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 (%)