with syndrome-specific antimicrobial stewardship efforts.[1] We adapted and validated the performance of an inpatient CAP electronic phenotype for antimicrobial stewardship interventions. **Methods:** An automated scoring system was created within the EHR (Epic Systems) to identify hospitalized patients with CAP based on the variables and logic listed in Fig. 1B. We adapted a score used by the Michigan Hospital Medicine Safety Consortium (HMS) to identify patients with CAP, with additions made to improve sensitivity (Fig. 1).[1] The score can be displayed in a column within the EHR patient list (Fig. 2). We validated the electronic phenotype via chart review of all hospitalized patients on systemic antimicrobials admitted to a medicine team consecutively between November 8 and 18, 2021. Patients who were readmitted within the validation time frame were excluded. We assessed the performance of the electronic phenotype by comparing the score to manual chart review, where "CAP diagnosis" was defined as (1) mention of "pneumonia" or "CAP" as part of the differential diagnosis in the admission documentation, (2) antimicrobials were started within 48 hours of admission, and (3) radiographic findings were suggestive of pneumonia. After initial evaluation, the scoring system was adjusted, and performance was re-evaluated during prospective audit and feedback performed on EHR CAP–positive patients over 13 days between July 2022 and December 2022. **Results:** We included 191 patients in our initial validation cohort. The CAP score had high sensitivity (95.83%), specificity (92.2%), and negative predictive value (99.35%), though lower positive predictive value (63.89%) was noted (Table 2). The rules were further refined to include bloodstream infection only with *Haemophilus influenza* or *Streptococcus pneumoniae* in rule 2B, and azithromycin was removed from "CAP antibiotics." After these changes, repeated evaluation of 88 patients with positive CAP EHR score was performed, and only 20 (23%) were considered false-positive results. **Conclusions:** Electronic phenotypes can be used to create automated tools to identify patients with CAP with reasonable performance. Data from this tool can be used to guide more focused antimicrobial stewardship interventions and clinical decision support in the future. **Reference:** Vaughn VM, et al. A statewide collaborative quality initiative to improve antibiotic duration and outcomes in patients hospitalized with uncomplicated community-acquired pneumonia. *Clin Infect Dis* 2022;75:460–467.
Disclosures: None

Figure 1: EHR Rules for identifying CAP at HMS vs. Stanford

A) HMS Rules

Rule 1: CAP Antibiotic* orders administered during encounter within 48 hours of admission
AND
Rule 2: Active order for a CAP Antibiotic ordered for a "pulmonary" indication
CAP EHR POSITIVE: IF Rule 1 AND Rule 2 present, THEN Positive

*CAP Antibiotic = ampicillin/sulbactam, azithromycin, cefepime, ceftriaxone, levofloxacin, moxifloxacin, piperacillin/tazobactam, vancomycin

B) Stanford adjusted Rules

Rule 1: CAP Antibiotic§ orders administered during encounter within 48 hours of admission (Score = 100,000)		
AND		
Rule 2: Any ONE of the following criteria met:		
Added Score for each rule:		
Rule 2A	1	Active order for a CAP Antibiotic ordered for a "pulmonary" indication
Rule 2B	10	CAP Antibiotic ordered with an indication of "bloodstream infection" AND CXR† ordered that admission
Rule 2C	100	CAP Antibiotic ordered with indication of "other" AND CXR ordered
Rule 2D	1000	CAP Antibiotic ordered AND Positive respiratory culture¶
Rule 2E	10,000	CAP Antibiotic ordered AND RVP‡ ordered
CAP EHR SCORE POSITIVE: Add scores from Rule 1 and Rule 2. If SUM >100,000, then Positive Score		

§CAP Antibiotic = amoxicillin/clavulanate, ampicillin/sulbactam, azithromycin, cefepime, ceftriaxone, cefpodoxime, doxycycline, levofloxacin, meropenem, moxifloxacin, piperacillin/tazobactam, vancomycin
†CXR = Chest X-ray
¶Positive Respiratory Culture = Respiratory culture marked as "abnormal result" in EHR. Note: respiratory cultures with growth of flora are not marked as "abnormal result" in Stanford's EHR
‡RVP = Respiratory Viral Panel; RT-PCR including influenza A/B, respiratory syncytial virus, parainfluenza 1/2/3/4, metapneumovirus, rhinovirus, adenovirus

Table 1: Validation of CAP "electronic phenotype"

		CAP Diagnosis on Clinical Chart Review		
		Yes	No	Total
"CAP" electronic phenotype	Positive	23	13	36
	Negative	1	154	155
	Total	24	167	191

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Presentation Type:
Poster Presentation - Oral Presentation
Subject Category: Infection Control in Low- and Middle-Income Countries

Hyperendemic carbapenem-resistant *Acinetobacter baumannii* at a hospital in Botswana: Insights from whole-genome sequencing

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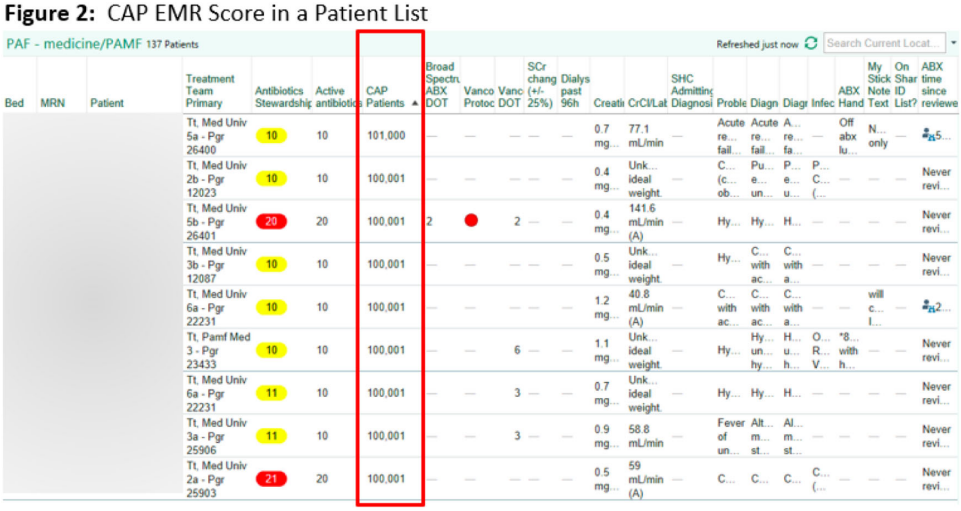
Figure 2: CAP EMR Score in a Patient List



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Background: Carbapenem-resistant *Acinetobacter baumannii* (CRAB) has emerged as a major cause of bloodstream infection among hospitalized patients in low- and middle-income countries (LMICs). CRAB infections can be difficult to treat and are devastating in neonates (~30% mortality). CRAB outbreaks are hypothesized to arise from reservoirs in the hospital environment, but outbreak investigations in LMICs seldom incorporate whole-genome sequencing (WGS). **Methods:** WGS (Illumina NextSeq) was performed at the National Institute for Communicable Diseases (South Africa) on 43 preserved *A. baumannii* isolates from a 530-bed referral hospital in Gaborone, Botswana, from March 2021–August 2022. This included 23 blood-culture isolates from 21 unique patients (aged 2 days–69 years) and 20 environmental isolates collected at the 36-bed neonatal unit in April–June 2021. Infections were considered healthcare-associated if the culture was obtained >72 hours after hospital arrival (or sooner in inborn infants). Blood cultures were incubated using an automated system (BACT/ALERT, BioMérieux) and were identified using manual methods. Environmental isolates were identified using selective or differential chromogenic media (CHROMagarTM). Taxonomic assignment, multilocus sequence typing (MLST), antimicrobial resistance gene identification, and phylogenetic analyses were performed using publicly accessible analysis pipelines. Single-nucleotide polymorphism (SNP) matrices were used to assess clonal lineage. **Results:** All 23 blood isolates and 5 (25%) of 20 environmental isolates were confirmed as *A. baumannii*; thus, 28 *A. baumannii* isolates were included in the phylogenetic analysis. MLST revealed that 22 (79%) of 28 isolates were sequence type 1 (ST1), including all 19 healthcare-associated blood isolates and 3 (60%) of 5 environmental isolates. Genes encoding for carbapenemases (*bla*NDM-1, *bla*OXA-23) and biocide resistance (*qac*E) were present in all 22 ST1 isolates; colistin resistance genes were not identified. Phylogenetic analysis of the ST1 clade demonstrated spatial clustering by hospital unit. Related isolates spanned wide ranges in time (>1 year), suggesting ongoing transmission from environmental sources (Fig. 1). An exclusively neonatal clade (0–2 SNPs) containing all 8 neonatal blood isolates was closely associated with 3 environmental isolates from the neonatal unit: a sink drain, bed rail, and a healthcare worker's hand. **Conclusions:** WGS analysis of clinical and environmental *A. baumannii* revealed the presence of unit-specific CRAB clones, with evidence of ongoing transmission likely driven by persistent environmental reservoirs. This research highlights the potential of WGS to detect hospital outbreaks and reaffirms the importance of environmental sampling to identify and remediate reservoirs (eg, sinks) and vehicles (eg, hands and equipment) within the healthcare environment.
Disclosures: None

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Presentation Type:
Poster Presentation - Oral Presentation
Subject Category: Long-term Care
Transmission of multidrug-resistant organisms by VA CLC residents: A multisite prospective study

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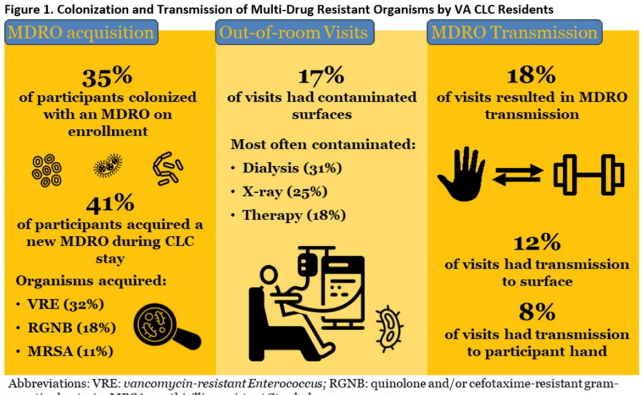
Background: Veterans Health Administration (VHA) community living centers (CLCs) provide postacute and long-term care. CLC veterans visit myriad locations outside their rooms (eg, rehabilitation, dialysis). Pathogen transmission during out-of-room visits is unknown. **Methods:** We recruited newly admitted veterans at 3 CLCs. After obtaining informed consent, we cultured nares, groin, hands, and 7 surfaces in the patient rooms. We accompanied veterans to up to 5 out-of-room visits and cultured patients' hands and surfaces they touched. We tested for multidrug-resistant organisms (MDROs) including methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus* (VRE), and quinolone, carbapenem, and/or ceftazidime-resistant gram-negative bacteria (R-GNB). We defined transmission as a positive culture following an initial negative culture during the same visit. **Results:** We enrolled 137 veterans (median follow-up, 29 days; mean, 5.9 visits); 97% were postacute patients. We conducted 539 patient-room sampling visits (mean, 3.9 per veteran; 5,490 swabs) and accompanied 97 veterans to 266 out-of-room sampling visits (mean, 2.7 per veteran; 2,360 swabs). Of 137 patients, 47 (35%) were colonized with an MDRO at enrollment and 74 (58%) of 128 patients were colonized on any follow-up patient-room visits. Of 133 patients, 55 (41%) acquired a new MDRO, most often VRE (31 of 97, 32%). In patient rooms, toilet seats [114 (21%) of 538], curtains [101 (19%) of 530] and bedrails [98 (18%) of 539] were most frequently conta-

Figure 1. Colonization and Transmission of Multi-Drug Resistant Organisms by VA CLC Residents



Abbreviations: VRE: *vancomycin-resistant Enterococcus;* RGNB: quinolone and/or cefotaxime-resistant gram-negative bacteria; MRSA: *methicillin-resistant Staphylococcus aureus*

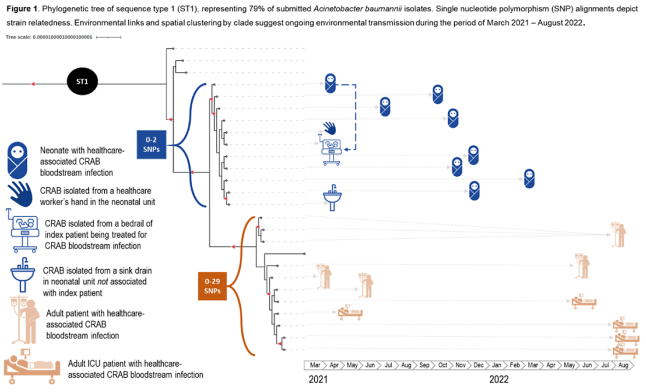


Figure 2. Transmission Rates by Out-of-Room Visit Type