higher HCW immunization and reduced incidence of HAI, data in acute care are lacking compared to the nursing home setting. **Objective:** Our goal was to assess the association between HCW influenza immunization and the incidence of HAI across 2 acute-care facilities. **Methods:** A multicenter prospective cohort study was undertaken at 2 acute-care hospitals including 1 university and 1 community-based academic hospital. Any patient prospectively identified with HAI was included between 2013–2014 and 2018–2019, whereas 2017–2018 was excluded due to vaccine mismatch. The HCW influenza immunization rate was defined as the proportion of HCWs (nurses and other allied and support staff but excluding physicians) immunized prior to December 15. A case of HAI was defined as laboratory-confirmed influenza A or B with symptom onset >72 hours after admission. The association between inpatient ward HCW influenza immunization rate and the incidence of HAI was compared using a Poisson regression analysis adjusting for hospital and influenza season. **Results:** Over 5 influenza seasons, the incidences of HAI at either facility were 0.24 and 0.22 per 1,000 patient days, whereas the median HCW influenza immunization rates were 57.3% (IQR, 42.5%–66.4%) and 66.6% (IQR, 50.6%–76.8%), respectively. When adjusting for hospital and influenza season in the multivariate analysis, HCW influenza immunization rates of 65% and 70% were not associated with HAI incidence. In contrast, HCW influenza immunization rates ≥75% was associated with a trend toward reduced HAI (IRR, 0.65; 95% CI, 0.39–1.08; $P = .096$) whereas inpatient wards above 80% immunization had significantly lower risk of HAI (IRR, 0.28; 95% CI, 0.089–0.89; $P = .03$). **Conclusions:** The risk of HAI across 2 acute-care hospitals was significantly lower among inpatient wards achieving HCW influenza immunization rates >80%. Acute-care facilities should aim for this minimum HCW immunization rate to protect patients from the complications of HAI.

Presentation Type:
Poster Presentation
Missing the Point in Point Prevalence: Harnessing EMR Data to Identify Epi-Linked Patients in an Outbreak Investigation

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Background: A critical step during outbreak investigations is actively screening for additional cases to assess ongoing transmission. In the healthcare setting, one widely used method is point-prevalence screening on the whole unit where a positive patient is housed. Although this point-prevalence approach captures the "place," it can miss the "person" and "time" elements that define the population-at-risk. Methods: At University of North Carolina (UNC) Hospitals, we used business intelligence tools to build a query that harnesses the admission, discharge, and transfer (ADT) data from the electronic medical record (EMR). Using this data identifies every patient who overlapped in time and space with a positive patient. An additional query identifies currently admitted overlap patients and their current location. During an outbreak investigation, an analyst executes these queries in the mornings when surveillance screens are scheduled. The queries generate a list of patients to screen that are prioritized on the number of days they were in the same unit with the positive patient. This overlap methodology successfully captures the person, place, and time associated with possible disease transmission. We implemented the overlap method for the last 3 months following 1 year of point-prevalence approach screening during a novel disease outbreak at UNC Hospitals. Results: In total, 4,385 unique patients overlapped with previously identified infected or colonized patients, of which 781 (17.8%) from 40 departments were screened over 15 months. During a subsequent, currently ongoing, outbreak, we are utilizing the overlap method and in 6 weeks have already screened 161 of the 1,234 overlapping patients (13%). After 3 rounds of overlap screening, we have already been able to identify 1 additional positive patient. This patient was on the same unit as patient zero 4 months prior but was readmitted to a unit that would not have received a point-prevalence screen using the standard approach. **Conclusions:** Surveillance screening is a time-consuming, resource-intensive effort that requires collaboration between infection prevention, clinical staff, patients, and the laboratory. By harnessing EMR ADT data, we can better target the population at risk and more efficiently utilize resources during outbreak investigations. In addition, the overlap method fills a gap in the current CDC guidelines by focusing on patients who were on the same unit with any positive patient, including those who discharged and readmitted. Most importantly, we identified an additional positive patient that would not have been detected through a point-prevalence screen, helping us prevent further disease transmission.

Presentation Type:
Poster Presentation
Modeling Transmission of Human Metapneumovirus in a Long-Term Care Facility

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Background: In September 2019, the Louisiana Department of Health (LDH) was notified of a possible outbreak of influenza in a nursing home. Upon investigation, the infectious agent was determined to be human metapneumovirus (HMPV). By the conclusion of the outbreak, 35 (31.3%) symptomatic cases were identified of which 15 were laboratory-confirmed HMPV. Public health coordination, infection control interventions, environmental cleaning audits, halting new admissions, and ceasing group activities are credited with stopping transmission. Considering the high attack rate, LDH epidemiologists examined scenarios wherein the aforementioned interventions were not utilized. The aim of this analysis is to describe transmission of HMPV in a 112-bed nursing home using mathematical models under conditions wherein interventions were not readily implemented. **Methods:** Two deterministic and 1 stochastic susceptible–preinfectious–infectious–recovered (SEIR) models are presented. Although recovered persons can be susceptible to HMPV following an infection experience, the potential for reinfection was not considered for this analysis. Fixed variables considered include a 5-day incubation period, basic reproduction number of 2, 14-day infectious period, and 112 susceptible patients. Three counterfactual modeling conditions are considered: delaying notification of an outbreak to public health epidemiologists (model 1), staff hand hygiene compliance of 50% (model 2), and continuing to accept new admissions (model 3). Average rate of recovery per day was and other metrics are used to demonstrate the number of susceptible individuals. Excel workbooks developed by Vynnycky and White (2010) were used for analysis. **Results:** In model 1, the average rate of onset of

infectiousness per day = 0.20, and the average recovery rate per day = 0.07. With no notification to public health epidemiologists, all 112 patients would have been infected with HMPV after 94 days. The reproductive number was doubled to 4 in model 2 to posit poor healthcare worker hand hygiene of 50% compliance. Given this, the number of days until all patients are infected with HMPV decreases to 39 days. Finally, the stochastic scenario (model 3) demonstrates that the number of newly infected persons per day = 0.86, and the hazard rate for infectious individuals becoming immune = 0.07. **Conclusions:** Infection control interventions are extremely useful for containing viral respiratory diseases for which there is no vaccine or treatment. Mathematical models can communicate utility of public health interventions in the presence of outbreaks. These models demonstrate worst-case scenarios for infection spread.
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Poster Presentation
Modified Veterans Health Administration *Clostridioides difficile* Infection (CDI) Prevention Bundle: Progress Over 8 Years Decreasing CDI Laboratory-Identified (LabID) Events at a Large Veterans Affairs Medical Center

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Background: In March 2012, the Veterans' Health Administration (VHA) published the Guideline for the Prevention of *Clostridium difficile* infection (CDI) in VHA Inpatient Acute-Care Facilities, with a goal of 30% reduction of cases within 2 years. In March 2011, this facility, along with 31 others, served as a pilot site to develop the guidelines. **Methods:** The CDI prevention bundle was implemented to prevent new onset CDI cases in the facility with 4 core measures: (1) environmental cleaning (EMS), (2) hand hygiene, (3) contact precautions, and (4) cultural transformation. Education was provided to EMS staff, nursing, and care providers on the CDI case definition, criteria for testing, empiric isolation for patients with diarrhea, hand hygiene, and PPE to control spread. In 2014, antimicrobial stewardship was added, and within 5 years an algorithm for isolation and testing was published. Cases were reviewed weekly using TheraDoc software and were reported monthly to the national VHA Inpatient Evaluation Center (IPEC). Isolation was communicated using a ward roster/isolation list in TheraDoc for all unit champions to consult daily. CDI cases were classified using NHSN definitions for a laboratory-identified (LabID) event, recurrent cases, and community-onset cases. Real-time case review and weekly multidisciplinary case discussions identified opportunities for improved compliance with the core measures. **Results:** Over an 8-year period, CDI healthcare-onset LabID events decreased by 73%. The cases decreased from 149 to 40 over the 8-year period.

The infection rate decreased 70% from 16.19 per 10,000 bed days of care in FY2011 (October 2010) to 4.88 in FY2019. The incidence of community onset infections increased from 75 in FY2011 to a high of 146 in FY2018 for a rate of 8.15 to 18.17. In FY2019, there was a decrease in both LabID events and community-onset cases to lows of 40 and 102, respectively. Inappropriate testing decreased by 84% from 50 in FY2011 to 8 in FY2019. **Conclusions:** A multidisciplinary team approach that included support from leadership and clinical providers as well as front line staff involvement, daily rounding, and case review by infection preventionists has reduced all CDI cases over an 8-year period using the modified VHA CDI bundle. TheraDoc enabled case review, correct isolation, changes to cleaning practices, and more appropriate lab testing. The antimicrobial stewardship program that includes clinical pharmacists working daily with providers was a strong driver for change.
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Poster Presentation
Molecular Epidemiology of *Bordetella pertussis* Strains Isolated in Vietnam During 2015–2017

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Background: Whooping cough is a serious respiratory illness in infants caused by *Bordetella pertussis*. In spite of the vaccination program, the incidence rates of whooping cough per 100,000 population in Vietnam increased from 0.33 in 2015 to 0.58 in 2017. If this represents a pertussis resurgence, contributors may include pathogen adaptation, the spread of specific variants, vaccine failure, and failure to effectively treat cases and contacts. There has been little research in Vietnam on *B. pertussis* strains. Therefore, we investigated the molecular epidemiology of circulating *B. pertussis* strains in Southern Vietnam by applying multilocus sequence typing (MLST) for 7 housekeeping genes and 4 antigenic determinant genes as components in the acellular vaccine including prn, ptxP, ptxS1, and fim3. **Methods:** DNA was extracted from 15 isolates collected from 263 case patients during 2015–2017 and was subject to MLST using primers and cycling conditions from the *Bordetella* pubMLST website (www.Pubmlst.org/Bordetella/). The products were analyzed using BioEdit version 7.2.5 software and then were aligned and compared to reference sequences of each genotype in the database. The evolutionary relationship among sequence types (STs) from housekeeping genes was performed as a minimum spanning tree via the goeBURST algorithm, whereas the correlation of different variants from 4 antigenic determinant genes was built up and clarified with phylogenetic trees based on the UPGMA method by MEGA 7 program. **Results:** The 15 isolates were all classified as ST2 (100%) by MLST of housekeeping genes, and they belonged to a common global clonal group (Fig. 1). Sequencing of antigenic determinant genes *prn2 – ptxP3 – ptxS1-1 – fim3-1* determined that all were identical to each another and the reference sequences (Fig. 2). **Conclusions:** *B. pertussis* isolates circulating in Southern Vietnam appeared to be the same as the common global strain. Few isolates were available for testing;