between July 2017 and June 2020. Additional data on potential risk factors for SSI were obtained electronically from hospital data marts and the Division of Cardiac Surgery database, including demographics, comorbidities, number of arterial grafts, surgical approach, surgeon, and discharge location. Using standard NNHS definitions, infection control practitioners identified post-CABG deep and organ-space SSIs. Patient and procedure characteristics were evaluated as potential risk factors for deep and organ-space SSI using the Fisher exact test. Results: Of 1,591 CABG procedures performed during the study period, 1,244 (78.2%) were performed using a SIMA technique and 347 (21.8%) were performed using a BIMA technique. The overall post-CABG SSI incidence was 1.2 per 100 procedures, with 1.0 SSIs per 100 SIMA procedures and 1.7 SSIs per 100 BIMA procedures. Table 1 demonstrates an increase over time in proportion of CABG procedures performed using SIMA and skeletonized IMA grafts. We also observed a decrease in overall SSI incidence over this period. See Table 2 for univariate predictors of post-CABG SSI. Conclusions: Female sex, BMI ≥ 40, age ≥ 75 years, diabetes, and discharge to a rehabilitation setting were associated with development of post-CABG SSI. Although the overall incidence of deep and organ-space SSI in our cohort was very low, making it difficult to draw conclusions about potentially modifiable risk factors, an increase in the use of SIMA and skeletonized grafts appears to be accompanied by a decrease in SSI incidence. More data from our institution and others are needed to determine the significance of this trend.

Funding: No

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2021;1(Suppl. S1):S77–S78
doi:10.1017/ash.2021.152

Presentation Type: Poster Presentation
Subject Category: SSI

The Impact of Narrowing Perioperative Antibiotic Prophylaxis for Left-Ventricular-Assist Device Implantation
Lauren Allen; Rachel Bartash; Kelsie Cowman; Yi Guo; Grace Minamoto; Snehel Patel; Sasha Vukelj; Daryl Nnani and Daphenie Fauvel

Background: Left-ventricular-assist device (LVAD)–related infections occur in 20%–40% of LVAD recipients and may result in up to 10% of LVAD-related deaths. Optimal surgical infection prophylaxis for LVAD implantation is not well defined. Our institution historically used a 4-drug surgical infection prophylaxis regimen of fluconazole, ciprofloxacin, rifampin, and vancomycin as recommended by the device manufacturer. In January 2020, a 2-drug surgical infection prophylaxis regimen of vancomycin and ceftazolin was implemented to reduce broad-spectrum antibiotic use while preserving gram-positive coverage. The primary objective of this study was to compare LVAD-associated infection rates before and after changing surgical infection prophylaxis.

Methods: A retrospective review of patients who underwent LVAD implantation between January 2018 and January 1, 2021, was performed. Definitions of LVAD-associated infections and non-LVAD infections were based on the International Society for Heart and Lung Transplantation guidelines. Infection rates at 2 weeks and 30 days after implantation and 30-day mortality were compared between the 4-drug surgical infection prophylaxis regimen (January 2018–December 2019) and the 2-drug regimen (January 2020–January 2021). Additional data collected included demographics, cause of cardiomypathy, type of infection, and causative organism. Results: In total, 51 patients were in the 4-drug surgical infection prophylaxis group and 23 patients were in the 2-drug surgical infection prophylaxis group. Baseline characteristics between the groups were similar. The cause of cardiomyopathy in both groups was predominantly nonischemic (67% vs 70%, P = .81), and most patients received a Heartmate III device (84% vs 100%, P = .06). There was no statistical difference between infection rates in the 4-drug and 2-drug prophylaxis groups at 2 weeks or 30 days (Table 1). The 30-day mortality rate was 4% in the 4-drug group versus 13% in the 2-drug group (P = .17). No deaths were due to infections. Gram-negative and fungal LVAD–associated infections were rare: 4% versus 4% (P = .99) for gram-negative infections and 2% versus 0% (P = .99) for fungal infections. The most commonly isolated organisms were Staphylococcus aureus and coagulase-negative Staphylococcus in both groups. Pneumonia was the most common infection in both groups (Figure 1).

Conclusions: We did not observe a significant increase in infection or mortality with narrowing of perioperative antibiotics. However, these results should be interpreted cautiously given the small sample size. Larger studies are needed to confirm these findings.

Funding: No

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2021;1(Suppl. S1):S78

Presentation Type: Surveillance/Public Health
Subject Category: Surveillance/Public Health
Prevalence of Healthcare-Associated Infections at the National Hospital During the COVID-19 Pandemic in Peru
Jussara Huamani and Walter Prudencio

Background: Healthcare-associated infections are important because they constitute a public health problem due to the increase in morbidity and mortality that they produce in hospitalized patients, increased hospitalization costs due to prolonged stay, expensive antibiotic treatments and surgical reinterventions, not counting the social costs due to loss of wages and production, among others. Methods: We report the specific prevalence of healthcare-associated infections (HCAs) in Edgardo Rebagliati Martin National Hospital, Peru, in 2020. We performed a descriptive cross-sectional study from July 27 to July 31, 2020. The medical records of hospitalized patients were reviewed according to the inclusion criteria. STATA software was used for descriptive statistical analyses. Results: In total, 1,217 hospitalized patients were included in the study. The prevalence of HCAI was 12.2% (149 patients). The prevalence of HCAI in areas where patients with the diagnosis of COVID-19 were hospitalized was higher (8.1%) than in common hospitalization areas (4.1%). Men represented 92% of the total

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number of patients with HCAIs. The most frequent infections were clinically defined pneumonia (30.9%) and bloodstream infections (20.1%). The most frequently isolated microorganism was *Pseudomonas aeruginosa*. The prevalence of HCAI was 12.2%. The most frequent infections were clinically defined pneumonia (30.9%) and bloodstream infections (20.1%). The most frequent infections were clinical pneumonia (30.9%) and bloodstream infections (20.1%). The most frequent microorganism was *Pseudomonas aeruginosa*. The prevalence of HCAI was 12.2%. The most frequent infections were clinically defined pneumonia (30.9%) and bloodstream infections (20.1%). The most frequent microorganism was *Pseudomonas aeruginosa*.

**Background:** NDM/OXA-23 carbapenemase-producing *Acinetobacter baumannii* isolates have been reported worldwide, but rarely in the United States. A California acute-care hospital (ACH) A identified 3 patients with pan-nonsusceptible *A. baumannii* during May–June 2020, prompting a public health investigation to prevent further transmission among the regional healthcare network. **Methods:** A clinical isolate was defined as NDM/OXA-23–producing *A. baumannii* from a patient at ACH A or B, or an epidemiologically linked patient identified through colonization screening during May 2020–January 2021. ACHs A and B are sentinel sites for carbapenem-resistant *A. baumannii* surveillance through the Antibiotic Resistance Laboratory Network (AR Lab Network), where isolates are tested for carbapenemase genes. The California Department of Public Health with 3 local health departments conducted an epidemiological investigation, contact tracing, colonization screening, and whole-genome sequencing (WGS). **Results:** In total, 11 cases were identified during May 2020–January 2021, including 3 cases at ACH A during May–June 2020, and 8 additional cases during November 2020–January 2021: 5 at ACH A, 1 at ACH B, and 2 at skilled nursing facility (SNF) A. All isolates from ACHs A and B were identified through testing at the AR Lab Network. Of the 11 patients (including the index patient), 4 had exposure at SNF A, where 2 cases were identified through colonization screening. Screening conducted at ACH A and 5 other long-term care facilities (LTFCs) identified no additional cases. WGS results for the first 8 cases identified showed 2–13 single-nucleotide polymorphism differences. Antibiotic resistance genes for all isolates sequenced included NDM-1 and OXA-23. **Conclusions:** This investigation highlights the importance of enhanced novel MDRO surveillance in public health laboratory surveillance allows early detection of novel multidrug-resistant organisms (MDROs), which enabled outbreak identification and public health response. A high COVID-19 burden and related changes in infection control practices have been associated with MDRO transmission elsewhere in California. This factor might have contributed to spread at ACH A and hampered earlier screening efforts at SNF A, likely leading to undetected transmission. Extensive movement of positive patients among a regional healthcare network including at least 6 ACHs and 7 LTFCs likely contributed to the prolonged duration of this outbreak. This investigation highlights the importance of enhanced novel MDRO surveillance strategies coupled with significant infection prevention and control practices as important factors in identifying outbreaks and preventing further transmission in regional networks.

**Presentation Type:** Poster Presentation

**Subject Category:** Surveillance/Public Health

**Multifacility Outbreak of NDM/OXA-23–Producing Acinetobacter baumannii in California, 2020–2021**

Diana Holden; Tisha Mitsunaga; Denise Sanford; Tanya Fryer; June Nash; Emily Schneider; Rituparna Mukhopadhyay; Erin Epstein and Matthew Sylvester

**Background:** NDM/OXA-23 carbapenemase-producing *Acinetobacter baumannii* isolates have been reported worldwide, but rarely in the United States. A California acute-care hospital (ACH) A identified 3 patients with pan-nonsusceptible *A. baumannii* during May–June 2020, prompting a public health investigation to prevent further transmission among the regional healthcare network. **Methods:** A clinical isolate was defined as NDM/OXA-23–producing *A. baumannii* from a patient at ACH A or B, or an epidemiologically linked patient identified through colonization screening during May 2020–January 2021. ACHs A and B are sentinel sites for carbapenem-resistant *A. baumannii* surveillance through the Antibiotic Resistance Laboratory Network (AR Lab Network), where isolates are tested for carbapenemase genes. The California Department of Public Health with 3 local health departments conducted an epidemiological investigation, contact tracing, colonization screening, and whole-genome sequencing (WGS). **Results:** In total, 11 cases were identified during May 2020–January 2021, including 3 cases at ACH A during May–June 2020, and 8 additional cases during November 2020–January 2021: 5 at ACH A, 1 at ACH B, and 2 at skilled nursing facility (SNF) A. All isolates from ACHs A and B were identified through testing at the AR Lab Network. Of the 11 patients (including the index patient), 4 had exposure at SNF A, where 2 cases were identified through colonization screening. Screening conducted at ACH A and 5 other long-term care facilities (LTFCs) identified no additional cases. WGS results for the first 8 cases identified showed 2–13 single-nucleotide polymorphism differences. Antibiotic resistance genes for all isolates sequenced included NDM-1 and OXA-23. **Conclusions:** This investigation highlights the importance of enhanced novel MDRO surveillance in public health laboratory surveillance allows early detection of novel multidrug-resistant organisms (MDROs), which enabled outbreak identification and public health response. A high COVID-19 burden and related changes in infection control practices have been associated with MDRO transmission elsewhere in California. This factor might have contributed to spread at ACH A and hampered earlier screening efforts at SNF A, likely leading to undetected transmission. Extensive movement of positive patients among a regional healthcare network including at least 6 ACHs and 7 LTFCs likely contributed to the prolonged duration of this outbreak. This investigation highlights the importance of enhanced novel MDRO surveillance strategies coupled with significant infection prevention and control practices as important factors in identifying outbreaks and preventing further transmission in regional networks.