elements of antimicrobial stewardship. Based on information obtained from the Infection Control Assessment and Response (ICAR) Program, the 2 core elements most infrequently achieved by LTCFs are tracking and reporting. Currently, minimal data are available on antibiotic use (AU) in LTCFs in Tennessee. To address both issues, the Tennessee Department of Health (TDH) developed a monthly antibiotic use (AU) point-prevalence (PP) survey to provide LTCFs with a free tool to both track and report their AU and to gather data on how LTCFs are using antibiotics. **Methods:** We used REDCap to create a questionnaire to collect information on selected antibiotics administered in Tennessee LTCFs. This self-administered survey was promoted through the TDH monthly antimicrobial stewardship and infection control (ASIC) call as well as at various conferences and speaking engagements across the state. Antimicrobial stewardship leads for each facility were targeted. Antibiotics were grouped into 4 classes according to their indications: *C. difficile* infections, urinary tract infections, skin and soft-tissue infections (SSTIs) and respiratory infections. We determined AU percentage by dividing the number of days of therapy for a drug by a facility's average census. Individualized reports are provided to each participating facility on a quarterly basis. **Results:** Currently, 16 facilities have participated in the survey. Overall, 40.7% of antibiotics prescribed were in the common for SSTI category and 39.3% were common for respiratory infections. The top 33 most commonly prescribed antibiotics were amoxicillin (156 days of therapy [DOT]), nitrofurantoin (92 DOT), and levofloxacin (88 DOT). The average percentage of residents on antimicrobials on the day of survey was 12.3%; within this group, 57% of antibiotics were initiated in the LTCF, whereas 43% were present upon admission. **Conclusions:** Early results from the TDH AU PP survey revealed that drugs commonly used for SSTIs and respiratory infection were the most common antibiotic prescriptions and a potential area of focus for TDH's antimicrobial stewardship efforts. None of the 3 most frequently prescribed antibiotics, however, fall under the SSTI indication, despite SSTI being the most commonly prescribed indication based on the survey's evaluation metrics. This finding could be related to the larger number of antibiotics that fall under the SSTI indication. Preliminary data are being used to guide the direction of TDH's future ASIC calls to better suit disease states, which have room for improvement.

Presentation Type:
Poster Presentation
Developing a Clinically Informed Compartmental Mathematical Model of Pediatric Norovirus Transmission—A Feasibility Study

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Background: Norovirus causes a significant disease burden of 20 million cases per year in the United States. Hospitals and long-term care facilities constitute the most commonly reported settings for noroviral outbreaks and clusters and thus represent a critically important site for prevention. Our institutional surveillance and

Figure 1: Norovirus SEIR Model

States: S_x = Susceptible class of entity x; E_x = Exposed class of entity x; I_x = Infectious class of entity x; R_x = Recovered/Immune class of entity x.
Transitions: $\beta_y I_x$ = Force of infection on the preceding compartment exerted by the compartment of infected from population x; σ_x = instantaneous transition rate from exposed to infectious classes; γ_1 = instantaneous transition rate from infectious to recovered/immune classes.
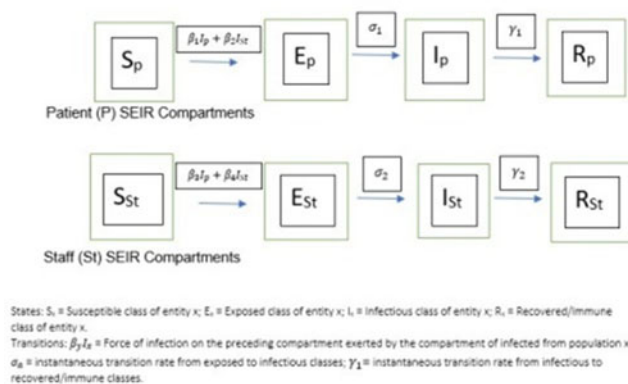
Fig. 1.

response system identified 10–14 clusters or outbreaks of gastrointestinal viral disease per year, predominantly affecting staff. We sought to develop a compartmental mathematical model to examine the potential efficacy of various infection control practices in the management of noroviral clusters. **Methods:** We developed a set of parallel compartments representing both patient and staff categories (nursing, nurse assistants, etc) involved in a prototypical outbreak, using a 38-bed mixed medium- and high-acuity medical unit as the model basis. A susceptible–exposed–infected–recovered/immune (SEIR) model structure was used (Fig. 1). We conducted interviews with infection preventionists and nursing management to parameterize the model with data on (1) staff-to-patient ratios, (2) staff-patient contact time, (3) staff-staff contact time, (4) spatial distribution of patient assignments, and (5) baseline and intraoutbreak infection prevention practices. With these data, we proceeded to develop submodels, building on the primary model, that examined the effects of additional parallel compartmentalization of granular groups of staff, including resident physicians, environmental services, and clinical nursing assistants. Model parameters for these subanalyses were informed by interviews with clinical experts and review of internal data. **Results and Conclusions:** An SEIR model was developed that allowed for examination of a modeled outbreak of norovirus and comparison with a known prior outbreak on the same modeled unit for fidelity. Submodeling was performed with more staffing detail, allowing for the addition of further parallel SEIR tracks that delineated more granular staffing patterns. Staff interviews proved critical in the parameterization of these submodels, allowing for a more faithful representation of real-world dynamics. This work, through modification of model parameterization, can be used to assess the efficacy of hypothetical infection control interventions (eg, earlier unit closure, longer staff furlough) in altering transmission dynamics during an outbreak.

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Presentation Type:
Poster Presentation
Developing a Public Health Model for Regional Infection Prevention Collaboration Among Healthcare Facility Networks
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Background: Antimicrobial resistance (AR), including *Clostridioides difficile* infection (CDI), can spread across the healthcare continuum when patients move between facilities. In 2015, the CDC recommended that healthcare facilities (HCFs) and local public health departments (LPH) coordinate their efforts to prevent the spread of AR and CDI. Accordingly, the California Department of Public Health (CDPH) Healthcare-Associated Infections (HAI) Program developed a model for implementing regionally based AR/CDI prevention collaboratives within HCF networks. **Methods:** The CDPH HAI Program began identifying regions in California with high AR/CDI incidence or risk for AR/CDI emergence using NHSN data. During 2015–2019, we organized AR/CDI prevention collaboratives in these regions. We recruited HCFs for participation by presenting at local professional organization meetings and engaging skilled nursing facility corporate leadership. HAI Program infection preventionists conducted onsite infection prevention assessments at each participating HCF. HAI Program and LPH staff convened quarterly in-person learning and discussion sessions focused on infection prevention and antimicrobial stewardship best practices. Participating HCFs committed to facility-tailored process improvement plans and conducted self-assessments to evaluate infection prevention practice changes at the conclusion of the collaborative. For CDI-focused collaboratives, we used data reported to CDPH via NHSN to assess changes in hospital- and community-onset CDI incidence among participating hospitals before and after the collaboratives. **Results:** Since 2015, 205 HCFs in 15 LPH jurisdictions have participated in 6 regional AR/CDI prevention collaboratives. Participating HCFs reported improved implementation of AR/CDI prevention strategies. For CDI-focused collaboratives, hospital-onset CDI incidence decreased by ~3% per month among participating hospitals. The collaboratives created forums for communication and relationship building, which previously did not exist among LPH and the HCF networks. We used our experience and feedback from partners to develop an HAI Program AR Prevention Collaborative Tool Kit to help LPHs and healthcare organizations develop and implement regional AR/CDI prevention collaboratives in other at-risk or high AR/CDI prevalence areas in California. The tool kit includes materials developed for each of our collaboratives, which may be adapted to meet local needs. **Conclusions:** Regionally coordinated AR/CDI prevention initiatives among LPHs and HCFs can contribute to increased AR awareness, improved AR prevention practices, and decreased AR/CDI incidence. The effectiveness of regional AR/CDI prevention collaboratives may be the result of concurrent efforts to improve AR prevention practices both within individual HCFs and across patient sharing networks.

Presentation Type:
Poster Presentation
Development of a New High-Throughput Multilocus Sequence Typing Method to Monitor Causative Agents of Nosocomial Infections
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Background: Nosocomial infections cause 4%–56% mortality in newborns. Several epidemiological studies have shown that transmission of opportunistic pathogens from the sink to the patient, including *Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*, and *Serratia marcescens* are associated with nosocomial infections in neonatal intensive care units (NICUs). In this project, we aimed to develop fast, accurate, and high-throughput multilocus sequence typing assays (HiMLST-Illumina) to detect opportunistic pathogens to assess their distribution in the sink environment of NICUs and their transfer to patients. **Methods:** Genome sequences of *P. aeruginosa* (n = 45), *S. maltophilia* (n = 23) and *S. marcescens* (n = 34) strains were retrieved from public genome databases to build their pangenomes, using the open-source PGAdb-builder server. The core genome was identified for each opportunistic pathogen and was searched for genes displaying the highest polymorphism. The minimal number of loci to include in a HiMLST-Illumina assay was determined by comparing topology of phylogenetic trees of concatenated loci based on genome similarity, computed as the average nucleotide identity (ANI) score. The primers used for HiMLST-Illumina schemes were designed *in silico* on a conserved domain and were tested on reference strains of each species. **Results:** Bioinformatics analyses showed that 3–4 loci (<300 base pairs per locus) distinguished strains with the same performances than ANI scores. The assays were tested using opportunistic pathogen isolates and environmental DNA originating from NICU sinks. The HiMLST-Illumina analysis of environmental DNA revealed the presence of at least 1 of the 3 studied opportunistic pathogens in 50% of sampled drains (n = 20). In a previous sampling, *P. aeruginosa* was isolated on selective culture media before and 48 hours after disinfection of a sink drain with chlorine. *S. marcescens* was also isolated from another sink 2 weeks after disinfection. Identification of the isolates was confirmed by HiMLST-Illumina analyses and will be typed to compare with clinical isolates. **Conclusions:** Initial in silico tests predict a high discriminating power of the HiMLST-Illumina method, suggesting that it would be possible to quickly identify strains of interest in a large number of samples. The power of this method is also in the possibility for molecular typing without a need for cultivation. Preliminary results suggest that sinks are readily colonized by opportunistic pathogens. This HiMLST-Illumina scheme will be applied in a 2-year intensive survey of NICUs in 3 hospitals in Montreal to evaluate the performance of new sink designs in limiting bioaerosol production and transmission of opportunistic pathogens to patients.