screening and isolation precautions; however, a significant increase was seen among the patients at site B (Fig. 1, infection rates). Furthermore, there was a significant decrease in VRE clinical isolate, infection, and bacteremia incidence following the reinstatement of screening in the ICU and transplant programs at site A, but no effect was seen in the other programs (Fig. 2, infection rates). **Conclusions:** The risk associated with discontinuing VRE screening and isolation measures appears depend on the subgroup of patients within a hospital environment. Furthermore, risk-based or unit-based VRE screening and isolation appears to be effective at controlling VRE incidence, even after measures had previously been discontinued. Additional study of other inpatient settings is warranted to determine the effects of screening and isolation for VRE on other patient subgroups.

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Presentation Type:

Poster Presentation

When Legionnaires' Disease Isn't: Case Presentation and Implications of the Council of State and Territorial Epidemiologists (CSTE) Changes to Case Definitions

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Background: Most cases of Legionnaires' disease are diagnosed by the urinary antigen test (UAT). Single cases of suspected healthcare-acquired Legionnaires' disease are often investigated by local and state health departments. Such investigations can result in disruptive and expensive interventions. We report a case of a urineantigen–positive patient whose clinical presentation was inconsistent with Legionnaires' disease. Within the same year, an employee at this hospital was diagnosed with presumed communityacquired Legionnaires' disease; however, the case was considered by the health department to be healthcare acquired. The

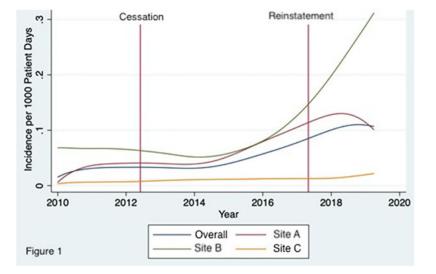
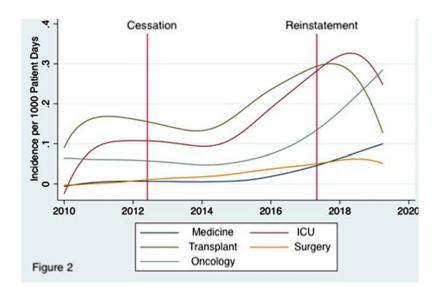


Fig. 1.



occurrence of 2 cases, as determined by the health department, fulfilled the definition for an outbreak investigation and triggered water restrictions and extensive testing of the environment and patients for *Legionella*. The cases and the implications of these actions are reviewed in the context of new information about false-positive urinary-antigen tests and changes to the outbreak case definitions for Legionnaires' disease by the Council of State and Territorial Epidemiologists (CTSE). This includes "probable" cases that have no positive diagnostic tests.

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Whole-Genome Sequencing Reveals Diversity of Carbapenem-Resistant *Pseudomonas aeruginosa* Collected Through the Emerging Infections Program

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Background: Carbapenem-resistant Pseudomonas aeruginosa (CRPA) is a frequent cause of healthcare-associated infections (HAIs). The CDC Emerging Infections Program (EIP) conducted population and laboratory-based surveillance of CRPA in selected areas in 8 states from August 1, 2016, through July 31, 2018. We aimed to describe the molecular epidemiology and mechanisms of resistance of CRPA isolates collected through this surveillance. Methods: We defined a case as the first isolate of P. aeruginosa resistant to imipenem, meropenem, or doripenem from the lower respiratory tract, urine, wounds, or normally sterile sites identified from a resident of the EIP catchment area in a 30-day period; EIP sites submitted a systematic random sample of isolates to CDC for further characterization. Of 1,021 CRPA clinical isolates submitted, 707 have been sequenced to date using an Illumina MiSeq. Sequenced genomes were classified using the 7-gene multilocus sequence typing (MLST) scheme, and a core genome MLST

