Presentation Type:
Poster Presentation
Subject Category: Microbiology
Assessment of Microbial Transmission by Insect Vectors in Healthcare Settings: A Systematic Review
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Background: Multi-drug resistance is increasing, and insects may serve as critical reservoirs for these bacteria. While insects are part of the world's natural flora and exist even in healthcare settings, their presence is often overlooked or disregarded. Current healthcare safety guidelines focus on keeping insects out but fail to address their potential contribution to nosocomial pathogen transmission, This study aims to determine the extent of knowledge regarding microbial transmission by insects in a healthcare setting. **Methods:** The systematic literature search utilized subject headings and preferred index terms such as "insects," "microbial transmissions," "insect vector," "insecta," and "cross infection" to construct a reproducible MEDLINE search within PubMed. This search was translated across Embase, CENTRAL, and select supplemental resources. Retrieved studies exceeded 1000 records, which were deduplicated using Covidence software, leaving 655 eligible articles for screening. A total of 36 peer-reviewed studies documenting insects in healthcare settings (e.g., hospitals, clinics, rehabilitation centers, ambulatory centers) were included and underwent data extraction and analysis. Excluded studies were non-English without translation or irrelevant to healthcare. Outcomes included identification of colonizing organisms, evidence of microbial transmission, and prevalence of multidrug-resistant pathogens carried by insects. Risk of bias was evaluated using the LEGEND criteria, and extracted data were synthesized following the Cochrane Review for Systematic Reviews in conjunction with the Joanna Briggs Institute (JBI) frameworks. **Results:** Of the analyzed studies the majority were from low- to middle-income countries and included the study of common insects such as cockroaches, ants, and various classes of flies. Studies included the examination of external surfaces and internal contents of the insects via evidence-based, aseptic collection and laboratory processes. Few studies demonstrated the likely transmission of bacteria via insect vector, though all studies demonstrated robust colonization of insect vectors with pathogenic microbes including multi-drug resistant bacteria. **Conclusion:** This review highlights the potential role of insects in microbial transmission in healthcare settings. However, most studies failed to establish a direct link between insects and pathogen transmission. Further research into areas such as multi-drug resistance transmission via insect vectors is needed.

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Presentation Type:
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Subject Category: Molecular Epidemiology
Genomic Characterization of Extended-Spectrum Beta Lactamase (ESBL)-Producing Klebsiella pneumoniae in Transplant Recipients
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Background: Multidrug-resistant organisms (MDRO), including those producing extended-spectrum beta lactamases (ESBL) are increasing. Infections, especially with MDRO, lead to increased healthcare costs. Bloodstream infections (BSI) caused by ESBL-producing Klebsiella pneumoniae increased at our institution in 2021-2022. An assessment as to whether these organisms were acquired during hospitalization or other healthcare exposures was conducted. **Methods:** The rates of ESBL-producing Klebsiella BSI per 1000 hospitalizations in 2021 and 2022 in transplant recipients and non-transplant patients were compared. From 1/1/2021 to 06/30/2023, 49 adult patients at an academic medical center had Klebsiella pneumoniae BSI with ceftriaxone resistance and a high probability of carrying an ESBL. Of these, 20 were transplant recipients and 29 were non-transplant patients. We performed whole-genome sequencing on the 28 available unique patient isolates (12 transplant; 16 non-transplant) to assess relatedness. Additional data were collected by chart review on transplant recipients. BugSeq bioinformatics pipeline and refMLST were utilized on the sequenced isolates to assess clonality, defined as ≤20 allele difference between two isolates. **Results:** The rate of ESBL-producing Klebsiella BSI increased universally from 2021 to 2022 but impacted the transplant cohort (0.3 to 3.6 per 1000 hospitalizations) more than the non-transplant cohort (0.2 to 0.5 per 1000 hospitalizations). Kidney and liver transplants were most often involved (5 out of 49 patients each). In the transplant cohort, bacteremia alone (45%, 9 out of 20) and urinary source (35%, 7 out of 20) were the most frequently identified etiologies. The most common sequence type was ST-307, accounting for 64% of total sequenced isolates (67% of transplant; 63% of non-transplant). The most common ESBL gene identified was blaCTX-M-15, identified in 24 isolates (86%). Less common resistance genes included blaSHV-12 (N=3) and blaCTX-M-3 (N=1). While there were 5 isolates within 20 allele differences (3 transplant; 2 non-transplant), they were separated in time and did not have obvious epidemiologic connections. While there was a change in TMP-SMX prophylaxis protocol during this time in kidney transplant recipients, it did not explain the increase observed in other transplant groups. **Conclusions:** There was a sharp increase in the number of BSI caused by ESBL-producing Klebsiella pneumoniae in the transplant pop-

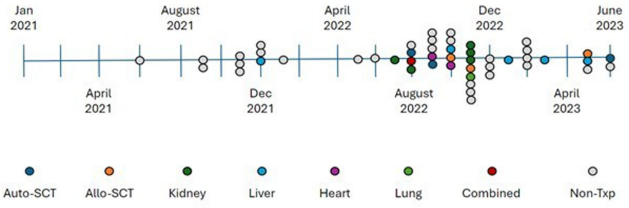

Figure 1. Timeline of Infections. Each circle represents a unique patient blood culture isolate.

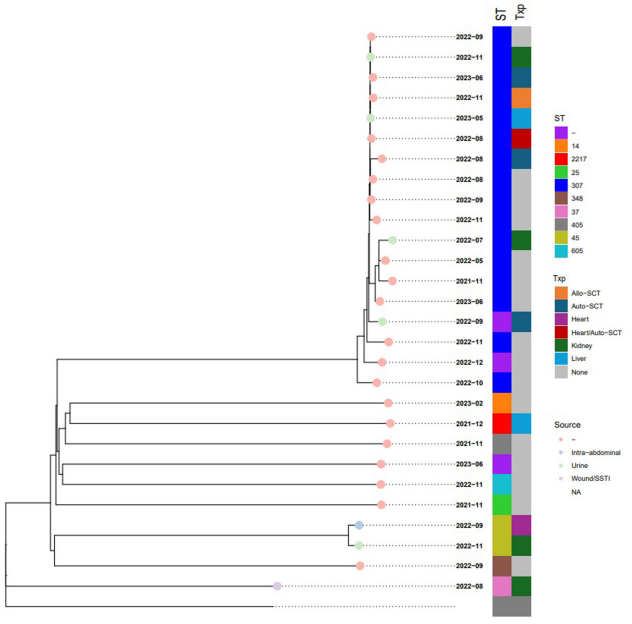

Figure 2. Neighbor-joining tree showing the allele distances between sequenced isolates. Leaves are annotated with suspected source and month of blood culture collection. The tree was rooted on the reference *K pneumoniae* HS11286 (RefSeq GCF_000240185.1). ST = sequence type. Txp = type of transplant.

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ulation between 2021 and 2022. A molecular epidemiologic analysis ruled out clonal transmission from breakdown of infection prevention practices as the cause. No other common epidemiologic link was identified. This demonstrates the application of whole-genome sequencing in excluding a clonal outbreak from a common source within an institution.

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Reduction of MRSA Bacteremia LabID Events in a Large Community Tertiary Care Facility

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Background: Methicillin-resistant Staphylococcus aureus (MRSA) bacteremia is a reportable hospital -acquired condition that can cause significant harm to hospitalized patients. Our facility, a 629 bed acute tertiary care hospital, continued to observe Healthcare Facility-Onset (HO) MRSA bacteremia rates above the corporate goal despite our housewide MRSA decolonization protocol consisting of daily chlorhexidine gluconate bathing (CHG) and an alcohol nasal antiseptic twice per day for all adult inpatients ≥ 18 years of age. This prompted us to conduct a gap analysis and evidence-based practice review to address our current MRSA decolonization practices. **Methods:** In January 2024, a revised MRSA decolonization protocol was implemented for our adult inpatient population consisting of the addition of nasal mupirocin twice per day for 5 days for all Intensive Care Unit (ICU) patients, MRSA nasal screening for high-risk patients, and implementation of contact precautions (gown, gloves) for patients identified or known with MRSA colonization and/or infection. The nasal alcohol antiseptic was removed from the revised protocol. Multidisciplinary education on the protocol changes (MRSA screening, isolation, and discontinuation of the nasal antiseptic) were disseminated to nursing, pharmacy, and the medical staff. Mupirocin was added to the standing ICU order set in the electronic medical record (EMR). Pre-intervention (February 2023 - January 2024) and Post-intervention (February 2024-October 2024) time periods were used to assess the impact on the rate of HO MRSA bacteremia and were obtained from The National Healthcare Safety Network (NHSN) standardized infection ratio (SIR) 2015 baseline with analysis using the NHSN statistics calculator. **Results:** Following implementation of the decolonization protocol, the MRSA bacteremia cumulative SIR decreased 91% from 1.077 to 0.096 which was statistically significant with a two-tailed p-value of 0.0021 (95% Confidence interval: -99.6, -49.5). The housewide MRSA bacteremia rate decreased from 1.05 infections per 10,000 patient days to 0.090 per 10,000 patient days which reflected a significant decrease (p: 0.0016). The ICU MRSA bacteremia rate also showed statistical significance with a decrease from 4.2 per 10,000 patient days to 0.00 per 10,000 patient days (p: 0.0477). **Conclusion:** Revising the MRSA decolonization protocol significantly decreased our MRSA bacteremia rates. This included re-implementation of contact precautions, screening high-risk patients that could be carriers of MRSA, and mupirocin decolonization for ICU patients. Facilities should consider evaluation of their MRSA decolonization, isolation, and screening practices if unable to decrease their HO MRSA bacteremia rates.

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Subject Category: MRSA/VRE
Clinical Characteristics and Antibiotic Exposure History in 75 Patients with Daptomycin-Nonsusceptible Enterococcus faecium

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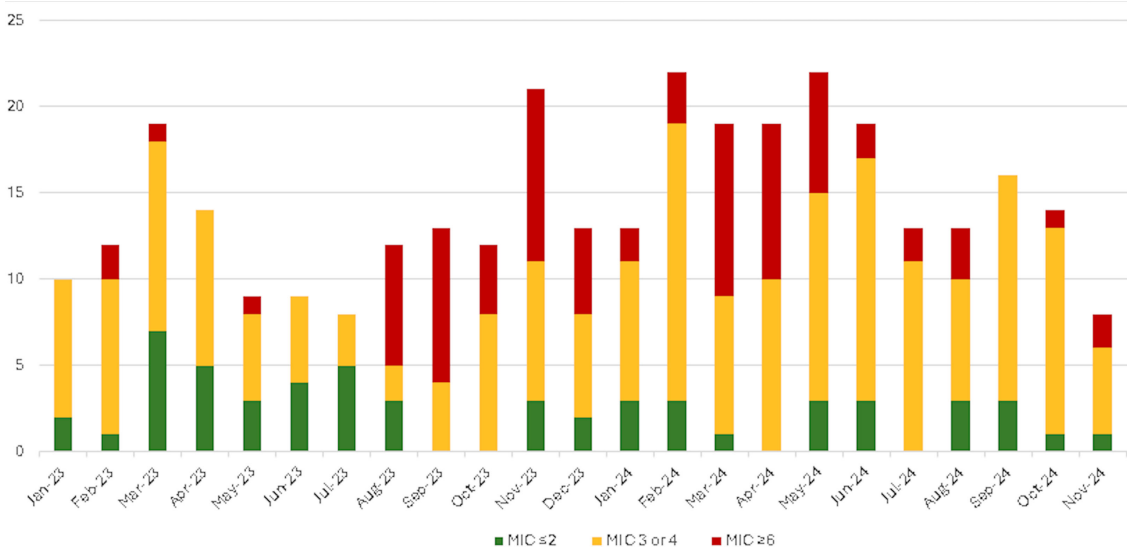
Background: Daptomycin-nonsusceptible Enterococcus faecium (DNS E. faecium) is an emerging multidrug-resistant pathogen associated with poor clinical outcomes. Prompted by an increase in DNS E. faecium at our institution in 2023 (Figure 1), we sought to characterize patient characteristics and generate hypotheses about potential risk factors. **Methods:** We conducted a retrospective case series of 75 patients with confirmed DNS E. faecium (MIC ≥6) across 10 hospitals (served by a single Microbiology laboratory) within the University of Maryland Medical System between January 1, 2023, and November 30, 2024. Data collected included demographics (age, gender, race, ethnicity), clinical history (prior Enterococcus or VRE infections, immunosuppression), infection characteristics (site, Healthcare-associated (defined as onset >48 hours from admission) vs. Community-onset), and antibiotic exposure (vancomycin, daptomycin, linezolid, rifaximin) within 90 days. Immunosuppression was defined as corticosteroid use (≥10 mg prednisone for ≥5 days), chemotherapy,



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