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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

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s115–s116
doi:10.1017/ash.2023.395

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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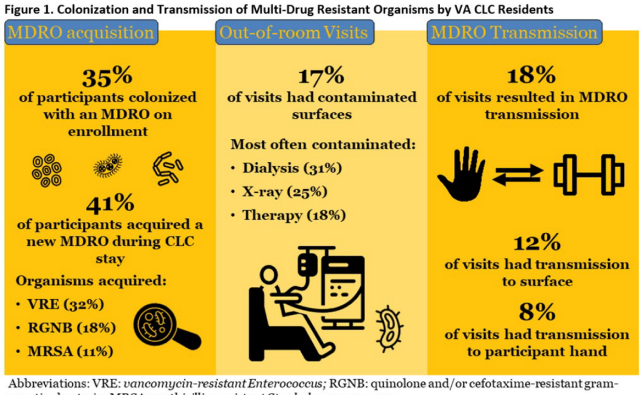
Background: Veterans Health Administration (VHA) community living centers (CLCs) provide postacute and long-term care. CLC veterans visit myriad locations outside their rooms (eg, rehabilitation, dialysis). Pathogen transmission during out-of-room visits is unknown. **Methods:** We recruited newly admitted 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*

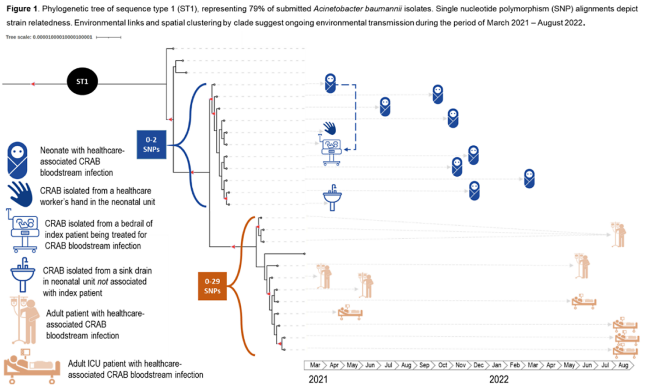
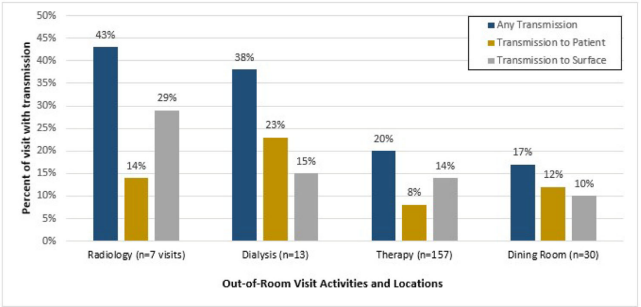


Figure 2. Transmission Rates by Out-of-Room Visit Type



minated. Among 266 out-of-room visits, 17% had surfaces contaminated with MDROs, most commonly involving dialysis [4 (31%) of 13], radiology [2 (25%) of 8], and rehabilitation therapy [29 (18%) of 159] (Fig. 1).Transmission of MDROs during out-of-room visits was common and occurred in 18% of visits with 8% (9 MRSA and 12 VRE) acquiring a new MDRO on their hands and 12% (9 MRSA and 23 VRE) of MDRO transmission occurring from hands to a surface that the patient touched (Fig. 1). In 18 (58%) of 31 cases, the organism transmitted to a surface was on patient hands at the start of the visit. Transmission was most common during visits to dialysis (3 to patients and 2 to surfaces), radiology (1 to a patient and 2 to surfaces), and rehabilitation therapy (13 to patients and 21 to surfaces) (Fig. 2). **Conclusions:** New MDRO acquisition during VHA CLC stay was common, and nearly one-fifth of out-of-room visits resulted in MDRO transmission. Our analyses suggest that veterans' hands may shed MDROs (MRSA and VRE) to surfaces. Interventions to reduce MDRO transmission during visits for rehabilitation, dialysis, and other therapies are needed.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s116–s117
doi:10.1017/ash.2023.396

Presentation Type:
Poster Presentation - Oral Presentation
Subject Category: Occupational Health
3D printers in hospitals: Reducing bacterial contamination on 3D-printed material
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Background: COVID-19 has presented hospitals with unique challenges. An SHEA Research Network survey showed that 40% reported "limited" or worse levels of personal protective equipment (PPE) and that 13% were self-producing PPE to address those deficits, including 3D-printed items. However, we do not know how efficiently, if at all, 3D-printed materials can be disinfected. Additionally, 2 filaments, PLACTIVE and PUREMENT, claim to be antimicrobial; they use copper nanocomposites and silver ions to reduce bacterial populations. We assessed how PLACTIVE and PUREMENT may be contaminated and how well they reduce contamination, and how readily polylactic acid (PLA), a standard 3D-printed material, may be disinfected. **Methods:** We grew methicillin-resistant and -susceptible *Staphylococcus aureus*, *Escherichia coli*, and *Klebsiella pneumoniae* on 3D-printed disks and conducted bacterial survival assays to determine whether bacteria grow on PLA, PLACTIVE, and PUREMENT. We performed a time series (with 3- and 24-hour dry times) followed by serial dilutions to attain colony-forming unit (CFU) averages for each strain per disk. To determine whether 3D-printed material can be cleaned, we used 70% EtOH on PLA only. We conducted the same time series followed by a disinfectant time series (with dry times 30 seconds, 2.5, minutes, 5 minutes, and 10 minutes). Again, serial dilutions were performed to attain the PLA CFU averages with disinfectant. The CFU averages from the control group (PLA) and testing group (PLACTIVE and PUREMENT) were compared to see how well the antimicrobial material decreased bacterial load. We also compared the CFU averages of PLA with and without disinfectant to see how well 70% EtOH decreased bacterial load. **Results:** 3D-printed material is readily contaminated with bacteria common in hospitals and can sustain that contamination. Antimicrobial materials, PLACTIVE and PUREMENT, had lower levels of bacterial contamination when compared to PLA. However, disinfected disks had lower overall CFU averages than those that were not, but the level of disinfection was variable and bacterial populations recovered hours after disinfection application. **Conclusions:** Proper disinfection and using appropriate 3D-printed materials are essential to limiting bacterial contamination. 3D printers and their products can be invaluable for hospitals, especially when supplies are low and healthcare worker safety is paramount. Environmental services should be made aware of the presence of antimicrobial 3D-printed materials, and patients should be discouraged from printing their own items for use in hospital environments.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s117
doi:10.1017/ash.2023.397

Presentation Type:
Poster Presentation - Oral Presentation
Subject Category: Other
Active surveillance and contact precautions for preventing MRSA healthcare-associated infections during the COVID-19 pandemic
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Background: Statistically significant decreases in methicillin-resistant *Staphylococcus aureus* (MRSA) healthcare-associated infections (HAIs) occurred in Veterans Health Administration (VA) facilities from 2007 to 2019 using active surveillance for facility admissions and contact precautions for patients colonized (CPC) or infected (CPI) with MRSA, but the value of these interventions is controversial. **Objective:** To determine the impact of active surveillance, CPC, and CPI on prevention MRSA HAIs, we conducted a prospective cohort study between July 2020 and June 2022 in all 123 acute-care VA medical facilities. In April 2020, all facilities were given the option to suspend any combination of active surveillance, CPC, or CPI to free up laboratory resources for COVID-19 testing and conserve personal protective equipment. We measured MRSA HAIs (cases per 1,000 patient days) in intensive care units (ICUs) and non-ICUs by the infection control policy. **Results:** During the analysis period, there were 917,591 admissions, 5,225,174 patient days, and 568 MRSA HAIs. Only 20% of facilities continued all 3 MRSA infection control measures in July 2020, but this rate increased to 57% by June 2022. The MRSA HAI rate for all infection sites in non-ICUs was 0.07 (95% CI, 0.05–0.08) for