1253. Healthcare-Associated Transmission of *Burkholderia cepacia* Complex Associated With Extrinsically Contaminated Nasal Spray

Dat Tran, MD, MS; Maureen Cassidy, MT, MPH; Tara Buehring, MPH and Rebecca Pierce, PhD[1]; [1]Public Health Division, Oregon Health Authority, Portland, Oregon

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Background. *Burkholderia cepacia* complex (Bcc) species can contaminate medical devices and water-based 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 laboratorian 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 polyposis 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 principles 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

Rajal Mody, MD, MPH[1,2]; Jean Rainbow, RN, MPH[2]; Beth Ferguson, PharmD, BCPS[3]; Cody Wiberg, PharmD, MS, RPh[3]; Trudy Kupferschmidt, MT(ASCP)[2]; Liz Horn, MT(ASCP)[2]; Maroya Spalding Walters, PhD, ScM[4]; Ryan Fagan, MD[5]; Greta Chen, MD[6] and Karla Rosenman, MD[7]; [1]Division of State and Local Readiness, Office of Public Health Preparedness and Response, Centers for Disease Control and Prevention, Atlanta, Georgia, [2]Minnesota Department of Health, St. Paul, Minnesota, [3]Minnesota Board of Pharmacy, Minneapolis, Minnesota, [4]Division of Healthcare Quality Promotion, National Center for Emerging and Zoonotic Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, [5]Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, Georgia, [6]Park Nicollet, Maple Grove, Minnesota, [7]Park Nicollet, Saint Louis Park, Minnesota

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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 chain (Chain X); one lesion had been diagnosed as a nontuberculous mycobacteria (NTM) infection. We investigated to identify the etiology, determine contributing transmission factors, and to prevent additional cases.

Methods. We defined a case as a skin or soft tissue lesion with a suspected infectious etiology in a Minnesota resident occurring within three months after HCG injection at or near an injection site. To find cases we sent health alerts to clinicians and clinical laboratories throughout Minnesota with diagnostic guidance, and we requested Chain X to notify all exposed patients. We visited two Chain X clinics to assess infection control practices, to collect invoices for product traceback, and to collect products for microbiological testing. All NTM isolates were identified by line probe assay and subtyped by pulsed-field gel electrophoresis (PFGE) at MDH.

Results. We identified six cases with illness onset dates ranging from April to November 2016. All patients were adult women who did not share HCG vials. Four patients had clinical specimens that grew NTM; all isolates were identified as *Mycobacterium chelonae* that were indistinguishable by PFGE. Three patients with confirmed *M. chelonae* infection obtained HCG at Clinic A, and one from Clinic B, but sharing of reconstituted HCG by the two clinics could not be excluded. We identified several infection control breaches at both clinics including improper reconstitution of HCG and incorrect use of single use vials. The most likely source of the HCG was an unregistered out-of-state compounding pharmacy.

Conclusion. This common source outbreak was likely due to contamination introduced either at a weight loss clinic or a compounding pharmacy. HCG injections are not US FDA-approved for weight loss, and their use may involve compounded products dispensed by alternative care settings that lack infection control expertise and regulatory oversight. This outbreak highlights the important role physician reporting of disease clusters plays in uncovering unsafe practices.

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

1255. First Outbreak Due to Vancomycin-Resistant *Enterococcus* Epidemic Clone ST796 in Europe

Nasstasja Wassilew, MD[1]; Eveline Rolli, Mrs[1]; Yvonne Fietze, Mrs[1]; Carlo Casanova, PhD[2]; Helena Seth-Smith, PhD[3,4]; Adrian Egli, MD[3,4]; Jonas Marschall, MD[1] and Niccolo Buetti, MD[1]; [1]Infectious Diseases and Hospital Epidemiology, University Hospital Bern, Bern, Switzerland, [2]Institute for Infectious Diseases, University of Bern, Bern, Switzerland, [3]Applied Microbiology Research, Department of Biomedicine, University of Basel, Basel, Switzerland, [4]Department of Clinical Microbiology, University Hospital Basel, Basel, Switzerland

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Background. 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 meticulous 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 1,200 patients. Three out of six hospitals within the Bern University Hospital group were affected. Eighty-three patients (6.9%) were colonized with VR *Enterococcus faecium*. Of those, 76 (91.6%) had a strain carrying *vanB*, 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 links were found 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.

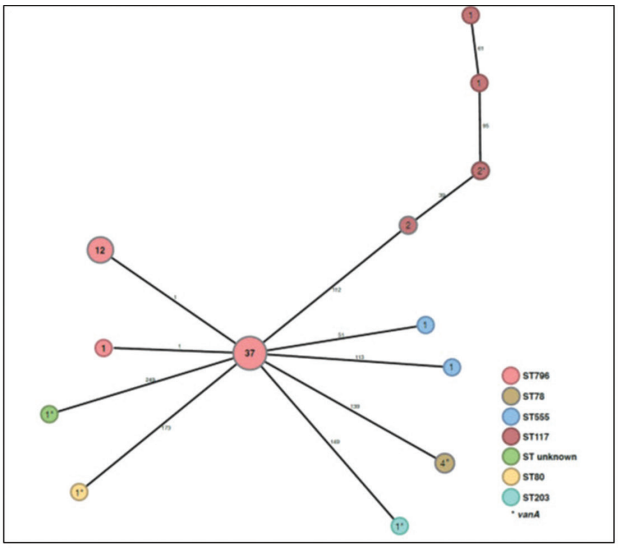

Figure: Core Genome MLST (cgMLST) multiple spanning tree of *Enterococcus faecium* isolates from University Hospital Bern. The cgMLST analysis is based on 1423 loci (3) and was performed in Ridom Seqsphere v4.1.6. Number of isolates belonging to each cluster is shown in the circles, and the number of allele differences between clusters is presented on the connecting lines. Outbreak strains carry *vanB* and belong to ST796: this cluster is highlighted. Strains carrying *vanA* are indicated with an asterisk. Other, non-VRE isolates are shown for context.

References

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