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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Presentation Type:
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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Presentation Type:
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;

Group(s): 0
STs = 7
isolates = 244
edges = 21 [7 10 4]
forest edges = 6 [6 0 0]
edges without ties = 4
tiebreaks by SLV = 2
tiebreaks by DLV = 0
tiebreaks by TLV = 0
tiebreaks by FRQ = 0
tiebreaks by ID = 0

VIETNAM

- country: Spain ST (MLST):2 (n = 80, 32.79%)
- country: USA ST (MLST):2 (n = 70, 28.69%)
- country: Czech Republic ST (MLST):2 (n = 58, 23.77 %)
- country: Vietnam ST (MLST):2 (n = 15, 6.15%)
- country: Spain ST (MLST):87 (n = 8, 3.28%)
- country: USA ST (MLST):79 (n = 4, 1.64%)
- country: USA ST (MLST):1 (n = 2, 0.82%)
- country: Austria ST (MLST):86 (n = 1, 0.41%)
- country: China ST (MLST):1 (n = 1, 0.41%)
- country: Japan ST (MLST):1 (n = 1, 0.41%)
- country: Spain ST (MLST):83 (n = 1, 0.41%)
- country: The Netherlands ST (MLST):2 (n = 1, 0.41%)
- country: USA ST (MLST):24 (n = 1, 0.41%)
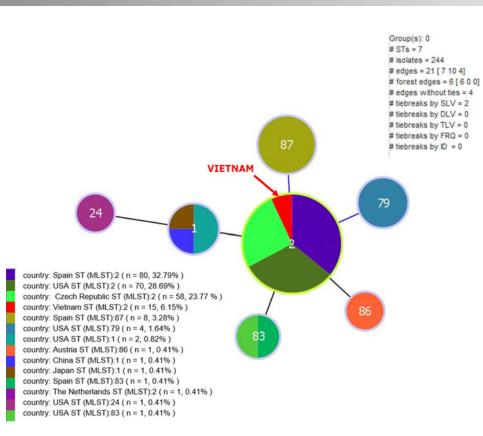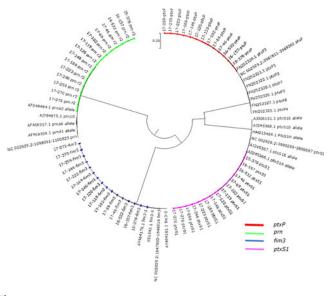- country: USA ST (MLST):83 (n = 1, 0.41%)

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

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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