescription antibiotic use. **Financial support:** HSQR-R 5R01HS026901-04

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Poster Presentation - Top Oral Abstract

Subject Category: Molecular Epidemiology

Real-time whole-genome sequencing surveillance for outbreak detection and intervention

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Background: Detecting healthcare-associated transmission and outbreaks often relies on reactive whole-genome sequencing (WGS), which occurs after the suspected transmission has occurred. Additionally, reactive WGS frequently misidentifies transmission and misses transmission when it has occurred. We initiated weekly real-time WGS to detect bacterial transmission and direct infection prevention interventions. We describe our experience after 1 year of real-time WGS surveillance at the University of Pittsburgh Medical Center–Presbyterian Hospital, a large, tertiary-care facility. **Methods:** Weekly WGS surveillance was performed from November 1, 2021, to October 31, 2022. Cultured isolates of select bacterial pathogens from patients who were hospitalized for ≥3 days or had a recent healthcare exposure in the prior 30 days were collected and sequenced. Isolates that were ≤15 single-nucleotide polymorphisms (SNPs) were considered genetically related clusters except for *Clostridioides difficile* (≤2 SNPs). Genetically related clusters were investigated for epidemiological links and interventions to interrupt transmission were implemented at the discretion of the infection prevention team. We analyzed subsequent infections that occurred within an outbreak after an intervention was in place. **Results:** In total, 1,909 isolates were sequenced. Of 1,633 unique patient isolates clustered by sequence type, 74 clusters were identified comprising 210 (12.9%) patient isolates

Table 1. Isolates sequenced and clusters detected

Organism	Sequenced	Unique Patient	Clusters	Clustered Isolates (%)
<i>Acinetobacter</i> species	52	50	5	11 (22.0)
<i>Burkholderia</i> species	6	4		
<i>Citrobacter</i> species	30	29		
<i>Clostridioides difficile</i>	100	98	3	8 (8.2)
<i>Enterobacter</i> species	35	34	2	4 (11.8)
<i>Escherichia coli</i>	128	109	5	11 (10.1)
<i>Klebsiella</i> species, not <i>pneumoniae</i>	21	21		
<i>Klebsiella pneumoniae</i> , ESBL producing	90	67	6	23 (34.3)
Methicillin-resistant <i>Staphylococcus aureus</i>	248	221	9	21 (9.5)
<i>Proteus</i> species	228	189	3	6 (3.2)
<i>Providencia</i> species	24	23		
<i>Pseudomonas aeruginosa</i>	558	438	20	50 (11.4)
<i>Pseudomonas</i> species, not <i>aeruginosa</i>	14	14		
<i>Serratia</i> species	153	135	3	6 (4.4)
<i>Stenotrophomonas maltophilia</i>	98	85	1	2 (2.4)
Vancomycin-resistant <i>Enterococcus faecium</i>	124	116	17	68 (58.6)
TOTAL	1909	1633	74	210 (12.9)

Table 2. Cluster size and distribution by species

Organism	Number of Clusters by Cluster Size (Patients)											
	2	3	4	5	6	7	8	9	10	11	12	
<i>Acinetobacter</i> species	4	1										
<i>Clostridioides difficile</i>	2		1									
<i>Enterobacter</i> species	2											
<i>Escherichia coli</i>	4	1										
<i>Klebsiella pneumoniae</i> , ESBL producing	4				1			1				
Methicillin-resistant <i>Staphylococcus aureus</i>	6	3										
<i>Proteus</i> species	3											
<i>Pseudomonas aeruginosa</i>	16	1	1	1	1							
<i>Serratia</i> species	3											
<i>Stenotrophomonas maltophilia</i>	1											
Vancomycin-resistant <i>Enterococcus faecium</i>	7	5	1			2		1				1

(Table 1). The median time from culture date to sequencing was 14 days (IQR, 5.25). The median cluster size was 2 (IQR, 1) (Table 2). Overall, 118 patient isolates (56.2%) had an epidemiological link to a prior isolate, indicating potential transmission. Of 74 clusters, 66 (89.2%) received infection prevention interventions after notification based upon epidemiological data. The infection prevention team performed 69 total interventions, which included unit education (n = 28), hand hygiene observations (n = 16), enhanced cleaning (n = 16), environmental cultures or removal of endoscope (n = 7), and enhanced microbiology surveillance (n = 2). The 59 subsequent infections after infection prevention notification included 17 (28.8%) with no clear epidemiological link, and 41 (69.5%) with an epidemiological link either to a new transmission route (n = 37) or the same route prior to infection prevention intervention (n = 4). Only 1 (1.7%) subsequent infection within a cluster occurred after an infection prevention intervention from the same potential route, which was a suspected unit-based transmission of vancomycin-resistant *Enterococcus faecium*. **Conclusions:** Real-time WGS was effective at detecting genetically related clusters, finding potential sources, and halting further transmission after interventions by the infection prevention team. Quick turnaround times from patient culture to sequencing and analysis were vital for successful WGS surveillance. Real-time WGS surveillance has the potential to substantially shift the infection prevention paradigm for outbreak detection.

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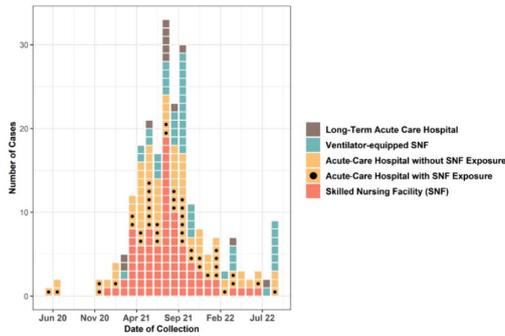
Subject Category: Outbreaks

Patient and facility characteristics of an NDM-producing *Acinetobacter baumannii* outbreak in California, 2020–2022

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Background: Carbapenem-resistant *Acinetobacter baumannii* (CRAB) are bacteria that cause healthcare-associated infections and outbreaks. Most produce carbapenemases like New Delhi metallo-β-lactamase (NDM), which are more commonly found in carbapenem-resistant Enterobacterales but rarely in CRAB. In 2018, selected laboratories began participating in a public health sentinel surveillance program by routinely submitting CRAB and other antimicrobial-resistant isolates to the AR Laboratory Network for specialized testing. In May 2020, the Antimicrobial Resistance Laboratory Network detected the first NDM-CRAB case in California, triggering an investigation. Initial whole-genome sequencing of subsequent isolates indicated high relatedness. **Methods:** We defined confirmed cases as patients with NDM detected in CRAB isolates and probable cases as NDM detected in a screening swab from a patient epidemiologically linked to a known case(s) with specimens collected during May 2020–September 2022. We defined outbreak facilities as having (1) 1 or more newly identified cases during a point-prevalence survey in response to a known case or (2) at least 2 cases identified within 4 weeks of each other that were epidemiologically linked. We analyzed demographic and specimen characteristics, as well as healthcare exposure history using R Studio version 1.3.959 software. **Results:** Of 230 total patients, 176 (77%) were confirmed and 54 (23%) were probable cases; 150 (65%) were identified

Figure 1: Confirmed and Probable NDM-CRAB Cases by Collection Facility Type, May 2020–September 2022 (N=230)



through colonization screening. Among 176 NDM-CRAB isolates, the most common specimen sources were respiratory (n = 29), wound (n = 28), and urine (n = 24), and 87 (49%) of 176 isolates were nonsusceptible to all antimicrobials tested. Among patients, median age was 65 years (range, 24–97), 127 (55%) were male, 37 (15%) were Hispanic or Latino, and 100 (43%) were White. We identified 37 outbreak facilities across 13 counties, including 25 acute-care hospitals (ACHs), 6 skilled nursing facilities (SNFs), 5 ventilator-equipped SNFs (vSNFs), and 1 long-term ACH. We identified 125 cases (54%) in SNFs and vSNFs and 93 cases (40%) in ACHs; among ACH patients, 43 (46%) had been SNF or vSNF residents within the prior year. No patients reported international exposure. **Conclusions:** The first known case of NDM-CRAB in California was detected by sentinel surveillance. In this extensive regional outbreak, most cases were identified by screening at public health and clinical laboratories. Transmission occurred across healthcare settings connected by patient sharing, underscoring the importance of communication, active surveillance, and implementation of infection prevention and control practices to mitigate spread within and between facilities. Expanding these efforts, with support and resources from public health departments, is key to detecting, characterizing, and containing future outbreaks of antimicrobial-resistant pathogens.

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Subject Category: Antibiotic Stewardship

Three-day antibiotic duration in patients with pneumonia: A sixty-eight-hospital cohort

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Background: Since 2019, community-acquired pneumonia (CAP) guidelines have recommended hospitalized patients be treated until clinical

“stability and for no less than 5 days.” However, randomized trials have reported that, in patients who stabilize by hospital day 3, very short antibiotic durations (eg, 3 days) are noninferior to longer durations. How these trial results relate to real-world practice is unknown. **Methods:** Using a 68-hospital cohort study of hospitalized, general-care adults with CAP, we aimed to (1) quantify the percentage of patients who—according to trial criteria—qualify for a 3-day antibiotic duration, (2) quantify the percentage who actually received a 3-day duration, and (3) assess 30-day outcomes. Patients were considered to have CAP if they had a pneumonia discharge diagnosis and met clinical criteria for CAP. Patients with concomitant infections (including COVID-19), admission to intensive care, or severe immunocompromise were not included. **Results:** Between February 23, 2017, and August 3, 2022, 36,064 patients with CAP were included. Of those, 48.2% (9,826 of 36,064) were excluded due to a condition or organism ineligible for the 3-day treatment (Fig. 1). Of the 18,690 patients remaining, 52.6% (9,826) were unstable on day 3 and thus were ineligible for the 3-day treatment. Therefore, of all 36,064 patients, only 8,864 (24.6%) would be eligible under trial criteria for a 3-day treatment. Notably, 5,493 (55.9%) of 9,826 patients unstable on day 3 would be eligible for 5 days of treatment under national guidelines. In practice, use of 3–4-day treatment was rare, occurring in 599 (6.8%) of 8,864 patients eligible for a 3-day treatment versus 660 (6.7%) of 9,826 patients unstable on day 3 (P = .945). Use of 3–4-day treatment increased over time and comorbidities that could mimic CAP or a negative procalcitonin were more common in patients who received a 3–4-day treatment whereas specific symptoms of CAP were less common (Fig. 2). After adjustments, patients eligible for a 3-day duration who received a 3–4 day treatment versus a ≥5-day treatment had higher 30-day mortality (aOR, 1.87; 95% CI, 1.32–2.64) and readmission (aOR, 1.35; 95% CI, 1.17–1.56). **Conclusions:** Across 68 hospitals, <25% of patients hospitalized with CAP would be eligible for a 3-day antibiotic treatment. Though increasing over time, there was little use of 3–4-day treatments and, when prescribed, outcomes were worse, potentially due to CAP misdiagnosis. Given the small number of patients eligible for 3-day treatment, and the potential harm with too-short durations, it may be prudent to focus on increasing the use of 5-day treatments.

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Subject Category: Antibiotic Stewardship

High prevalence of antibiotic use in a tertiary-care hospital in Sierra Leone: We need to handle antibiotics with care

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Background: Antimicrobial resistance (AMR) is a global public health concern that has the potential to reverse decades of progress aimed at decreasing morbidity and mortality attributed to infectious diseases. In 2019, ~5 million deaths were associated with AMR, of which 1.2 million were attributed to antibacterial-resistant infections. Healthcare facilities where antimicrobials are frequently used are high-risk settings for the selection and spread of resistant bacteria, and they further contribute to the increase in the burden of AMR. We have documented the prevalence and indication of antibiotic use in a tertiary-care referral hospital in Freetown, Sierra Leone. **Methods:** This point-prevalence survey was conducted at Connaught hospital, a tertiary-care hospital in Sierra Leone, in November 2021. The hospital offers a range of medical and surgical services through 25 units and has 16 wards with >300 beds. Data on patient-level antibiotic use, including indications for use, were extracted from medical records using WHO point-prevalence survey (PPS) forms that had been pretested and validated. Data collection was conducted in all the wards over a 10-day period by trained healthcare personnel. On the day of the survey, only the medical records of patients on admission

