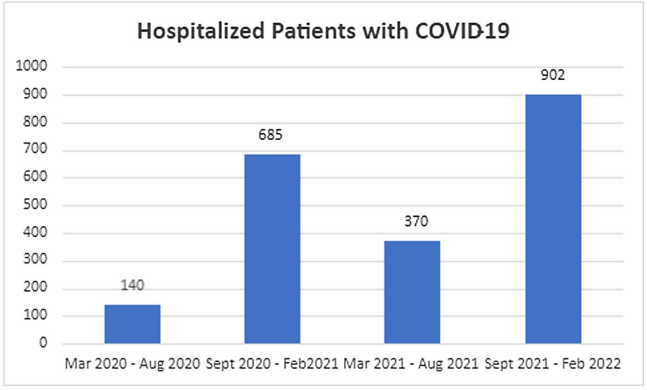
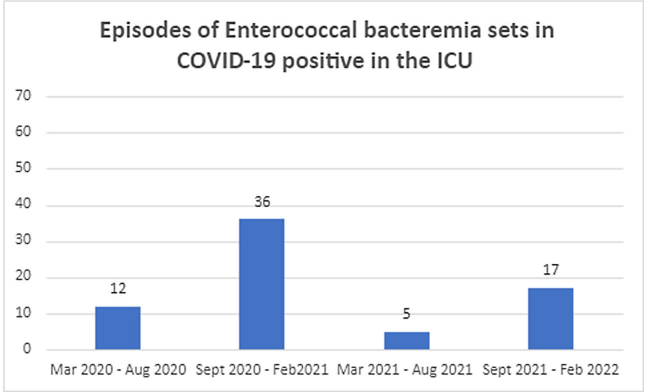
Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Outbreaks
Enterococcal Bacteremia outbreaks during SARS-COV-2 in Intensive Care Unit (ICU): The role of Strain Identification
Sharanjeet K. Thind, Mercy Hospital, Oklahoma City; Ghias Sheikh, Mercy Hospital, Oklahoma City; Syeda Sahra, OUHSC; Dena R. Shibib, University of Oklahoma Health Sciences Center; Awais Bajwa, University of Oklahoma Health Sciences Center; Houssein A. Youness, University of Oklahoma Health Sciences Center and Christopher Gentry, University of Oklahoma Health Sciences Center

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.





Antimicrobial Stewardship & Healthcare Epidemiology 2024;4(Suppl. S1):s124
doi:10.1017/ash.2024.282

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Outbreaks
Whole Genome Sequencing for the Identification of a Streptococcus agalactiae Outbreak in Neonatal Intensive Care Unit
Halima Dabaja Younis, Sinai Health System- Toronto; Allison McGeer, Sinai Health System- Toronto; Vanessa Allen, Sinai Health System- Toronto; Angelie Seguban, Sinai Health System- Toronto; Andrea Morillo, Sinai Health System- Toronto; Irene Martin, National Microbiology Laboratory, Public Health Agency of Canada; Alyssa Golden, Public Health Agency of Canada - National Microbiology Laboratory and Jennie Johnstone, Public Health Agency of Canada - National Microbiology Laboratory

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