the considerable proportion of IPC resources dedicated to daily education and feedback in clinical areas, the IPC teams reported that improvement was often difficult to achieve. **Conclusion:** Given the high burden of CROs and limited IPC resources, detailed knowledge of IPC opportunities for improvement will help hospitals target novel interventions for CRO prevention and containment. Further investigation of colonization rates and effective performance improvement methods in these settings is needed.
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Impact of Transitioning to Single-Patient Rooms on Prevention of Multidrug-Resistant Organisms in a Resource-Limited Facility

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Background: Healthcare-associated infections (HAI) substantially increase hospital costs and lead to poor patient outcomes, particularly when caused by multidrug-resistant organisms (MDRO). To decrease MDRO transmission, isolation of colonized or infected patients in single rooms is recommended. However, single-patient isolation rooms are expensive to build and often unavailable in resource-limited hospitals. In 2023, an intensive care unit (ICU) at a large Brazilian tertiary hospital relocated from a space with an open floor plan to a newly built location with single-patient rooms. We evaluated the impact of this transition on acquisition of carbapenem-resistant Enterobacterales (CRE) colonization, HAI, and compliance with Hand Hygiene (HH) and Contact Precaution (CP) activities. **Methods:** We compared rates of CRE colonization acquisition, CRE colonization pressure, HAI, and compliance with HH and CP between pre- (March 1, 2022 – Feb 28, 2023) and post-implementation of single-rooms (March 1, 2023 - October 31, 2023) in a 12-bed surgical ICU. All patients were screened for CRE colonization on admission to the unit and weekly until discharge using rectal swab cultures. Colonization pressure was defined as the ratio of CRE-positive patient-days (PDs) to the total number of PDs. Rates of central-line associated blood-stream infections, ventilator-associated pneumonia, and catheter-associated urinary tract infections were monitored. HH and CP compliance were monitored weekly by infection prevention staff outside of the unit. Poisson regression and multiple linear regression were used to compare rates between pre- and post-implementation periods. **Results:** Healthcare acquisition of CRE colonization remainedstable between pre- and post-implementation (incidence rate ratio: 0.88 (95%CI, 0.73-1.05; P=0.16) despite an increase in CRE colonization pressure of 8.6% over baseline (from 7.84% pre- to 16.39% post-implementation (95% confidence interval [CI], 4.13-12.96%; P=.001)). The latter was driven by reduced turnover of CRE-colonized patients in the post-implementation period (mean patient-day reduced by 10.33; 95%CI, 3.06-17.61; P=0.006). Incidence of HAIs also remained stable (global incidence 3.12 vs 3.30, pre- and post-intervention, respectively; P=0.2). HH compliance was high prior to the transition (95.7%) and increased slightly but not significantly post-intervention (97.5%; P=0.3). CP compliance improved by 9.83%, especially in gown and glove changes after each patient interaction, from 90.62% pre- to 100% post-implementation (95%CI, 1.52-17.22; P=.02). Conclusion The move to an ICU with exclusively single-patient rooms was associated with increase in CP compliance. This could help explain why HAI incidence and healthcare acquisition of CRE colonization remained stable despite a significant increase in CRE colonization pressure.
Disclosure: Matias Salomao: Speaker - Cepheid

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Assessment of 19 Operation Room and Sterile Processing Units in Puerto Rico, 2023: Preliminary Findings using a new ICAR Tool

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Background: Infection prevention and control assessments in healthcare settings serve as a primary resource for obtaining data and providing recommendations based on safety, compliance, and quality assurance guidelines. In Puerto Rico (PR), surgical site infections are underreported in the Epi Info platform used by the Puerto Rico Department of Health (PRDOH), mainly due to the complexity of their identification. By focusing on evaluating Operating Rooms/Sterile Processing and Distribution (OR/SPD) units in acute care facilities (ACFs), our goal is to generate new data within the Healthcare-Associated Infection/Antibiotic Resistance (HAI/AR) Program, specifically related to patient management throughout preoperative, intraoperative, and postoperative phases, as well as reprocessing practices. **Methods:** Nineteen evaluations of ACFs' OR/SPDs were conducted from May through December 2023. Direct observations, file reviews, and personnel assessments were performed using an infection control assessment and response (ICAR) tool developed collaboratively by a team from an acute facility in PR and the HAI/AR Program staff. This ICAR Tool was customized based on guidelines from the certified Board for Sterile Processing and Distribution (CBSPD), the Association of periOperative Registered Nurses (AORN), and the Association for the Advancement of Medical Instrumentation (AAMI), among other regulatory agencies. The Division of Health Quality Promotion (DHQP) reviewed and approved the tool for use in these evaluations. **Results:** Key findings indicate that 32% of Sterile Processing Department (SPD) units restrict access to dedicated personnel with available manufacturer's instructions, yet only 36% of SPD personnel are certified in CBSPD and packaging practices. Only 10% of facilities had a water treatment system for sterilization and Immediate Use Steam Sterilization (IUSS) policies. Notably, 84% of endoscopy areas require additional equipment for cultivating endoscopes, and no facility possessed a borescope for visually inspecting endoscope lumens. Tray inspection occurred in 21%, and only 31% of staff knew the Spaulding Classification and Class V Indicators.

Conclusion: These data underscore the necessity of evaluating OR/SPD units in ACFs to provide updated recommendations and mitigate the incidence of surgical site infections (SSI). They offer insight into the structural and functional status of OR/SPD units in Puerto Rico, aligning reporting with OR/SPD practices to enhance patient care and minimize infection risks.

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Rapid Genomic Characterization of High-Risk, Antibiotic Resistant Pathogens Using Long-Read Sequencing to Identify Nosocomial

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Background: Current epidemiological methods have limitations in identifying transmission of bacteria causing healthcare-associated infections (HAIs). Recent whole genome sequencing (WGS) studies found that genetically related strains can cause HAIs without meeting standard epidemiologic definitions, but these results could not provide data in a timely fashion needed for intervention. Given recent advances in Oxford Nanopore Technologies (ONT) sequencing, we sought to establish a validated ONT pipeline capable of providing accurate WGS-based comparisons of clinical pathogens within a short time frame that would allow for infection control interventions. **Method:** Using electronic medical record data, we identified potential healthcare acquisition of methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant enterococci (VRE), and carbapenem-resistant gram-negative rods. Bacterial genomic DNA was directly extracted from clinical microbiology lab plates. Sequencing was conducted with the ONT MinION sequencer and R10.4.1 flow cell. MINTyper for single nucleotide polymorphism (SNP) calling and Ridom SeqSphere+ for core genome MLST were used to determine genetic relatedness. The main outcome was time from pathogen identification to completed genetic analysis. **Result:** The weekly workflow, from genomic DNA extraction to complete data analysis, averaged 2.6 days with a standard deviation of 1.3 days. (range: 1 to 6 days). Starting in August 2023, we have sequenced a total of 177 bacterial isolates from 156 unique patients. Isolates came from blood (38%), tissue/wound/body fluid (24%), urinary tract (20%), respiratory tract (16%), and rectal swab (2%). To date, six genetically related clusters have been identified. Three clusters involved ST117 vancomycin-resistant Enterococcus faecium (VREfm), comprising a total of 13 unique patients distributed as 2, 3, and 8 patients in each group, with pairwise SNP differences of 20, 11, and 14. Patients within the same clusters showed epidemiological links through overlapping admissions and temporally shared ICU stays. Additionally, another cluster consisted of five genetically related ST633 Pseudomonas aeruginosa isolates, with a pairwise SNP difference of 57.5. Each patient in this cluster had potential epidemiological links through overlapping admission times, despite the absence of identified shared spaces. The last two clusters involved Klebsiella pneumoniae and Escherichia coli (two cases each), with pairwise SNP differences of 18 and 9, respectively. In both cases, each patient showed potential epidemiological links through overlapping admission times. **Conclusion:** Our stand-alone ONT pipeline was able to rapidly and accurately detect genetically related AMR pathogens, aligning closely with epidemiological data. Our approach has the potential to assist in the efficient detection and deployment of preventative measures against healthcare-associated infection transmission.

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Evaluation of Empiric Antibacterial Treatment and Subsequent De-escalation for Febrile Neutropenia

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Background: Febrile neutropenia (FN) is the most common complication of chemotherapy-induced neutropenia that affects over 80% of patients with hematologic malignancies. National guidance and randomized controlled trial data demonstrate empiric antimicrobial therapy (EAT) can be discontinued after 72 hours of apyrexia and clinical recovery regardless of absolute neutrophil count (ANC). A 2019 internal study identified opportunity for improvement for targeted de-escalation. We aimed to reevaluate duration of EAT in patients with FN without a documented source of infection. **Methods:** A pharmacovigilance platform identified 110 patients from January to September 2023 without identified source of infection. Data collection was performed via manual chart review. Historic patient data from our 2019 cohort (n=50) was available in our research repository. The primary outcome was the duration of EAT in patients with at least 72 hours of apyrexia and clinical recovery, defined as normalization of vital signs. Secondary outcomes included adverse events associated with EAT, and initiation of intravenous vancomycin. **Results:** Baseline characteristics for 2023 were similar to historic, median age was 67.5 years, 56% were male, and median ANC at fever onset was 150 cells/μL. EAT was continued in 29 patients (58%) despite defervescence and stabilization versus 35 (70%) in 2019 (figure 1). Average duration (LOT) of EAT beyond clinical stabilization was 6 versus 7 days. Adverse effects due to EAT occurred in 13 patients

Table 1:

Outcomes	2019 (n = 50)	2023 (n = 50)
Total LOT mean (± SD)	11 (8)	8 (4)
EAT continued post defervescence & clinical stability, n (%)	35 (70)	29 (58)
Duration of EAT beyond clinical stability, mean (± SD)	7 (±6)	6 (±6)
Adverse Events, n (%)		
LFT abnormalities (≥4x ULN)	1 (2)	4 (8)
Acute Kidney Injury	2 (4)	2 (4)
C. difficile infection	1 (2)	7 (14)

Figure 1: Patients Continued on EAT continued Post Defervescence & Clinical Stability (%)