contacting the primary team. Twenty-five patient encounters were timed with a mean of 4.7 minutes documented per encounter. Over a 9-month period after initiation of the automated time-based resolution, the monthly mean number of patients with CP for MRSA and VRE which were automatically discontinued was 247 and 100, respectively. Projected IP time savings over the same 9-month period for MRSA and VRE were 174.1 and 70.5 hours, respectively. Over a 5-month period after initiation of automated ordering of MRSA polymerase chain reaction (PCR)/culture, as well as VRE culture for test-based evaluation, the monthly mean number of MRSA culture, MRSA PCR, and VRE culture automatically ordered for patients on CP for MRSA and VRE were 176, 24, and 145, respectively. Projected IP time savings over the same 5-month period for MRSA and VRE were 78.3 and 56.8 hours, respectively.
Conclusion: Healthcare systems that enhance their EHR with CDSS to automate CP evaluations may improve frontline clinician workflow, patient flow and bed capacity, while optimizing use of IP resources.

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Assessing Mupirocin Resistance in MRSA Isolates in Hospitals in Cleveland, OH and Detroit, MI

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Background: Methicillin-resistant Staphylococcus aureus (MRSA) is a common pathogen responsible for nosocomial and community-acquired infections with high morbidity and mortality1. MRSA nasal colonization is a major risk factor for developing infection in the hospital setting2,3. Decolonization of MRSA carriers is a strategy to decrease recurrence or to prevent new MRSA infections3,4. Decolonization with nasal mupirocin 2% and chlorhexidine baths has been shown to decrease the risk of MRSA infection after hospital discharge3. Mupirocin is an RNA synthetase inhibitor with activity against MRSA5. Resistance of MRSA isolates to mupirocin has been described previously6. As topical disinfectants play a crucial role in prevention of MRSA infection in a variety of settings, it is important to monitor the emergence of resistance. The goal of this study was to determine the prevalence of mupirocin resistance among MRSA samples isolated from two different regions in the United States (U.S). **Methods:** Our study had a total of 474 MRSA samples that were obtained from hospitals in Detroit, MI (287 samples) and Cleveland, OH (187 samples). After whole genome sequencing using NextSeq (Illumina Inc., CA) platform the data was analyzed using ResFinder 4.1, to identify antimicrobial resistance which can be either acquired or chromosomally mediated mutations. To visualize the presence of genes of interest the resistance genes were tallied on a spread sheet. **Results:** Mupirocin resistance gene was detected in five of 287 (1.74%) MRSA samples from the Detroit hospitals, all of which were associated with the mupA gene. Samples collected from the Cleveland area hospital demonstrated mupirocin resistance in seven samples of 187 (3.74%), all associated again with the mupA gene. One sample from the Detroit group showed resistance to both mupirocin and chlorhexidine. **Conclusions:** Prevalence of mupirocin resistance gene varied between the two hospital locations. Resistance to mupirocin has been documented in association with mutations in the mupA gene as well as chromosomal point mutations that can lead to either low or high-level resistance7,8. Although the mechanisms are not fully clear, mupA gene has been associated with high-level resistance9. Mupirocin resistance among MRSA isolates has increased over time9. MRSA infections remain an important etiology of nosocomial and community-acquired infections and common practice to combat this issue is universal decolonization with mupirocin10. It is critical to understand and monitor for development of mupirocin resistance as mupirocin remains one of the most effective tools to prevent invasive infection with MRSA in many patient populations.

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S. aureus Surveillance and Decolonization Associated with Decreased MRSA, but not MSSA, Infections in the Neonatal ICU

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Background: Invasive Staphylococcus aureus infections cause significant morbidity and mortality in neonatal intensive care unit (NICU) infants.1 Colonization (asymptomatic carriage in the nose, skin, or gut) is a risk factor for subsequent invasive infection (e.g., pneumonia, bone infections, bloodstream infections, etc.). Active surveillance and decolonization measures for S. aureus-colonized infants have been associated with decreased invasive infection rates. 2-4 **Methods:** A methicillin-resistant S. aureus (MRSA) surveillance and decolonization program, consisting of admission and weekly MRSA nasal cultures followed by intranasal mupirocin plus chlorhexidine baths for colonized infants, was implemented in our level IV NICU with 150 beds in 2006.5 Due to poor compliance with decolonization protocols5, existing practices were reviewed and multiple interventions to increase compliance were implemented in 2018. These renewed efforts included revision of the existing MRSA decolonization protocol, updating the associated electronic medical record order set, re-education of unit staff, and weekly review by the Infection Prevention (IP) and NICU leadership teams to ensure the decolonization protocol was followed for newly colonized infants. Mean MRSA bloodstream infection (BSI) rates were calculated quarterly pre- (January 2014-December 2017) and post- (January 2018-December 2023) implementation of renewed efforts and compared via unpaired t-test. In July 2020 a similar methicillin-susceptible S. aureus (MSSA) surveillance and decolonization program was implemented with an associated revision of existing documents, education campaign, and weekly review of infants with new MSSA colonization. Mean MSSA BSI rates pre- (July 2018-June 2020) and post- (July 2020-December 2023) implementation were compared via unpaired t-test. **Results:** Renewed implementation of MRSA surveillance and decolonization was associated with a sustained decrease in the mean MRSA BSI rate (Figure 1): 0.10 per 1000 patient-days pre-implementation, 0.03

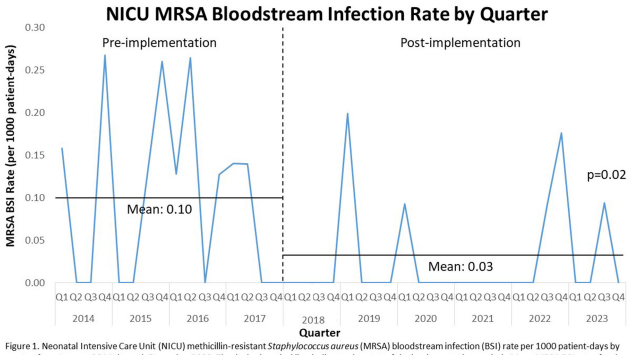

Figure 1. Neonatal Intensive Care Unit (NICU) methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infection (BSI) rate per 1000 patient-days by quarter from January 2014 through December 2023. The dashed vertical line indicates the start of the implementation period. Mean MRSA BSI rates for the pre- and post-implementation periods are indicated by the horizontal lines.

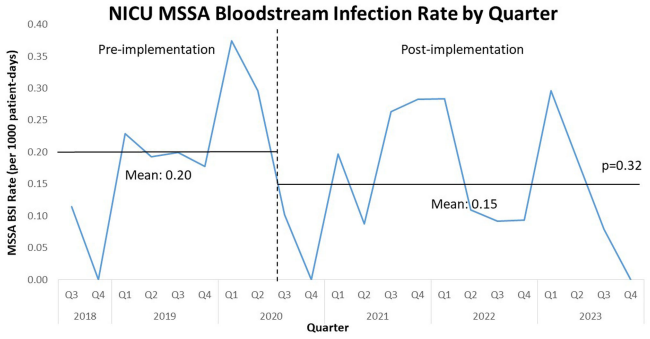

Figure 2. Neonatal Intensive Care Unit (NICU) methicillin-susceptible *Staphylococcus aureus* (MSSA) bloodstream infection (BSI) rate per 1000 patient-days by quarter from July 2018 through December 2023. The dashed vertical line indicates the start of the implementation period. Mean MSSA BSI rates for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

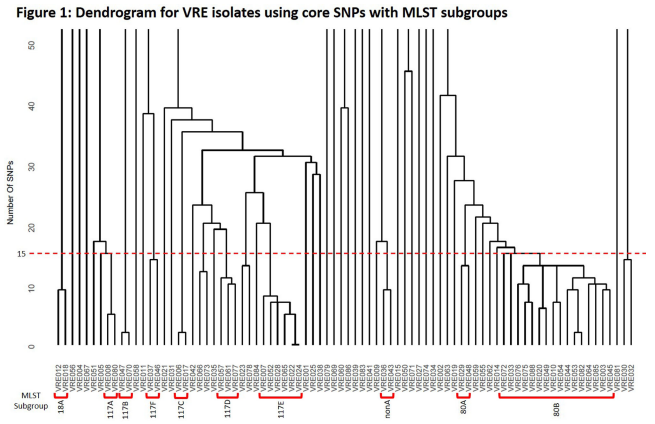

Figure 1: Dendrogram for VRE isolates using core SNPs with MLST subgroups

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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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