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**Background.** We performed an investigation after noting an increase in hospital-onset (HO) KPC-producing *Enterobacteriaceae* (KPC-E) infections in patients admitted to a tertiary referral hospital in North Carolina.

**Methods.** We defined pre-outbreak (January 1, 2017–June 30, 2017), outbreak (July 1, 2017–October 31, 2017), and post-outbreak (November 1, 2017–March 31, 2018) phases. A clinical case was defined as any positive clinical culture for KPC-E. HO was defined as a positive clinical or surveillance culture collected on hospital day ≥ 2. Patients were mapped in space and time to inform targeted environmental sampling. Whole genome sequencing (WGS) was performed on selected KPC *K. pneumoniae* environmental and patient isolates to determine relatedness.

In October 2017, a CRE prevention bundle was implemented that included daily communication of CRE patient movement, increased audits/feedback of HCW compliance with hand hygiene, enhanced cleaning and disinfection in CRE rooms and high-risk units with bleach and UVC disinfection, and weekly rectal surveillance screens in four adult ICUs.

**Results.** 0.67 clinical cases of KPC-E per month were observed during the pre-outbreak period compared with 3.75 clinical cases of KPC-E per month during the outbreak period. *K. pneumoniae* was the most common species (Figure 1). Mapping of patients revealed probable direct and indirect transmission between patients in multiple hospital units (Figure 2). Three patients who were non-sequentially admitted to the same ICU room over a 12-week span acquired KPC *K. pneumoniae* (Figure 2).

Environmental cultures from the in-room sink drain and P-trap grew KPC *K. pneumoniae* that was related to the patient isolates by WGS; the sink was removed. Although no additional clinical cases of KPC-E occurred after full implementation of the bundle and sink removal, we continued to observe acquisition of KPC-E rectal colonization in all four ICUs (Figure 3).

**Conclusion.** We describe a multispecies outbreak of KPC-E that was mitigated through evidence-based CRE control measures and removal of a colonized sink. However, ongoing low-level presumed transmission of KPC points to persistent environmental sources. Additional study is needed to understand the prevalence of CRE in hospital sinks, factors that drive drain colonization, and contribution of CRE in a sink to nosocomial transmission.

**Disclosure.** All authors: No reported disclosures.

1252. A Challenging *Burkholderia* Outbreak Investigation Across Multiple Units at an Academic Medical Center From June 2017 to February 2018

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**Background.** Most outbreak investigations involve short-term, geographically localized clusters. However, some organisms can form environmental reservoirs leading to more prolonged, widespread outbreaks. We describe a prolonged outbreak of *Burkholderia* at our institution.

**Methods.** An epidemiologic investigation was conducted. *Burkholderia* isolates were genotyped using pulsed-field gel electrophoresis (PFGE) and recA gene sequencing. Initial isolates were sent to a national reference laboratory for multilocus sequence typing (MLST).

**Results.** 32 patients on 12 units (see figure) had ≥1 positive culture for *Burkholderia* from June 2017 to February 2018. 21 had *B. cenocepacia* (PFGE pattern A, recA allele 365) and 11 had *B. cepacia* (PFGE pattern C, recA allele 53). MLST revealed that isolates with recA allele 365 were unique compared with previously identified *B. cenocepacia* strains. Of 32 patients, 28 (88%) had positive respiratory cultures. Of 32 patients, 3 (9%) had bacteremia. Thirty-day mortality was 4/29 (14%). A case-control study did not reveal a common point source. All surveillance cultures from asymptomatic patients were negative (n = 53). Two of nine sink drains in rooms of cases were positive for an unrelated strain of *B. cepacia*. Other environmental cultures were negative for *Burkholderia* (n = 49). Cases continued despite routine interventions (see figure), with some incident cases detected long after potential exposures. Ventilator/respiratory equipment (V/RE) cleaning was investigated. Multiple V/RE interventions were implemented: (1) ensuring a sterilization process for ventilator temperature probes (used in heated humidification) was occurring; (2) using disposable manometers on contact isolation patients; (3) reinforcing ventilator cleaning, including those in radiology suites after use.

**Conclusion.** No definitive source of the outbreak was found. New cases continued after reinforcement of basic infection control practices, but subsided after focused attention on V/RE cleaning practices. Control of this outbreak was challenging due to the complexity of a prolonged “latency period” for *Burkholderia*, difficulty identifying reservoirs, and multiple possible modes of transmission, especially for organisms like *Burkholderia* that can persist on environmental surfaces and equipment.

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1253. Healthcare-Associated Transmission of Burkholderia cepacia Complex Associated With Extrinsically Contaminated Nasal Spray
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Background. Burkholderia cepacia complex (Bcc) species can contaminate medical devices and products, resulting in outbreaks of healthcare-associated infections. In March 2018, we investigated a cluster of 20 patients with a sinus culture positive for Bcc seen at two affiliated ENT clinics in Oregon over a 2-month period, based on reporting by a laboratory in a central laboratory external to the clinics.

Methods. We conducted an epidemiologic investigation to identify potential causes for an apparent outbreak of Bcc, including review of health records and microbiologic reports, site visits, staff interviews, and cultures of common equipment and products.

Results. 20 patients (9 were female; age range 10 to 72 years, median age 54.5 years) had new positive Bcc cultures from the sinus. The absence of cystic fibrosis, immunosuppression or sinonasal polyps in all patients, scant growth of Bcc in most cases with isolation of another organism in some, and the use of Bcc-directed antibiotics in a minority of patients suggested the presence of a contamination source. All patients had received lidocaine/phenylephrine (L/P) via multidose nasal spray atomizers prior to endoscopically-directed sinus cultures. Site visits revealed improper medication dispensing and storage practices (e.g., no expiration date for L/P stock, storage of L/P-containing atomizers at room temperature), and inadequate instrument reprocessing and environmental cleaning. Cultures of L/P in 2/2 in-use atomizers and 1/1 opened stock bottle, as well as swabs of 3/3 spray mechanisms, grew Bcc. Cultures of L/P from the unopened, refrigerated stock bottle, a flexible endoscope and a rigid endoscope did not yield Bcc. No negative clinical sequelae in these patients were reported.

Conclusion. Contaminated multidose L/P nasal spray with Bcc resulted in nosocomial transmission at these clinics. This investigation highlights the important role of laboratorians in detecting Bcc contamination events that lead to colonization, and suboptimal reporting by clinicians in the outpatient setting. It also raises the question of how often such contamination events go undetected. Injection safety training needs to be broadened to “medication administration safety” training as one and only principle could have prevented this incident.

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1254. Outbreak of Mycobacterium chelonae Skin Infections Associated With Human Chorionic Gonadotropin Injections at Weight Loss Clinics
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Background. In December 2016, a dermatologist notified the Minnesota Department of Health (MDH) of three patients with skin lesions after self-administration of human chorionic gonadotropin (HCG) injections supplied by same weight loss clinic. A large outbreak with different clones of vancomycin-resistant enterococci (VRE) affected the Bern University Hospital group for several months. The aim of this study was to describe the extent of the outbreak, using whole-genome sequencing (WGS).

Methods. Triggered by two cases of VRE bloodstream infections on our hemato-oncology ward, an outbreak investigation was started. Microbiological diagnosis of VRE was obtained by culture and PCR. Epidemiological links were assessed by metagenomic chart review and supplemented with WGS analyses. Multiple infection control measures were implemented to avoid further transmissions.

Results. Between December 2017 and April 2018, 2,877 screening samples were obtained from 1,201 patients. Three out of six hospitals within the Bern University Hospital group were affected. Eighty-three patients (6.9%) were colonized with VRE enterococcus faecium. Of those, 76 (91.6%) had a strain carrying vanA, with 70 (84%) isolates virtually identical (separated by up to two alleles) by cgMLST and identified as MLST type ST796 (figure). The remaining seven patients (8.4%) were colonized with vanA carrying strains from five different STs. Five patients (7%) developed an invasive infection with VRE ST796. Temporo-spatial clusters were seen in most patients carrying the outbreak strain. In order to control the outbreak, extensive infection control measures were implemented. By April 2018 the outbreak was contained with these specific measures.

Conclusion. This VRE outbreak was characterized by a rapid intra- and inter-institutional spread of the emergent clone ST796. This clone was recently described in Australia and New Zealand but never before in Europe.1,2 A multi-faceted infection control led to the containment of the outbreak.

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