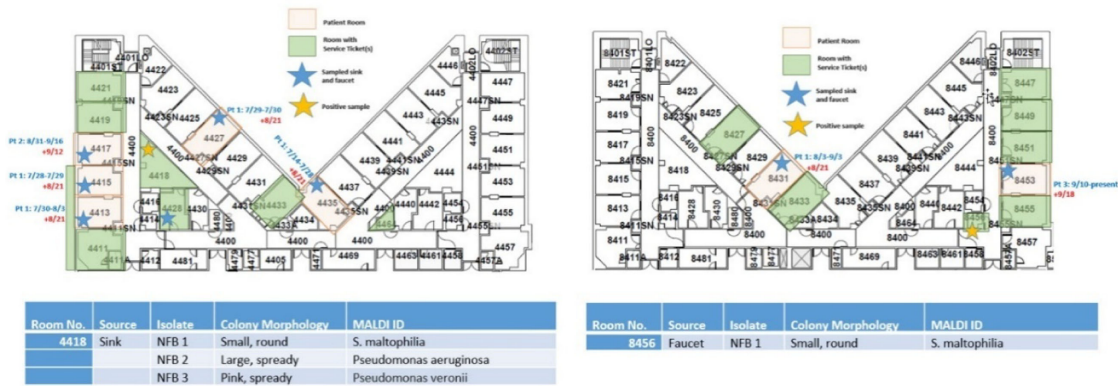
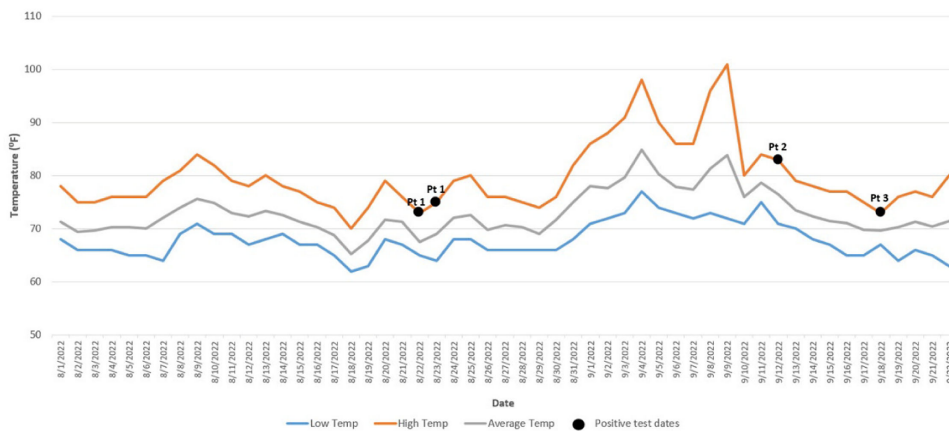


Map of patient rooms, environmental sampling locations and results



Temperature and timing of *Aeromonas* cultures



carbapenemases VIM-2 and KPC-3 in 1 isolate and OXA-232 in another. Of the 20 environmental samples, few gram-negative nonfermenting bacteria and no *Aeromonas* isolates were detected (Fig. 1). Elevated city did loosely proceed patient cases of *Aeromonas*, suggesting a possible role of higher temperature, which may have promoted the growth of *Aeromonas* during the periods of the 3 cases and thus may contribute to the nosocomial infections (Fig. 2). **Conclusions:** Although our investigation did not reveal a definitive cause for the *Aeromonas* cases, it did show the importance prompt identification and investigation can have on mitigating the spread of a cluster. Our facility has not identified any additional nosocomial cases. Monitoring water intrusion events and plans for remediation continue to be a priority.

Disclosures: None

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Presentation Type:

Poster Presentation - Poster Presentation

Subject Category: Outbreaks

Polyclonal *Burkholderia cepacia* complex outbreak caused by contaminated chlorhexidine gluconate solution

Christel Valdez; Cybele Abad; Karl Evans Henson; Mark Carascal and Raul Destura

Background: *Burkholderia cepacia* complex is an opportunistic environmental pathogen that has been linked to nosocomial outbreaks. We

describe an outbreak of bacteremia caused by *Burkholderia cenocepacia* from a contaminated chlorhexidine gluconate solution. **Methods:** The hospital infection control team carried out an outbreak investigation on February 21, 2021, when 3 adult hemodialysis patients developed *B. cenocepacia* bacteremia. Patient demographics and clinical profile were reviewed retrospectively. Potential sources of infection were identified,

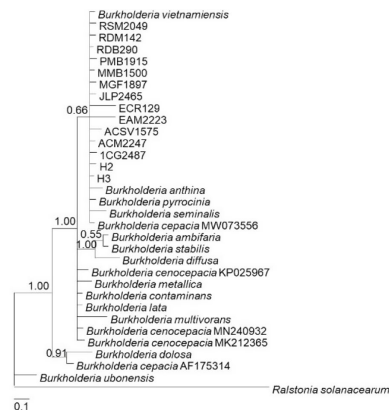


Figure 1. Bayesian inference tree of the sample sequences based on 563 nucleotides of the 16S rRNA gene and two majority consensus trees. The tree is rooted on the bacterium *Ralstonia solanacearum*. Numbers on nodes represent posterior probabilities.

and environmental screening was performed in several units. Processes of catheter care in the hemodialysis unit were reviewed. Water samples from the hemodialysis unit, and samples of solutions used in patient care were sent for culture. Isolates from patients and from environmental samples were sent for 16S rRNA gene sequencing to determine genetic relatedness. **Results:** In total, 16 patients, 8 of whom were male, developed *B. cenocepacia* bacteremia during the investigated period. The median age was 68 years (range, 19–83), and 15 of 16 had at least 1 comorbidity. All patients used a central venous catheter (CVC) for hemodialysis, and 11 (70%) of these 16 were temporary. Chlorhexidine gluconate solution was routinely used as part of CVC care and 1 bottle was shared among 4 hemodialysis stations. On suspicion of contamination, all identified chlorhexidine bottles were recalled on February 26, 2021, and random samples from 15 opened and 19 unopened bottles were sent for culture from the following units: hemodialysis (n = 2), ICU (n = 14), wards (n = 6), and 4 each from transplant surgery, and delivery suites. Of 34 sampled bottles, 17 grew *B. cenocepacia*: 8 opened and 9 unopened bottles. The Bayesian inference tree (Fig. 1) supports the hypothesis that patient samples and the samples from the chlorhexidine solutions were most probably related to each other based on the 16S rRNA sequences. However, the individual identities of the specific sample sequences could not be determined using the analyzed region of the gene, possibly due to low quality of the sequences received. No new cases of *B. cenocepacia* were identified after recall of the chlorhexidine

solution, and the outbreak was deemed resolved on March 24, 2021. **Conclusions:** Medical solutions routinely used in patient care can cause outbreaks and should be suspected as a potential source of infection by infection control teams.

Disclosures: None

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Presentation Type:

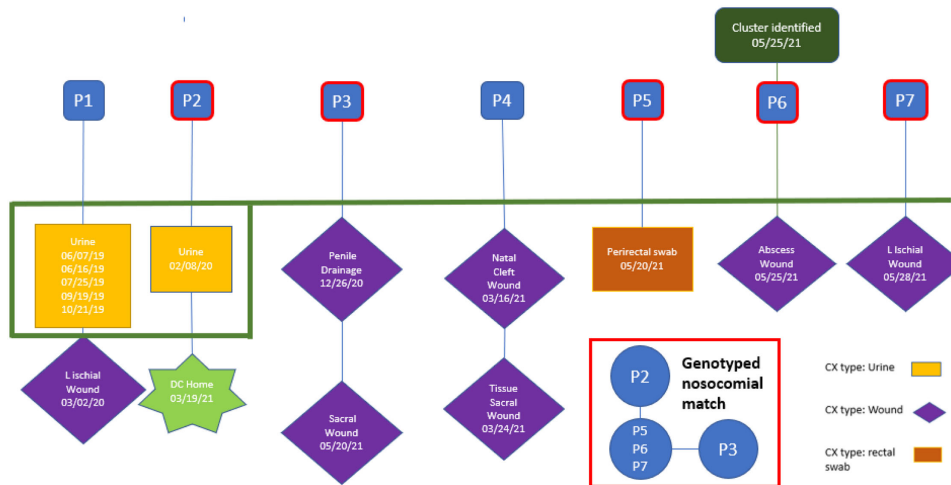
Poster Presentation - Poster Presentation

Subject Category: Outbreaks

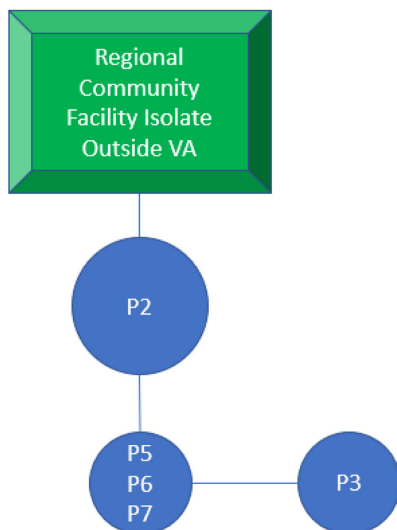
Multidrug-resistant *Acinetobacter* outbreak in spinal cord unit identified and stemmed through infection prevention epidemiologic efforts

Sean O’Neil; Delvina Ford; Erica Beck and Theresa Carroll

Background: Drug-resistant pathogens are a significant source of increased cost and patient complications in long-term and/or congregate care settings. Once introduced, depending on the environmental niche in which they establish and the mechanisms they employ for survival, they can be difficult to eradicate. We report the details of an epidemiologic investigation of a multidrug-resistant *Acinetobacter baumannii* (MDR-A) outbreak in a spinal cord intervention (SCI) unit within a Veterans Affairs facility in San Antonio, Texas, that was identified after back tracing



Carroll/Beck/Ford Infection Prevention



Five *A. baumannii* isolates belonged to sequence type (ST) ST-2 and a single isolate belonged to ST-1

Patient	Culture Results
P2	Urine 02/08/20
P3	Wound 12/26/20 Wound 05/20/21
P5	Perirectal Swab 05/20/21
P6	Wound 05/25/21
P7	Wound 05/28/21