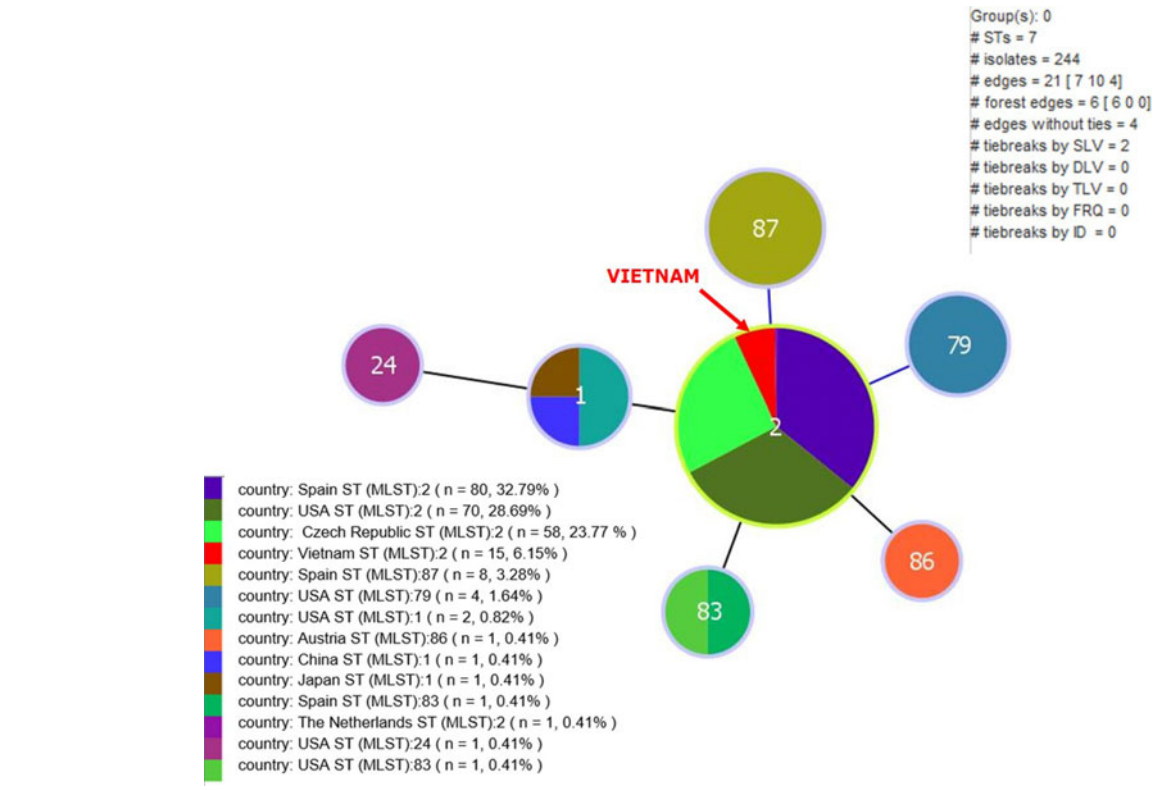

Fig. 1.

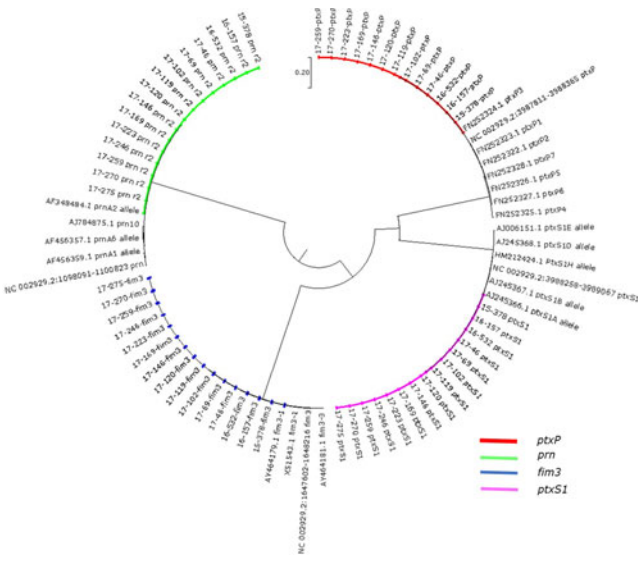

Fig. 2.

therefore, continued surveillance is important to confirm these findings and to monitor population changes over time.

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Presentation Type:
Poster Presentation

Molecular Landscape of Carbapenemase-Producing *Acinetobacter baumanii* in the United States

Kellan Burrell, Centers for Disease Control and Prevention; Jennifer Huang, Centers for Disease Control; Maria Karlsson, Centers for Disease Control and Prevention; Gillian McAllister, Centers for Disease Control and Prevention; Allison Brown, Centers for Disease Control and Prevention

Background: Carbapenem-resistant *Acinetobacter baumannii* (CRAB) are an urgent public health threat because they cause healthcare-associated infections that are difficult to treat and can spread in healthcare environments. *Acinetobacter* spp may develop resistance to carbapenems through various mechanisms, including decreased permeability, overexpression of efflux pumps, and production of carbapenemases. Carbapenemases found in CRAB commonly belong to the group of carbapenem-hydrolyzing class D β-lactamases, which can be either intrinsic or acquired. The most clinically relevant class D enzymes are the OXA-23-like, OXA-24/40–like, and OXA-58–like because they are commonly plasmid mediated and thereby have the potential for rapid dissemination. We describe the molecular epidemiology of CRAB in the United States using a convenience sample of isolates collected from reference submissions, an isolate-based surveillance system, and the Antibiotic Resistance Laboratory Network (ARLN). **Methods:** Beginning in August 2017, 7 public health laboratories in the ARLN began testing CRAB isolates submitted by participating sentinel clinical laboratories across their region. Carbapenem-resistant isolates were identified by resistance to imipenem, meropenem, or doripenem. Testing included molecular detection of 4 targeted carbapenemase genes: *bla*KPC, *bla*NDM, *bla*VIM, and *bla*IMP. Participating labs reported testing results to CDC at least monthly. A separate collection of isolates from CDC reference and surveillance activities between 2013 and 2015 underwent whole-genome sequencing (WGS) to evaluate the presence of

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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), *blaI*MP (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.
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Poster Presentation

Motivational Application of Standardized Antimicrobial Administration Ratios Within a Healthcare System

Stephanie Shealy, University of South Carolina College of Pharmacy and Prisma Health Richland; Joseph Kohn, Prisma Health – Midlands; Emily Yongue, Prisma Health – Midlands; Casey Troficanto, Prisma Health – Midlands; Brandon Bookstaver, University of South Carolina College of Pharmacy and Prisma Health Richland; Julie A. Justo, University of South Carolina College of Pharmacy and Prisma Health Richland; Michelle Crenshaw, Prisma Health – Midlands; Hana Winders, University of South Carolina College of Pharmacy; Sangita Dash, University of South Carolina, School of Medicine; Majdi Al-Hasan, University of South Carolina School of Medicine

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 postintervention 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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Poster Presentation

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

Sarah Hochman, NYU Langone Health; Anna Stachel, NYU Langone Health; Michael Phillips, NYU Langone Medical Center; Stephanie Sterling, NYU; Jennifer Lighter, NYU Langone Health; Maria Aguero-Rosenfeld, NYU Langone Health; Tamara King-Morrieson, NYU Langone

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

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