

acquired carbapenemase genes, including class D OXA-variants. **Results:** From August 2017 through July 2019, the ARLN tested 2,368 CRAB isolates across 44 states. Only 12 (0.5%) of these harbored a *bla*- gene: *bla*KPC ($n = 5$), *bla*NDM ($n = 5$), *bla*IMP ($n = 1$), and *bla*VIM ($n = 1$). Of 95 reference and surveillance isolates sequenced, none harbored these targeted carbapenemases. However, 69 (73%) harbored at least 1 acquired class D OXA gene; OXA-23 was the most commonly acquired OXA variant ($n = 46$, 48.4%). **Conclusions:** Using a multipronged approach, our studies indicate that the presence of class D β -lactamases of the OXA type are common in CRAB among surveillance and reference samples that underwent WGS analysis. Other acquired carbapenemases appear to be rare. To prevent the spread of highly resistant CRAB, particularly those carrying the targeted, emerging carbapenemase genes, continued testing, and rapid infection control are necessary to improve patient safety and maintain situational awareness. **Funding:** None
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Poster Presentation

Motivational Application of Standardized Antimicrobial Administration Ratios Within a Healthcare System

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Background: Hospitals in the United States have been encouraged to report antimicrobial use (AU) to the CDC NHSN since 2011. Through the NHSN Antimicrobial Use Option module, health systems may compare standardized antimicrobial administration ratios (SAARs) across specific facilities, patient care locations, time periods, and antimicrobial categories. To date, participation in the NHSN Antimicrobial Use Option remains voluntary and the value of reporting antimicrobial use and receiving monthly SAARs to multihospital healthcare systems has not been clearly demonstrated. In this cohort study, we examined potential applications of SAAR within a healthcare system comprising multiple local hospitals. **Methods:** Three hospitals within Prisma Health-Midlands (hospitals A, B, and C) became participants in the NHSN Antimicrobial Use Option in July 2017. SAAR reports were presented initially in October 2017 and regularly (every 3–4 months) thereafter during interprofessional antimicrobial stewardship system-wide meetings until end of study in June 2019. Through interfacility comparisons and by analyzing SAAR categories in specific patient-care locations, primary healthcare providers and pharmacists were advised to incorporate results into focused antimicrobial stewardship initiatives within their facility. Specific alerts were designed to promote early de-escalation of antipseudomonal β -lactams and vancomycin. The Student *t* test was used to compare mean SAAR in the preintervention period (July through October 2017) to the postintervention period (November 2017

through June 2019) for all antimicrobials and specific categories and locations within each hospital. **Results:** During the preintervention period, mean SAAR for all antimicrobials in hospitals A, B, and C were 0.69, 1.09, and 0.60, respectively. Notably, mean SAARs at hospitals A, B, and C in intensive care units (ICU) during the preintervention period were 0.67, 1.36, and 0.83 for broad-spectrum agents used for hospital-onset infections and 0.59, 1.27, and 0.68, respectively, for agents used for resistant gram-positive infections. After antimicrobial stewardship interventions, mean SAARs for all antimicrobials in hospital B decreased from 1.09 to 0.83 in the post-intervention period ($P < .001$). Mean SAARs decreased from 1.36 to 0.81 for broad-spectrum agents used for hospital-onset infections and from 1.27 to 0.72 for agents used for resistant gram-positive infections in ICU at hospital B ($P = .03$ and $P = .01$, respectively). No significant changes were noted in hospitals A and C. **Conclusions:** Reporting AU to the CDC NHSN and the assessment of SAARs across hospitals in a healthcare system had motivational effects on antimicrobial stewardship practices. Enhancement and customization of antimicrobial stewardship interventions was associated with significant and sustained reductions in SAARs for all antimicrobials and specific antimicrobial categories at those locations.

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Moving Beyond Contact Precautions: Implementation of a *Staphylococcus aureus* Screening and Decolonization Program

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Background: *Staphylococcus aureus*-colonized hospitalized patients are at risk for invasive infection and can transmit *S. aureus* to other patients in the absence of symptoms. Infection isolation precautions do not reduce the risk of infection in colonized patients and are untenable in health systems with high rates of *S. aureus* colonization. **Objective:** We implemented an inpatient *S. aureus* screening and targeted decolonization program across hospital campuses to reduce transmission and invasive infection. We screen and decolonize for methicillin-susceptible *S. aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA) because MSSA makes up more than half of all *S. aureus* isolated from clinical cultures in our health system. **Methods:** All medicine, pediatrics, and transplant patients receive *S. aureus* nares culture at admission and upon change in level of care for medicine, and at admission and weekly for pediatrics and transplant patients. All *S. aureus*-colonized patients receive decolonization with nasal mupirocin ointment and chlorhexidine baths. Two implementation frameworks guide our processes for *S. aureus* screening and decolonization: the Consolidated Framework for Implementation Research, to evaluate factors affecting implementation at different levels of the health system, and the Dynamic Sustainability Framework, to account for iterative changes as the hospital setting and patient population change over time. Implementation interventions focus on education of patients and bedside nurses who perform *S. aureus* screening and decolonization; utilization of the electronic health record to identify

patients for screening and/or decolonization and avoid human error; and introduction of a clinical nurse specialist to oversee the program and to provide iterative feedback. **Results:** At baseline, 21% of patients had *S. aureus* colonization, 20% of which was MRSA, and the MRSA bloodstream infection rate was 0.06 per 1,000 patient days. After program implementation, there was no change in *S. aureus* colonization and the MRSA bloodstream infection rate fell to 0.04 per 1,000 patient days. Screening compliance improved from 39% (N = 1,805) of eligible patients in the 6-month period before the introduction of the clinical nurse specialist to 52% (N = 2,024) after the introduction of the clinical nurse specialist. In the same periods, decolonization increased from 18.6% to 41% of eligible patients. **Conclusions:** We used 2 implementation frameworks to design our *S. aureus* screening and decolonization program and to make iterative changes to the program as it evolved to include new patient populations and different hospital settings. This resulted in a large-scale, sustainable, health system program for *S. aureus* control that avoids reliance on infection isolation precautions.

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Methicillin-Resistant *Staphylococcus aureus* (MRSA) Admission Screening in the Neonatal Intensive Care Unit (NICU): Algorithm for Hospital Transfers

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a frequent source of infection in the neonatal intensive care unit (NICU). Due to the serious consequences associated with MRSA infections in neonates, much effort has been made to prevent and control epidemics in NICUs. Since 2006, our hospital has performed MRSA nasal surveillance screening of all newborns in the NICU in accordance with the recommendations of the Chicago-Area Neonatal MRSA Working Group. In 2017, a MRSA infection was identified in a newborn shortly after transfer from an outside hospital and who had an initial negative MRSA admission screen. As a result, we modified the admission screening process for all transfers from outside NICUs. **Methods:** The Evanston Hospital Infant Special Care Unit is a level 3 NICU in the northern suburbs of Chicago with 44 NICU beds and 450 admissions per year. Effective July 1, 2017, all NICU transfers have a nasal MRSA screen performed upon admission and after 48 hours. The transferred baby is placed on contact isolation until both screening results return negative. Nasal MRSA testing is performed using both PCR on the BD MAX MRSA Assay platform and is confirmed by culture using MRSA CHROMagar TM. **Results:** Between July 1, 2017, and October 31, 2019, 112 neonates were transferred from outside NICUs. Moreover, 105 (94%) had at least 1 MRSA screen completed and 99 (88%) had both MRSA screens completed. Of 99 with 2 screens, only 1 neonate had an initial positive nasal MRSA screen. Of the remaining 98 negative babies, none had a repeat positive nasal MRSA screen within 48 hours of admission. Of 99 neonates with 2 serial admission MRSA screens, 82 (83%) were transferred within 48 hours of birth. In addition, 17 neonates were transferred >48 hours after birth, including the 1 MRSA-positive

baby. **Conclusions:** In an attempt to identify all potential MRSA-positive neonates transferred to our NICU, we instituted a policy of 2 admission nares swabs. However, our data suggest that a single initial MRSA swab may be sufficient. If continued collection of a second screen is performed, it may be sufficient to screen babies who have been hospitalized for at least 48 hours prior to transfer, which eliminates 83% of admission testing and results in a cost savings.

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Methicillin-Resistant *Staphylococcus aureus* (MRSA) Risk Factors: Comparison Between Acute-Care, and Subacute- and Long-Term Care Facilities in a Healthcare Network

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Background: The risk factors for methicillin-resistant *Staphylococcus aureus* (MRSA) colonization can differ between acute-care, subacute-care, and long-term care facilities, but comparative information is lacking. We compared risk factors for MRSA colonization contemporaneously between an acute-care hospital (ACH) and its affiliated intermediate- and long-term care facilities (ILTCFs). **Methods:** Serial cross-sectional studies were conducted in a 1,600-bed tertiary-care ACH and its 6 affiliated ILTCFs in Singapore, in June–July 2014–2016. Separate nasal, axillary, and groin swabs were taken and cultured for MRSA. MRSA isolates were subject to whole-genome sequencing. Clinical and epidemiological data were obtained from medical records. To account for clustering, multivariable 2-level multinomial logistic regression models were constructed to assess factors associated with colonization of specific MRSA clones, in the ACH and ILTCFs, respectively. **Results:** In total, 8,873 samples from 2,985 patients in the ACH and 7,172 samples from 2,409 patients and residents in ILTCFs were included in the study. Patients and residents in the ILTCFs (29.7%) were more likely to be colonized with MRSA than patients in the ACH (12.6%) ($P < .0001$). The predominant MRSA clones were clonal complexes (CC)22 (n = 692, 46.7%) and CC45 (n = 494, 33.4%), contributing to 80% of MRSA isolates. For ACH patients, after adjusting for age, gender, comorbidities, prior exposures to antibiotics and percutaneous devices, presence of wounds, and screening year, prior MRSA carriage in the preceding 12 months was the strongest predictor of colonization with all MRSA clones: CC22 (aOR, 14.71; 95% CI, 6.17–34.48); CC45 (aOR, 7.75; 95% CI, 2.70–22.22); and others (aOR, 22.22; 95% CI, 3.83–125.00). Hospital stay >14 days was also positively associated with colonization with MRSA CC22 (aOR, 2.67; 95% CI, 1.22–5.88), but not the other clones. For ILTCF patients and residents, after adjusting for age, comorbidities, prior exposure to antibiotics, presence of wounds, and screening year, prior MRSA carriage was a significant predictor of colonization with MRSA CC22 (aOR, 2.72; 95% CI, 1.35–5.46), and CC45 (aOR, 2.36; 95% CI, 1.06–5.24), but not with other clones. Additionally, prior exposure to a percutaneous device and being male were respectively positively associated with colonization by MRSA CC22 (aOR, 2.70; 95% CI, 1.19–6.17) and CC45 (aOR, 2.17; 95% CI, 1.11–4.26). **Conclusions:** Prior MRSA carriage was a common risk factor for colonization with the predominant