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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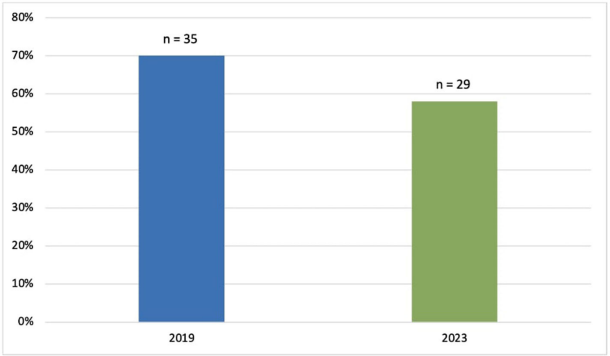
Background: Febrile neutropenia (FN) is the most common complication of chemotherapy-induced neutropenia that affects over 80% of patients with hematologic malignancies. National guidance and randomized controlled trial data demonstrate empiric antimicrobial therapy (EAT) can be discontinued after 72 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 (%)



in 2023 (26%) versus 4 (8%); of which, C. difficile infection (CDI) was the greatest contributor. Vancomycin was initiated in 31 patients (62%), 22 having no identifiable indication. **Conclusions:** Rates of EAT de-escalation for neutropenic patients after 72 hours of apyrexia and clinical stability improved by 12% as compared to 2019. Mean days of overall EAT was 3 days less in 2023. With a notable increase in CDI rates in 2023, dedicated time for antimicrobial stewardship review, clinician education and guideline driven alerts for review will be explored to help further improve practice.

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Subject Category: Infections in Immunocompromised Patients
Nosocomial Transmission of Mycobacterium tuberculosis in an Oncological Setting
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Objective: Mycobacterium tuberculosis (MTB) is a contagious airborne disease that is spread from person to person via particles in the air which are expelled when speaking or coughing1. This retrospective observational study aims to assess the nosocomial transmission of pulmonary MTB among inpatient roommates in a high-risk oncological population over a 14-year period. With limited studies on the transmissibility of MTB in such environments, the investigation focuses on evaluating the risk of nosocomial transmission and implementation of appropriate infection control measures. **Design:** A retrospective analysis from 2010 – April 2023 was conducted in an acute care, 500-bed oncological center. Following exposure workups performed by the Department of Infection Prevention and Control, 17 of 57 identified patients with active pulmonary MTB had inpatient stays with roommates. Source infectivity showed 7 AFB smear positive results, 4 MTB PCR positive results, and 14 MTB culture positive results. Some index patients had a combination of AFB, PCR and/or culture positivity. A high-risk exposure is defined as any patient who shared a room with an index patient for >4 cumulative hours during the infectious period. Infectious period was determined for each index patient based on the onset of symptoms and laboratory results. Workups identified 33 exposed roommates who were notified and advised to undergo testing, employing QuantifERON (QFT-GIT) serum test or Tuberculin skin (TST) PPD test at least 8 weeks following their last day of exposure. The overlap between inpatient roommates and index patients ranged from 1 to 4 days, averaging 1.5 days. **Results:** Of the 33 high-risk roommates, 14 (42%) patients were unable to provide follow-up testing for various reasons including: patient expiration prior to testing, patient transfer to hospice, and being lost to follow up. Nineteen (58%) patients completed post-exposure testing. 12 patients underwent PPD testing (63%) and 7 patients underwent QuantifERON testing (37%). Zero (0%) were found to have a positive QuantifERON or PPD following their exposure. 15.8% (N=3) of exposed patients had hematologic malignancies, and 84.2% (N=16) of exposed patients had solid tumor malignancies. **Conclusion:** The risk of active pulmonary MTB transmission in an oncological, inpatient setting was determined to be low. The absence of positive conversions among roommates of confirmed MTB patients underscores the effectiveness of infection control measures, emphasizing the importance of isolating confirmed or suspected cases promptly. Ongoing efforts should continue to focus on these preventive measures to mitigate the risk of MTB transmission in similar high-risk settings.

References: 1. How TB Spreads. CDC, 2023. https://www.cdc.gov/tb/topic/basics/howtbspreads.htm

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Subject Category: Leadership
Bridging the Gap: Specialized Training Programs for Infection Prevention Specialists Increase Certification Success
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Background: The role of the infection preventionist (IP) is complex and encompasses a range of responsibilities requiring extensive knowledge in infection control practices, data analysis, surveillance, performance improvement and collaboration with multidisciplinary teams. Infection prevention certification (CIC) by the certification Board of Infection Control (CBIC) is a standardized marker of knowledge and competencies required for practice in the field. In a 2020 survey of IPs, less than half were certified or planned to become certified. Of those that do take the certification exam, less than three quarters pass on their initial exam attempt. **Methods:** From 2017 to 2023, fifty-two new IPs were enrolled in a competency-based training program which combined didactic and applied learning on core IP job functions, and a structured mentoring program. The initial didactic phase consisted of evidence-based learning modules with validation of competency through post-training testing and practical demonstration. Education was provided by an advanced practice IP via remote webinars, which included discussion of questions, skills coaching, and review of post-tests. Novice IPs were partnered with at least two preceptors: one advanced practice lead preceptor guided the novice IPs through assigned education modules and oversaw program management and training benchmarks. A second, near-peer preceptor or mentor collaborated with the novice IP in the facility setting. Initial training focused on facility operations, surveillance, rounding and other facility specific activities. Facility mentors were responsible for combining education module topics with practical application of skills. Mentors guided novice IPs through National Healthcare Surveillance network (NHSN) surveillance training and validated surveillance and infection coding until the novice IP had an interrater reliability validation assessing surveillance competency. After the initial training phase, the novice IPs began preparation for certification. This phase included additional training modules aligned with the CBIC certification content outline and practice exams. **Results:** All 52 novice IPs completed the training program and attempted the CIC examination. The initial pass rate for the certification exam among IPs in the supervised training and mentorship program was 98.1% (n=51). This is 33% higher than the initial pass rate published by CBIC, which was 73.9% (Figure 1). **Conclusions:** Organizing evidence-based guidelines into topic-specific modules builds a foundation of infection prevention and control knowledge, which is enhanced through remote instruction and direct application of skills under a preceptor's supervision.

Figure 1: CIC Initial Test Pass Rate