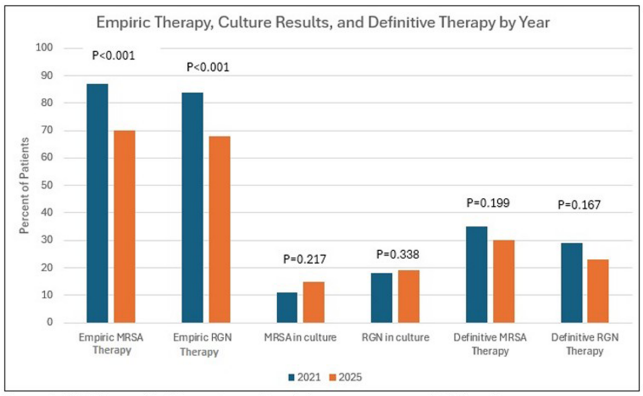


Figure 1. MRSA: methicillin-resistant *Staphylococcus aureus*. RGN: resistant gram-negatives.

Presentation Type:
Oral Presentation
Subject Category: C. difficile

Clostridioides difficile Whole Genome Sequencing Does Not Support Transmission from Environmental Contamination by Prior Room Occupants‡

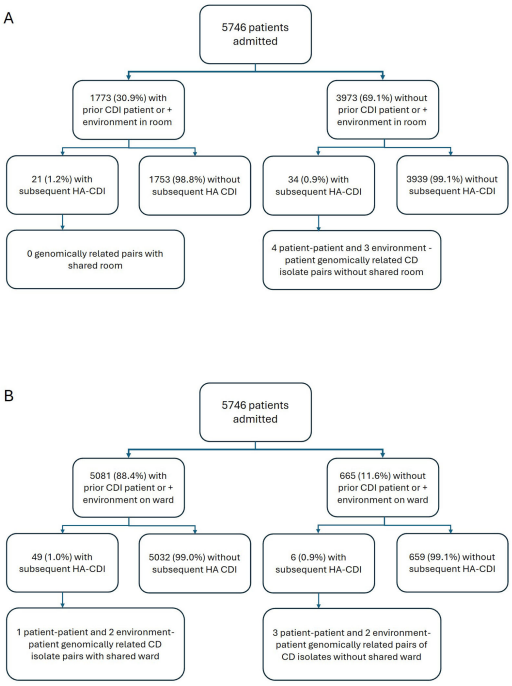
Sarah Redmond, Maria Torres-Teran[1], Jennifer Cadnum[1], Claire Kaple[2], Munok Hwang[3], Hosoon Choi[4], Piyali Chatterjee[4], Chetan Jinadatha[4] and Curtis Donskey[1]
[1]Cleveland VA Medical Center; [2]VANEOHS; [3]Central Texas VA Research Foundation and [4]Central Texas Veterans Health Care System

Background: Admission to a room previously occupied by a patient with Clostridioides difficile infection (CDI) has been identified as a risk for CDI. However, previous studies have not included molecular typing to definitively link healthcare-associated CDI (HA-CDI) cases to prior room occupants or to residual spore contamination on surfaces. **Methods:** In an acute care hospital, we conducted a 1-year cohort study to determine the proportion of HA-CDI cases linked to prior room occupants with CDI or to room surfaces remaining contaminated after post-discharge cleaning and disinfection. Cultures were collected from post-discharge CDI and non-CDI rooms. Whole genome sequencing was used to determine relatedness of isolates. We calculated the percentage of HA-CDI cases infected with isolates genomically related to prior room or ward-level exposures. **Results:** Of 5,746 patients admitted, 22 had community-associated CDI and 55 were diagnosed with HA-CDI. C. difficile was recovered from 79 of 327 (21%) post-discharge rooms, including 14 of 36 (39%) CDI rooms and 83 of 287 (29%) non-CDI rooms. Of 1,773 patients with room-level exposure to prior CDI patients or contaminated surfaces, 21 (1%) developed HA-CDI, but none were infected with genomically-related isolates (Figure 1.A). Of 49 patients developing HA-CDI after ward-level exposures, 3 were infected with isolates genomically related to prior CDI patients or contaminated surfaces on the ward (1.B). **Conclusion:** Despite frequent exposure to rooms previously occupied by patients with CDI or contaminated with C. difficile, no HA-CDI cases were linked to prior room exposures based on whole genome sequencing.

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‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.

Figure 1. Flow diagram for the new admissions during the study stratified based on room (A) or ward (B) level exposures to prior patients with *Clostridioides difficile* infection (CDI) and/or to prior environmental contamination. HA-CDI, healthcare-associated CDI.



Presentation Type:
Oral Presentation
Subject Category: CLABSI

Midlines for Outpatient Parenteral Antimicrobial Therapy: A Not-So-Safe Alternative to Peripherally Inserted Central Catheters?‡

Justin Kim[1], Guadalupe Ordaz-Nielsen[1], James Vu[2], Kim Tran[1], Ho Kim[3], Michael Schoeny[1] and Michael Lin[1]
[1]Rush University Medical Center; [2]UC Davis Medical Center and [3]Rush University

Background: The safety of midlines (MLs) versus peripherally inserted central catheters (PICCs) in the context of outpatient parenteral antimicrobial therapy (OPAT) is still debated. The Infectious Diseases Society of America guidelines currently offer a weak recommendation to consider MLs for antibiotic durations of <14 days. The purpose of this study was to quantify the ML complication rate compared to PICCs for OPAT. **Methods:** We performed a single-center, retrospective cohort study of MLs and PICCs placed by the bedside vascular access team for OPAT as recommended by the infectious diseases consult service at a 670-bed urban academic medical center. Between July 2019 and June 2022, 1351 catheters were placed in 1252 unique patients for OPAT. The primary exposure was the placement of a ML versus PICC, informed by selection guidelines from the Infusion Nurses Society. The primary outcome was any bloodstream infection (BSI) or superficial or deep venous thromboembolism (VTE) while the catheter was present. We estimated the hazard ratio (HR) of developing the outcome among MLs compared to PICCs using Cox proportional hazards models, accounting for multiple episodes of OPAT-related catheter placement over time in the same patient and adjusting for confounding by planned antibiotic duration of ≥14 days

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