Figure 1-1 Global Hepatitis Outbreak Surveillance Technology

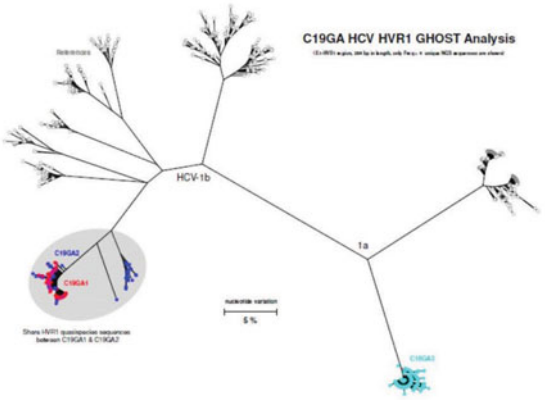

Figure 1-2 Genotypic Test Results

Specimen ID	HVR1 QS Seqs	Sequence ID	Genotype	HVR1 QS NGS	Molecular Analysis Comment
C19GA1	positive	C19GA1	1b	NGS	Share HVR1 quasispecies with C19GA2
C19GA2	positive	C19GA2	1b	NGS	Share HVR1 quasispecies with C19GA1
C19GA3	positive	C19GA3	1a	NGS	

Fig. 1.

of Healthcare Quality Promotion, NCEZID, CDC; Danae Bixler, Division of Viral Hepatitis, CDC; Tonya Hayden, Division of Viral Hepatitis, CDC; Po-Yi Ho, ORISE fellow; Sumathi Ramachandran, Division of Viral Hepatitis, CDC; Priti Patel, Centers For Disease Control and Prevention; Jeanne Negley, Georgia Department of Public Health

Background: Hepatitis C virus (HCV) transmission at outpatient hemodialysis clinics is well documented, but little is known about HCV transmission risks in long-term care facilities (LTCFs) providing hemodialysis services. LTCFs can provide onsite hemodialysis for residents by contracting with a licensed hemodialysis clinic to either provide its staff to the LTCF or to train LTCF staff as caregivers. In August 2019, the Georgia Department of Public Health (DPH) was notified about an HCV seroconversion in patient A at a LTCF providing onsite hemodialysis. **Methods:** Three residents (including patient A) were receiving hemodialysis at the LTCF in August 2019; patients B and C had chronic HCV infection upon admission. Records were reviewed for medical history, behavioral risk factors, and healthcare exposures. We conducted onsite infection control assessments and interviewed staff. Serum specimens were collected for all 3 patients in August 2019 and HCV tested for genetic similarity using Global Hepatitis Outbreak Surveillance Technology (GHOST). **Results:** The facility reported initiating onsite hemodialysis in November 2018; facility staff were trained by a dialysis provider. Patient A, admitted in September 2018, was anti-HCV negative in June 2019 and both anti-HCV and HCV RNA positive in July 2019. Patient B was admitted in December 2018, discharged for 1 month in May 2019, and then readmitted. Patients A and B reported previous injection drug use, and they were not observed by staff to use during their stay and had limited mobility. Patient A was wheelchair confined and B was bed confined. Patient C was admitted in May 2019. HCV samples from patients A and B both had HCV genotype 1b and demonstrated 100% genetic relatedness, indicating that patient B was the likely source. Patient C had HCV genotype 1a. Hemodialysis was provided to residents simultaneously in a converted resident room with 4 hemodialysis stations, and the LTCF operated 2 shifts, 3 times per week. We observed multiple infection control gaps, such as preparation of IV medications and inadequate disinfection in the shared dialysis treatment area. Recommendations addressing gaps were issued, and a follow-up site visit was conducted to validate implementation. With the exception of May 2019, patients A and B received hemodialysis on the same shift and days from December 2018 to September 2019. **Conclusions:** Phylogenetic and epidemiological results indicate HCV transmission likely occurred during hemodialysis services provided by the LTCF. As the provision of dialysis expands to nontraditional settings such as LTCFs, it is essential that proper infection control procedures and oversight are in place.

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Poster Presentation

High Burden of Resistant Gram-Negative Pathogens Causing Device-Associated Healthcare Infections in Saudi Arabia, 2008–2016

Hanan Balkhy, World Health Organization; Aiman Ramadan, Mansoura University; Majid Alshamrani, Ministry of National Guard Health Affairs; Asim Alsaedi, King Abdulaziz Medical City – Jeddah; Wafa Al Nasser, Ministry of National Guard Health Affairs; Ayman El Gammal, Ministry of National Guard Health Affairs; Sameera Aljohani, Ministry of National Guard Health Affairs; Yassen Arabi, Ministry of National Guard Health Affairs; Saad Alqahtani, Ministry of National Guard Health Affairs; Henry Baffoe-Bonnie, King Abdulaziz Medical City; Adel Alothman, Ministry of National Guard Health Affairs; Saad AlMohrij, Ministry of National Guard Health Affairs

Objectives: There is local and regional deficiency in the data examining the contribution of resistant pathogens to device-associated healthcare-associated infections (DA-HAIs). We examined such data in a multihospital system in Saudi Arabia in comparison with the US NHSN reports. **Methods:** Surveillance of DA-HAIs was prospectively conducted between 2008 and 2016 in 4 hospitals of Ministry of National Guard Health Affairs. Consecutive NHSN reports were used for comparison. Definitions and methodology of DA-HAIs and bacterial resistance were based on the NHSN reports. **Results:** In total, 1,260 pathogens causing 1,141 DA-HAI events were included. Gram-negative pathogens (GNPs) were responsible for 62.5% of DA-HAIs, with significantly higher *Klebsiella*, *Pseudomonas*, *Acinetobacter*, and *Enterobacter* than NHSN hospitals. Approximately 28.3% of GNPs and 23.5% of gram-positive pathogens (GPPs) exhibited some type of resistance. Nearly 34.3% of *Klebsiella* were cephalosporin-resistant; 4.8% of Enterobacteriaceae were carbapenem-resistant (CRE); 24.4% of *Staphylococcus aureus* were methicillin-resistant (MRSA; and 21.9% of *Enterococci* were Vancomycin-resistant (VRE). The multidrug resistance (MDR) rates were 65.0% for *Acinetobacter*, 26.4% for *Escherichia coli*, 23.0% for *Klebsiella*, and 14.9% for *Pseudomonas*. Resistant GNPs including cephalosporin-resistant *Klebsiella*, MDR *Klebsiella*, and MDR *Escherichia coli* were significantly more frequent than in

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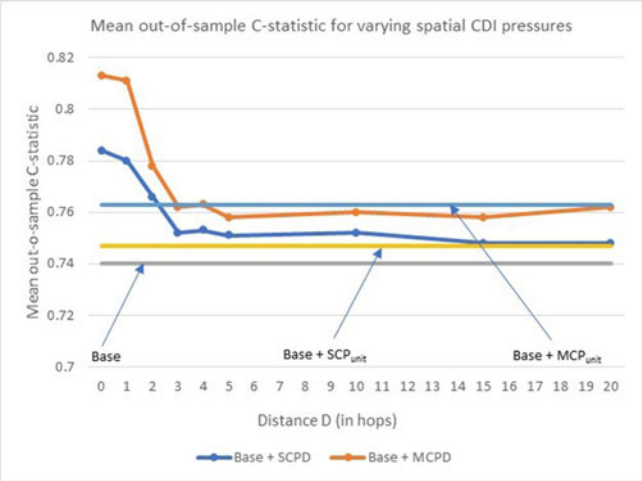

Fig. 1.

NHSN hospitals, whereas resistant GPPs including MRSA and VRE were significantly less frequent than in NHSN hospitals. **Conclusion:** Compared with American hospitals, GNPs that contribute to DA-HAIs in Saudi hospitals show more resistance. The higher resistance rates in *Klebsiella* and *Escherichia coli* are alarming and call for effective antimicrobial stewardship programs.

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Highly Local *Clostridioides difficile* Infection (CDI) Pressure as Risk Factors for CDI

Talal Riaz, The University of Iowa Abhijeet Kharkar, The University of Iowa; Nabeel Khan, The University of Iowa; Philip Polgreen, University of Iowa; Alberto Segre, Department of Computer Science; Daniel Sewell, University of Iowa; Sriram Pemmaraju, University of Iowa

Background. Colonization pressure at the unit level is known to be a risk factor for *Clostridioides difficile* infections in hospitals. Because *C. difficile* colonization is not routinely detected in clinical practice, only patients identified as having *C. difficile* infection (CDI) are included in these pressure calculations. We used data from the University of Iowa Hospitals and Clinics (UIHC) to determine whether highly local CDI pressure, due to patients in nearby rooms, is more strongly correlated with CDI than unit-level CDI pressure. **Methods:** We designed a base logistic regression model using variables known to be risk factors for CDI: age, antibiotic/gastric acid suppressor use, low albumin, prior hospitalization, comorbidities. To the base model, we add 2 measures, *mean colonization pressure* (MCP) and *sum colonization pressure* (SCP) of CDI at the unit level to obtain new models. To the base model, we also added CDI colonization pressure by considering CDI cases at different distance thresholds from the focal patient. Distances between patient rooms were extracted from hospital floor plans. **Results:** Adding unit-level CDI colonization pressures to the base model improved performance. However, adding CDI colonization pressures due to roommates and due to patients at different distances improved the model much more (Table 1). The top (resp. bottom) row shows in-sample (resp. out-of-sample) C-statistics for the base model, the base model with unit-level MCP, the base model with roommate MCP, and the base model with MCP from patients are different distances added as separate features. C-statistics for the base model and the base model with unit CDI pressure (SCP and MCP) are compared in Fig. 1 with C-statistics from the base model with CDI pressure from patients at distances D = 0, 1, 2, 3, 4, 5, 10, 15, 20 hops (1 hop = 5–6 meters). **Conclusions:** Our results support the hypothesis that unit CDI colonization pressure is a risk factor for CDI. However, by incorporating spatially granular notions of distances between patients in our analysis, we were able to demonstrate that the true source of CDI pressure at the UIHC is almost exclusively attributable to roommates and patients in adjacent rooms.

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Hospital Infections by *Stenotrophomonas maltophilia*: Results in Five Years of Multicentric Study

Luciana Tanure, UniBH (Centro Universitário de Belo Horizonte); Rafaela Pinho, Centro Universitário de Belo Horizonte – UniBH; Mayra de Oliveira , Centro Universitário de Belo Horizonte – UniBH; Daniela Ribeiro, Centro Universitário de Belo Horizonte – UniBH; Jose A. Ferreira, Federal University of Minas Gerais- UFMG Braulio Couto, Centro Universitário de Belo Horizonte – UniBH; Carlos Starling, Vera Cruz Hospital

Background: *Stenotrophomonas maltophilia* is an emerging pathogen responsible for high morbidity and mortality rates. Hospital infections caused by this bacteria, especially in intensive care centers, are concerning for the health system, given that the microorganism is multidrug resistant to most antimicrobials available. **Objective:** Therefore, the present study is built from an analysis of the variables related to nosocomial infections caused by *S. maltophilia* in hospitals in Brazil, to display points of major concern. **Methods:** We used the data collected by the Infection Prevention and Control Service to clarify the incidence rate of *Stenotrophomonas maltophilia* in Brazilian hospitals as well as the gross lethality of these infections and the profiles of infected patients. We collected and analyzed epidemiological data from 10 hospitals in Brazil for the period July 2014 to June 2019 according to the CDC NHSN protocol. **Results:** In 5 years, 93 *Stenotrophomonas maltophilia* infections were diagnosed in the hospitals analyzed. Overall, 61 occurred in men (66%) and 32 occurred in women (34%). Furthermore, 47 cases (51%) occurred in adult ICUs; 19 cases (20%) followed zascular surgery; 9 (10%) cases occurred in the neonatal ICU; 7 (8%) cases were from the medical clinic; and 11 (12%) were from other clinics. The incidence rate was 1.2 cases for 10,000 hospitalizations, ranging from 0.0 to 2.8 (Fig. 1). Patients' ages ranged from 0 to 90 years, with a mean of 55 years (SD, 26 years) and a median of 64 years. Time between admission and diagnosis of infection was 1 to 102 days, with a mean of 24 days (SD, 21 days) and a median of 17 days. The gross lethality for *S. maltophilia* infection was 43 of 93 (46%) (95% CI, 35.8%–56.9%). The frequencies of specific infections were as follows (Fig. 2): pneumonia, 26 (28%); tracheobronchitism, 22 (24%); primary bloodstream infection, 18 (19%); skin and soft-tissue infection, 13 (14%); local infection, 7 (8%); vascular access infection, 3 (3%);