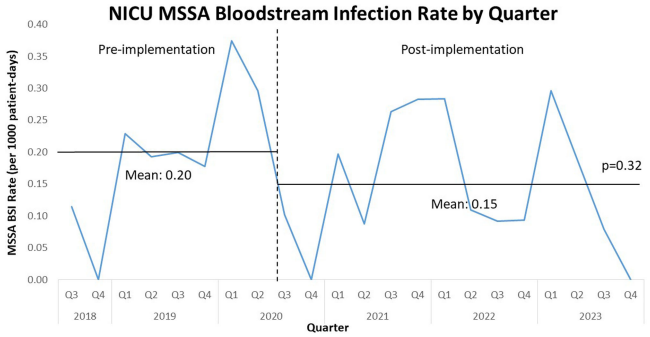

Figure 2. Neonatal Intensive Care Unit (NICU) methicillin-susceptible *Staphylococcus aureus* (MSSA) bloodstream infection (BSI) rate per 1000 patient-days by quarter from July 2018 through December 2023. The dashed vertical line indicates the start of the implementation period. Mean MSSA BSI rates for the pre- and post-implementation periods are indicated by the horizontal lines.

post-implementation (p=0.02). Following implementation of MSSA surveillance and decolonization, there was no statistically significant change in the mean MSSA BSI rate (Figure 2): 0.20 per 1000 patient-days pre-implementation, 0.15 post-implementation (p=0.32). **Conclusions:** Implementation of a robust MRSA surveillance and decolonization program in the NICU was associated with a sustained decrease in invasive MRSA infections. No change in invasive MSSA infection rates was observed following implementation of a similar protocol for MSSA. Additional research is needed to better understand the role of MSSA surveillance and decolonization in the NICU.

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: MRSA/VRE

Use of Whole Genome Sequencing for Investigation of Potential Hospital-Acquired Vancomycin Resistant Enterococcus

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Background: Whole genome sequencing (WGS) is a relatively new method for analyzing outbreaks and modes of transmission, particularly for multidrug resistant bacteria. This study sought to investigate clusters of patients with genetically related Vancomycin-Resistant Enterococcus spp. (VRE) bacteremia for shared hospital environmental exposures. **Methods:** All VRE blood culture isolates from patients from July 1, 2021 to June 30, 2022 underwent Illumina WGS. Core single nucleotide polymorphisms (SNPs) were identified, and multi-locus sequence typing (MLST) was performed across the VRE isolates. Clusters were defined as isolates with 15 or fewer core genome SNPs and were investigated for potential transmission routes. For each cluster, patients were evaluated in the 12 weeks before and after the first VRE isolate for shared hospital environmental exposures (hospital unit, patient rooms, procedural rooms, and radiology suites). Hospital units were comprised of patient rooms located geographically together on the same floor of the hospital. **Results:** A total of 82 VRE isolates underwent WGS. Thirty-eight (46%) clustered genetically with at least one other isolate. Clusters included 2 to 15 patients per group and represented 10 distinct MLST subgroups (Figure 1). Nine hundred and thirty-nine hospital environmental

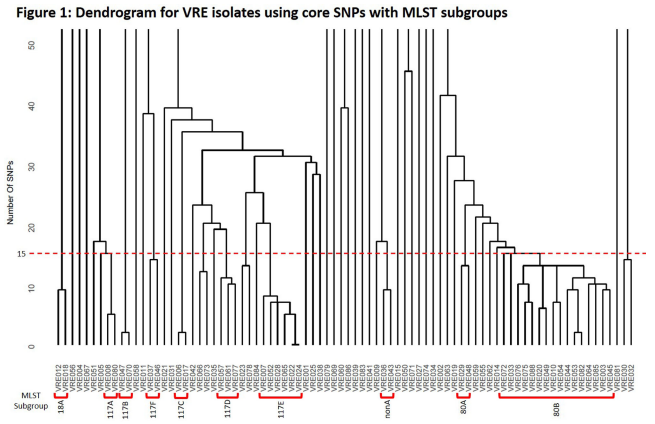

Figure 1: Dendrogram for VRE isolates using core SNPs with MLST subgroups

exposures were identified across the 38 patients. For each cluster, there was a total of 341 (36.3%) shared exposures. Shared environmental exposures occurred in radiology suites (35, 38.5%), patient rooms (32, 35.6%) and procedural rooms (23, 25.6%). Of the patients who shared the same hospital unit, 10 (31.3%) had the same patient room with 7 (70%) of them being in the emergency department (ED). Overall, the ED represented 7 (21.9%) of the shared hospital units. Each cluster had at least one shared hospital environmental exposure found. **Conclusions:** Use of WGS can help investigate outbreak clusters of resistant organisms such as VRE. In this study, nearly half of all VRE blood isolates were able to be segregated into clusters with at least one other isolate. Although VRE colonization of hospital rooms is well described, patient rooms represented the smallest proportion of shared hospital environmental exposures. This study thus suggests other environmental transmission routes such as radiology suites and procedural rooms warrant closer investigation.

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Presentation Type:
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MDRO Colonization Among Nursing Homes Patients: A Risk Classification Tool for Early Identification

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Background: Nursing homes (NHs) have high prevalence of multi-drug resistant organisms (MDROs) with rates exceeding those in hospitals. This study proposes quantifying patients' risk of MDRO colonization and creating a risk profile for the NH patient populations to assist in reducing MDRO burden in health care facilities. **Methods:** We assessed a risk classification model using data from a prospective cohort study (2018 Pathways study). Patient sample included 783 newly admitted patients followed for up to 180 days and 9,587 samples collected from patients during 2,089 visits. Individual risk factors of MDRO colonization were assessed using unadjusted logistic regression, and patients were risk classified based on number of risk factors. Multivariate regression was performed to obtain odds of MDRO colonization for patient risk groups adjusting for patient age, sex, race, and length of NH stay (LOS). The risk classification tool developed using Pathways data was also tested among a sample of NH residents from Veterans Administration (N=190). **Results:** The patient sample (Pathways data) was 43.2% male, 37.2% Black with a mean age 74 years. 69.3% were colonized with a MDRO during the study. In unadjusted regression, recent antibiotic use ($p<.001$), open wounds ($p<.05$), use of urinary catheter or feeding tube ($p<.001$), functional disability ($p<.001$), diabetes ($p<.01$), and preadmission hospital stay over 14

Figure 1

Adjusted[a] Association Between Number of Risk Factors and MDRO

Number of Risk Factors	%[b] (N)	OR (95% CI)	P value
None	45% (104)	1 [Reference]	
One	63% (263)	2.29 (1.39 - 3.74)	0.001
Two	73% (212)	3.74 (2.22 - 6.31)	<0.001
Three	84% (138)	6.17 (3.31 - 11.52)	<0.001
Four or more 1	91% (57)	8.89 (3.16 - 24.99)	<0.001

[a] Logistic regression model adjusted for patient age, race, sex, length of stay in study, and nursing facility. [b] Percentage of patients colonized with any MDRO during SNF stay.

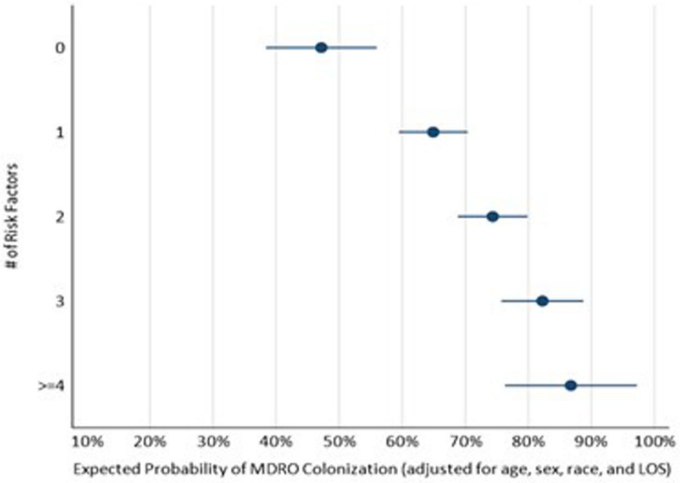
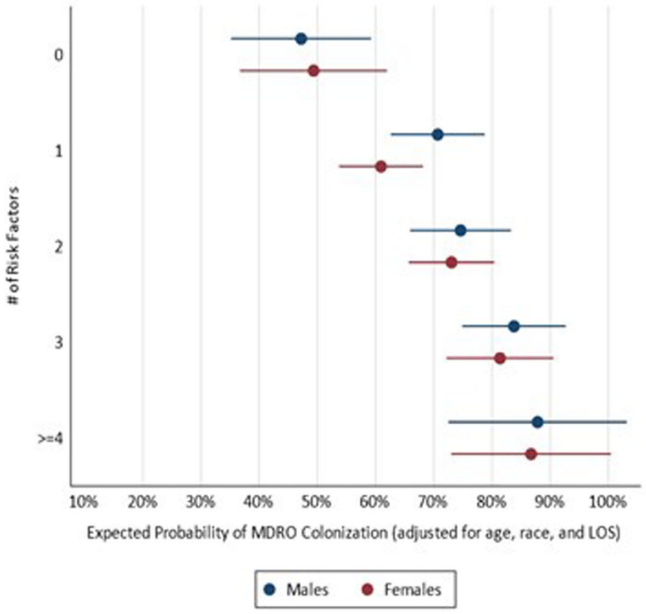
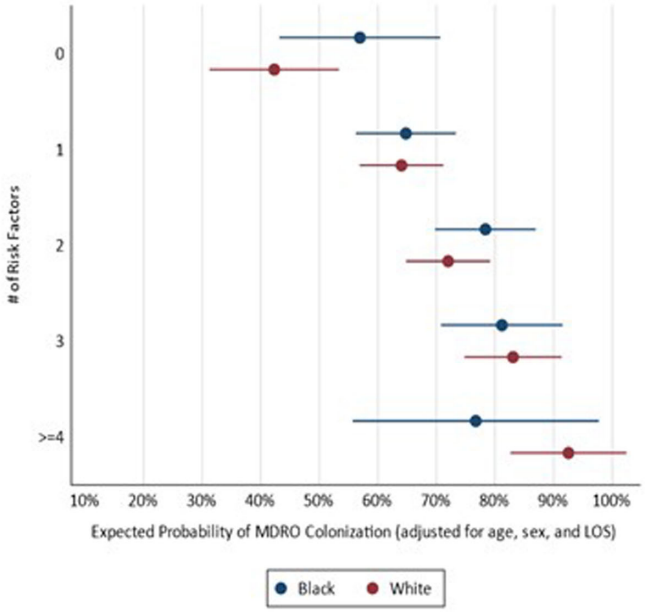


Figure 2





days (p<.001) were associated with colonization, while Charlson comorbidity score, age, sex, and race were not. In adjusted analysis (c-statistic=0.75), a patient's colonization risk increased with the number of risk factors (Figure 1), with 47.2% expected colonization among patients with none of the risk factors and 86.7% expected colonization among patients with four or more risk factors. The risk classification model had similar performance among male and female patients, and among Black and White patients (Figure 2). Secondary analysis using data obtained from separate, Veterans Administration facilities provided preliminary validation of the risk scoring tool. The model had acceptable fit (c-statistic=0.71). Veterans with four or more risk factors had 87.8% expected probability of MDRO colonization compared with 39.6% colonization among those without any risk factors. Veterans with less than four risk factors also had higher colonization, but these differences were not statistically significant. Conclusions. Despite system-wide efforts to reduce MDRO burden, prevalence of MDRO colonization remains high in NHs. The risk classification tool can assist in early identification of most vulnerable NH patients to direct targeted interventions such as education, enhanced environmental cleaning, and active surveillance.

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