Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Outbreaks
Enterococcal Bacteremia outbreaks during SARS-COV-2 in Intensive Care Unit (ICU): The role of Strain Identification
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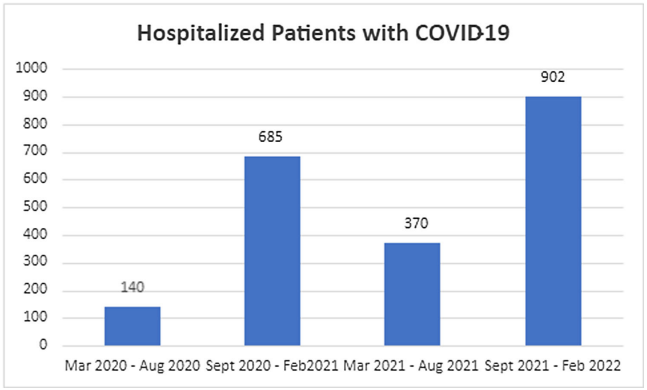
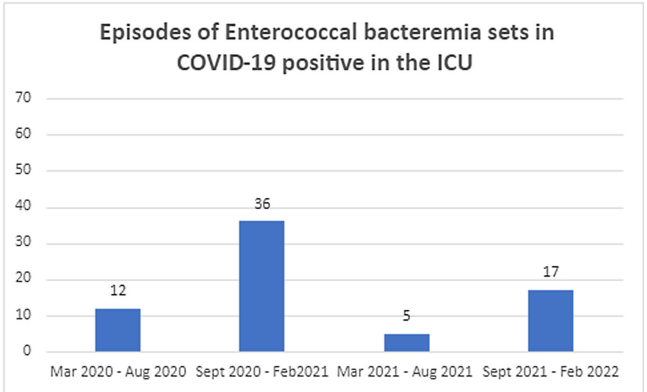
Background: An unprecedented burden of morbidity and mortality has been reported in patients admitted to healthcare facilities with SARS-COV-2 infection globally since March 2020. A higher incidence of ICU-acquired bloodstream infection has been described with the cumulative risk increased with the length of ICU stay, use of steroids, anti-inflammatory agents, and indwelling catheters. Additionally, SARS-COV-2 infection may increase the risk of bacteremia from gastrointestinal flora such as Enterococcus species by disrupting the gastrointestinal barrier and microbiome. **Methods:** We aimed to investigate the outbreaks of Enterococcus bacteremia in patients with SARS-COV-2 infection and included patients aged>18 years admitted to the ICU at the Oklahoma City Veterans Affairs Medical Center who were infected with SARS-COV-2 and were identified as having positive blood cultures for Enterococcus faecalis, Enterococcus faecium including vancomycin-resistant species and other bacterial or candida species between March 1, 2020, to March 9, 2022. We collected the following data: duration of hospitalization including ICU stay, unit and room location during the hospital stay, blood culture collection date and results, duration, and site of central line placement, duration of ventilation, administration of antimicrobials and COVID-19 directed therapeutics using computerized patient record system (CPRS). We sent 10 E. faecalis and 12 E. Faecium isolates for genetic analysis. DNA was sequestered from each isolate and multi-locus sequence typing (MLST) was performed by amplifying 7 regions of the E. faecalis genome and 7 regions of the E. faecium genome by polymerase chain reaction (PCR). Resulting amplicons were sequenced and allele type for each gene region and overall sequence type was determined using MLST database (http://pubmlst.org). **Results:** There were 22 episodes of enterococcal bacteremia in a 3-month duration in the ICU in 20 patients of which 17 were associated with another episode with the same strain (Figure-1-2). Central line placement was noted in 18/22 episodes. Genetic analysis by multi-locus sequence typing of enterococcal bacterial strains was performed by the Public Health Reference Laboratory, Palo Alto. Similar strains were localized to patients in the same geographical region in the ICU (Figure 3). The isolates from 2 other patients who presented with the same strain of Enterococcus but were never hospitalized at the same time during the COVID-19 pandemic were localized to another hospital where both had received care at different times. **Conclusion:** Higher rates of enterococcal bacteremia were reported during the SARS-COV-2 pandemic. Geographical proximity with strained infection control measures accounted for ICU outbreaks seen in our tertiary care setup.





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Whole Genome Sequencing for the Identification of a Streptococcus agalactiae Outbreak in Neonatal Intensive Care Unit
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Background: While Streptococcus agalactiae (Group B Streptococcus [GBS]) infections in infants usually result from maternal transmission, healthcare-associated cases, particularly in the neonatal intensive care unit (NICU), can occur. Whole genome sequencing (WGS) can aid in investigating GBS outbreaks among infants in hospital settings. The aim of the study is to describe the investigation of GBS infections in NICU using WGS. **Methods:** Infection prevention and control (IPAC) at our hospital monitors the occurrence of late-onset GBS disease (LOD) in our 57-bed NICU, which consists of all private rooms. The occurrence of 2 cases of LOD within 2 weeks triggered an investigation, including WGS of the two isolates and isolates causing invasive GBS during the last 6 months in the unit. GBS isolates underwent WGS using Illumina at Canada's National Microbiology Laboratory. All affected patients underwent

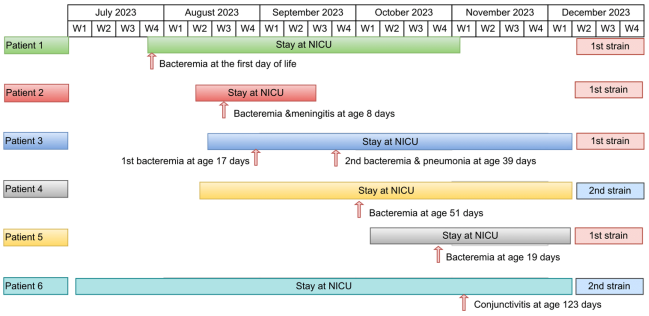

chart-review. Outbreak description and investigation: In August 2023, two NICU neonates (patients 2,3) experienced LOD two weeks apart, one with bacteremic meningitis and the other with two bacteremic episodes three weeks apart. While WGS was pending two additional cases of late-onset GBS bacteremia (patients 4,5) occurred. Isolates from Pts 2,3 and 5 were indistinguishable from each other and from an isolate from an infant admitted to the NICU with early onset bacteremia on July 27, 2023 (day 1 of life) (patient 1). Weekly point prevalence for throat and rectal colonization over 3 weeks identified five infants colonized with unrelated strains. An additional long-stay infant (patient 6) developed GBS conjunctivitis due to a strain indistinguishable from (patient 4) by pulse field gel electrophoresis, WGS for the second cluster is pending. IPAC interventions: Lapses in IPAC practices were observed, with no commonalities among cases other than similar geographic location within the unit. We hypothesized transmission was due to horizontal transmission between babies due to these lapses. Basic IPAC measures, including hand hygiene and environmental cleaning, were reinforced; Additional Precautions were not used due to private rooms' unit structure. No environmental samples were taken due to lack of an obvious environmental point or common source. Point prevalence monitoring persisted until no new cases related to the outbreak strains were further identified in three consecutive weekly point prevalence. **Conclusions:** Increased awareness of healthcare-associated transmission is crucial in NICU as LOD GBS emerges. WGS plays a key role in identifying transmission. Detecting a multi-strain outbreak can appropriately redirect investigations. Legend: Figure 1: Timeline of stay at NICU and infection timing for patients 1-6

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Outbreak of New Delhi Metallo-β-lactamase-producing Escherichia coli in a Neonatal Intensive Care Unit, New York State

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Background: Outbreaks of carbapenemase-producing (CP) organisms (CPOs), including carbapenem-resistant Enterobacterales (CRE), in neonatal intensive care units (NICUs) are not well documented. The Centers for Disease Control and Prevention (CDC) identifies CP-CRE as an urgent threat to United States (US) healthcare facilities. Wadsworth Center, the New York State (NYS) Department of Health's (NYSDOH's) public health laboratory, participates in CDC's Antimicrobial Resistance Laboratory Network to provide CPO identification, characterization, and surveillance. NYSDOH investigated an outbreak of CP-CRE Escherichia coli (E. coli) infections in NICU patients reported by one hospital. **Method:** Hospital A reported a CRE E. coli outbreak in their NICU to NYSDOH, as required by NYS Sanitary Code. In response, epidemiologists reviewed case data, conducted case finding, and provided infection control guidance to the hospital. Hospital A continued NICU clinical surveillance and conducted colonization screening to detect additional cases of CRE E. coli. The Wadsworth Center Antimicrobial Resistance Laboratory Network tested isolates from affected patients for CP genes and performed whole genome sequencing (WGS) to determine the CP gene variant, multilocus sequence type (MLST), and relatedness by mutation event (ME) analysis. NYSDOH epidemiologists assessed Hospital A's infection control practices in affected areas and provided recommendations. **Result:** Hospital A identified two CRE E. coli infections in NICU patients with overlapping admissions in June-July 2023. Retrospective surveillance identified a third CRE E. coli case in an adult medical intensive care unit patient on admission to Hospital A in June 2023, with prior hospitalization April-May 2023. WGS analysis identified the blaNDM-5 gene in all three CRE E. coli patient isolates. The two NICU patients' isolates had the same MLST (361/650) and differed by 9 MEs, indicating relatedness to each other and not the adult patient's (MLST 167/2). NICU patient colonization screening identified no additional blaNDM-5 E. coli cases. NYSDOH's NICU infection control assessment found that both cases were in adjacent isolettes within three feet of each other. Clean isolettes, equipment, and supplies for new admissions were stored in the clinical care space, not in a separate clean area. **Conclusion:** CP-CRE is an urgent threat to US healthcare facilities, including hospital NICUs. Though the incidence and prevalence of CP-CRE blaNDM-5 E. coli are not well-defined in NY, single healthcare-associated cases in NICU populations represent an outbreak. The Wadsworth Center Antimicrobial Resistance Laboratory Network's contributions complement traditional epidemiologic surveillance and investigation methods to provide more specific, comprehensive infection

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Not Your Usual Exposure: Tuberculosis Contact Investigation Related to Contaminated Bone Allograft

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Background: Mycobacterium tuberculosis transmission through contaminated bone allograft product is unusual and was first described in 2021 with a second outbreak in 2023. In July 2023, Michigan Medicine conducted contact tracing for healthcare personnel (HCP), patients, and visitors following exposure to an immunocompromised patient with surgical site infection and subsequent widely disseminated tuberculosis (bacteremia, pulmonary, lymphadenopathy) following spinal fusion with bone allograft in April 2023. The patient was in the emergency department, operating room (OR), and inpatient units for 9 days prior to initiation of Airborne Precautions (AP). **Methods:** Michigan Medicine is a 1,107 bed academic hospital. HCP are screened for tuberculosis with interferon-gamma release assay (IGRA) testing upon hire and following tuberculosis exposure. Exposure testing includes baseline IGRA testing and follow-up testing at 10-12 weeks post exposure. Exposure criteria for this investigation was defined as sharing room airspace with the tuberculosis patient prior to initiation of airborne precautions or Central Sterile Processing Department (CSPD) staff involved with instrument decontamination without the use of a respirator. Of note, universal masking with surgical masks was not required during this time for staff and patients/visitors, with the exception of CSPD and OR staff. Contact tracing was performed by Infection Prevention and Occupational Health Services managed all test results and conversions. **Results:** 176 employees from perioperative care areas (n=30), CSPD (n=7), OR (n=9) and inpatient units (n=130) were