

profile of the hospitals collected; and (3) an assessment of the predictive power of 5 types of MLP (backpropagation standard, momentum, resilient propagation, weight decay, and quick propagation) for SSI prediction. MLPs were tested with 3, 5, 7, and 10 hidden layer neurons and a database split for the resampling process (65% or 75% for testing and 35% or 25% for validation). The results were compared by measuring AUC (area under the curve; range, 0–1) presented for each of the configurations. **Results:** Of 1,246 records, 535 were intact for analysis. We obtained the following statistics: the average surgery time was 190 minutes (range, 145–217 minutes); the average age of the patients was 67 years (range, 9–103); the prosthetic implant index was 98.13%; the SSI rate was 1.49%, and the death rate was 1.21%. Regarding the prediction power, the maximum prediction power was 0.744. **Conclusions:** Despite the considerable loss rate of almost 60% of the database samples due to the presence of noise, it was possible to perform relevant sampling for the profile evaluation of hospitals in Belo Horizonte. For the predictive process, some configurations have results that reached 0.744, which indicates the usefulness of the structure for automated SSI monitoring for patients undergoing hip arthroplasty surgery. To optimize data collection and to enable other hospitals to use the SSI prediction tool (available in www.sacihweb.com), a mobile application was developed.

Funding: None

Disclosures: None

Doi:[10.1017/ice.2020.649](https://doi.org/10.1017/ice.2020.649)

Presentation Type:

Poster Presentation

Awareness of Antimicrobial Stewardship Interventions Within a Community Hospital Network

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Background: A system of 3 community hospitals in New Jersey has actively engaged in antimicrobial stewardship since November 2014. Consultations with infectious diseases specialists are mandatory for patients with sepsis, severe sepsis, septic shock, patients on 3 or more antibiotics, and for those diagnosed with *Clostridioides difficile* infection (CDI). A multidisciplinary team meets monthly and has begun to improve the appropriateness of antibiotics use and to reduce antibiotic days of therapy per 1,000 patient days. Recently, we participated in a targeted assessment program (TAP) for CDI, and we identified areas of opportunity for antimicrobial stewardship. **Methods:** The TAP survey was emailed to a wide distribution of employees in the hospital, primarily nurses, physicians, and others with a variable range of experience and for those working in the intensive care units and on the wards. Ultimately, the numbers of responses were 60 in hospital A, 88 in hospital B, and 124 in hospital C. **Results:** In hospital A, most respondents were nurses or nurse assistants or technicians (63%), and most of the total individuals surveyed worked outside the intensive care unit setting. In hospital B, nurses or nurse assistants or technicians comprised 69% of all responses. Hospital C had the highest percentage of physicians who responded (31%). One theme for all hospitals was that a little more than half of those surveyed felt that for patients with new or recent CDI infections, antibiotics prescribed for infections were reviewed by clinicians. Less than half of respondents believed that education was being given to patients and families about the risks of CDI from antibiotics. With

regard to high-risk CDI antibiotics, there was a general lack of knowledge that these were being monitored. For example, survey respondents felt that this was always monitored on clindamycin by only 33% of respondents in hospital A, 40% in hospital B, and 42% in hospital C. With regard to strategies to reduce the unnecessary use of fluoroquinolones, the response of “always” ranged from 35% to 47% of the time. **Conclusions:** Even though hospitals may have robust antimicrobial stewardship programs, it is important to survey frontline staff. Although all of the antimicrobial stewardship interventions, such as monitoring high-risk-CDI antibiotics, reducing high-risk CDI antibiotics, among others, are performed, there may be lack of knowledge that these initiatives are even being implemented. In this TAP against CDI, we found opportunities to share data with respondents to increase awareness of antimicrobial stewardship to further combat hospital-acquired infections.

Funding: None

Disclosures: None

Doi:[10.1017/ice.2020.650](https://doi.org/10.1017/ice.2020.650)

Presentation Type:

Poster Presentation

Bacterial Colonization of Waiting Rooms in a Newly Constructed Children's Outpatient Clinic: Construction Through 6 Months After Opening In Waiting Rooms

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Background: Healthcare-associated infections (HAIs) represent an ongoing problem for all clinics. Children's clinics have waiting rooms that include toys and activities to entertain children, possibly representing reservoirs for HAIs. This study focuses on a newly constructed children's outpatient clinic associated with a teaching hospital. We studied waiting room bacterial colonization of floors and play devices from the last phase of construction through 6 months of clinical use. **Methods:** Waiting room areas on the first 2 floors of the facility were studied due to high patient volume in those areas. In total, 16 locations were sampled: 11 on floors and 5 on play items. Using sterile double-transport swabs, all locations were sampled on 5 separate occasions over 2 months during the last phase of construction and 13 times over 6 months after the clinic was opened. After collection swabs were placed on ice, transported to a microbiology lab, and used to inoculate Hardy Diagnostics Cdiff Banana Broth (for *Clostridium difficile* - Cdiff), CHROM MRSA agar (for methicillin resistant *Staphylococcus aureus* - MRSA), *Pseudomonas* isolation agar (for *Pseudomonas* spp and *P. aeruginosa*), and tryptic soy agar to detect *Bacillus* spp. Media were incubated for 48 hours at 37°C and were scored for bacterial presence based on observation of colonies or change in the medium. **Results:** During the construction phase, waiting-room-floor bacterial colonies were dominated by *Bacillus* spp, and first-floor waiting rooms had nearly 7 times more colonies than those on the second floor ($P < .05$). A similar pattern was observed for *C. difficile* and MRSA. No *Pseudomonas* spp were observed during construction. Once patients were present, *Bacillus* spp contamination dropped for the first floor, but increased for the second floor. All other bacterial types (*C. difficile*, MRSA,



Fig. 1.

Pseudomonas spp, and *P. aeruginosa*) increased on the second floor after the clinic opened (eg, from 23% to 42% for *C. difficile* and from 7% to 46% for MRSA; $P < .05$). The play devices showed small increases in bacterial load after clinic opening, most notably *Pseudomonas* spp. **Conclusions:** This study provides evidence that a shift from bacterial species associated with soil (eg, *Bacillus* spp) toward species commonly associated with humans occurred in waiting rooms after construction in this children's outpatient clinic. Increases for MRSA, *Pseudomonas* spp, and *P. aeruginosa* were linked to patient presence. These data suggest that patients, their families, and clinic staff transport bacteria into clinic waiting

rooms. This outpatient clinic environmental contamination may increase potential for HAIs and may represent a target for intervention.

Funding: None

Disclosures: None

Doi:10.1017/ice.2020.651

Presentation Type:

Poster Presentation

Bad Bugs Move Alike: Regional Transmission of Antibiotic-Resistant Organisms

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Background: Upon admission, 56.8% of patients entering 6 Michigan nursing facilities from regional acute-care hospitals (ACHs) were colonized with 1 or more antibiotic-resistant organisms (AROs) (Mody 2018, CID). This observation raises 2 questions critical to regional infection control strategies: (1) Is the high ARO burden entering nursing facilities driven by dominant epidemic lineages or diverse circulating strains? and (2) What are the relative roles of patient characteristics (eg, high-risk patients) and exposure to specific ACHs (eg, high-risk facilities) in determining whether patients are colonized with AROs upon nursing facility admission? Here, we integrated whole-genome sequencing, patient transfer, and clinical data to answer these questions for the 4 most prevalent ARO species in the region: methicillin-resistant *Staphylococcus aureus*

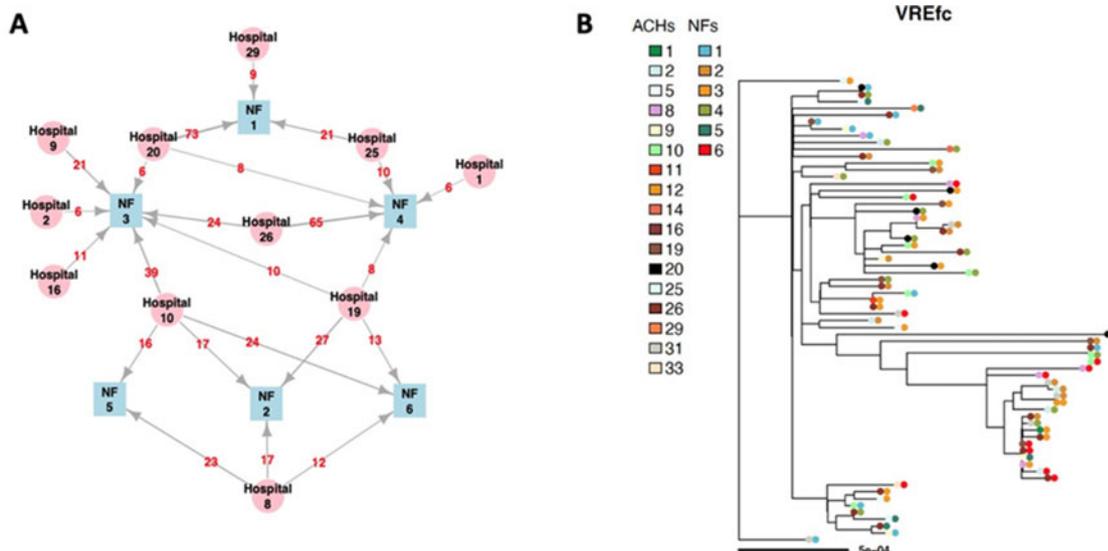


Figure 1. A) Visualization of patient sharing network involving six nursing facilities (NFs; blue nodes) and 11 acute-care hospitals (pink nodes) in southeast Michigan, 2013–2016. Directed arrows represent patient flow from an ACH to a NF, with the number of patients transferred shown in red. **B)** A representative phylogenetic tree (vancomycin-resistant *Enterococcus faecalis*; VREfc) labeled with nursing facilities (NFs) and acute-care hospitals (ACHs) to demonstrate the intermixing of strains across facilities. The trees were inferred from maximum likelihood (RAxML) analysis. Tip colours indicate different NFs and ACHs, and scale bar represents substitutions per nucleotide site.

Fig. 1.