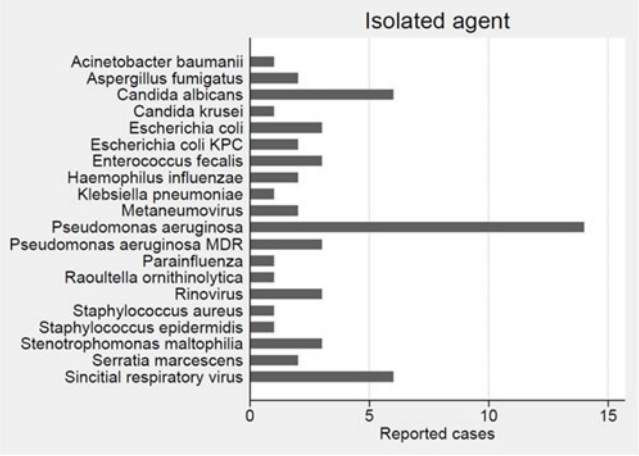


**Fig. 2.**

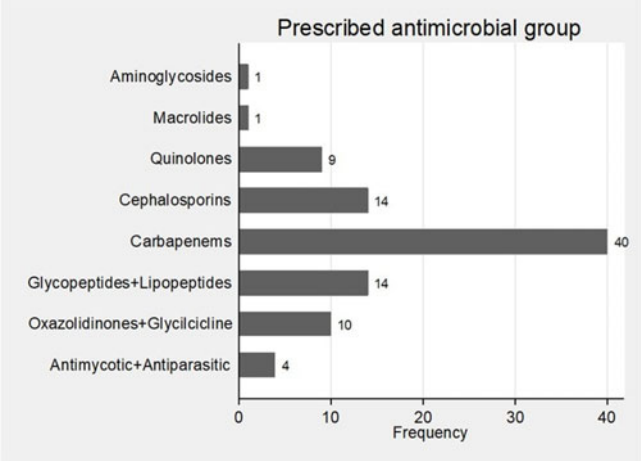


**Fig. 3.**

47 cases (43.93%) from 2017, 38 cases (35.51%) from 2018, and 20.56% from 2019. The month that reported the highest frequency was February, with 17 cases (15.89%). The median age was 63 years (range, 0–97 years; IQR, 36). The most affected age group was ≥65 years (48.60%), and the most affected 5-year age group was 75–79 years (13.08%). Moreover, 60 cases (56.07%) were men and 47 (43.93%) were women. Regarding the reason for discharge, 71% were discharged due to improvement, 27% died, and 2% were transferred to another healthcare facility. Also, 17 patients (15.89%) required re-admission due to respiratory illness within 72 hours of previous discharge. The most common diagnosis was a solid malignant neoplasm (20.19%), followed by heart or vascular malformation or anomaly (12.50%). The mean inpatient hospital stay was 39.95 days (±46.40; median, 27 days, range, 2–317 days; IQR 35 days). The median time elapsed until detection was 14 days. The hospitalization area with the most cases was the intensive care unit, with 24 cases (22.43%); the service with most cases was oncology with 21 cases (20.56%). The most isolated pathogen was *Pseudomonas aeruginosa* (14%). Moreover, 59% were gram-negative, 36% were gram-positive, 19.67% were viruses, and 14.75% were fungi. Our accumulated-incidence-rate was 0.58 cases per 1,000 patient days and our case-fatality-rate was 25.23%. Furthermore, 41% of cases required invasive mechanical ventilation, 52.34% required noninvasive mechanical ventilation, 5% cases had an endo-pleural tube, 9.35% had a nasogastric tube, and 41.12% had a central venous catheter. The most-prescribed antimicrobial was meropenem (33.33%), and meropenem-resistance was 61.54%. **Conclusions:** Infection prevention efforts should target oncological patients, critical-care units, and the elderly. We must reinforce our antimicrobial policy due to our overprescription of carbapenems. Early detection is needed to reduce mortality.

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**Disclosures:** None
Doi:10.1017/ice.2020.806

**Presentation Type:**
Poster Presentation

**Hepatitis A Virus Survival on Drug Paraphernalia**

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**Background:** The ongoing hepatitis A outbreak in the United States has concerned public health authorities since March 2017. The outbreak has already spread throughout 30 states and includes primarily homeless individuals and persons who use drugs, including persons who inject drugs (PWIDs). Contaminated drug injection paraphernalia and sharing of these items are suspected to be one of multiple causes of hepatitis A virus (HAV) transmission in those populations. **Methods:** We used a standard plaque assay to investigate HAV infectivity. Liquid suspensions of HAV were tested to examine the effects of time and temperature on viral infectivity. We also examined HAV survival on commonly used drug paraphernalia, such as needles, syringes, cookers, tourniquets, and cotton balls/filters frequently shared among PWIDs. We investigated the effect of low pH on HAV survival using citric acid, which is frequently used by PWIDs during dose preparation. We also compared the plaque assay results with those concurrently obtained by RT-PCR to establish whether viral HAV RNA levels could be used as surrogates for plaque assay results. **Results:** We found that HAV suspended in PBS at room temperature was able to infect FRhk4 cells for >17 weeks. HAV remained viable in syringes and needles (ie, semidry conditions) for up to 10 weeks depending on the size of the needles and the syringe dead volume. HAV survival in dry conditions on cooker, tourniquet, and cotton balls/filter surfaces did not exceed 4 weeks. HAV retained its infectivity for >10 weeks at pH as low as 2. PCR results suggest that RNA is amplified from both infectious and noninfectious HAV. **Conclusions:** Our findings show that HAV can survive and remain infective in the PWID setting for 4–10 weeks depending on the type of paraphernalia examined. These findings suggest that sharing drug paraphernalia by the homeless and PWIDs can potentially facilitate the transmission of HAV within these populations. Moreover, our results confirm that the plaque assay is currently the only reliable method to determine the infectivity of HAV in vitro.

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**Disclosures:** None
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**Presentation Type:**
Poster Presentation

**Hepatitis C Virus Transmission at a Long-Term Care Facility (LTCF) Providing Hemodialysis Services—Georgia, United States, 2019**

JoAnna Wagner, Georgia Department of Public Health; Ami Gandhi, Georgia Department of Public Health; Bill Johnson, Georgia Department of Public Health; Nicole Gualandi, Division

Figure 1-1 Global Hepatitis Outbreak Surveillance Technology

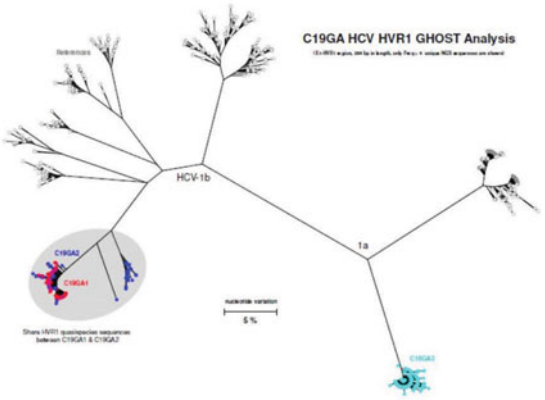


Figure 1-2 Genotypic Test Results

| 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**

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**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