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Letter to the Editor

Outbreak of *Serratia marcescens* bacteremia in pediatric patients epidemiologically linked to pre-filled heparin flushes

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To the Editor—On January 20, 2018, a case of *Serratia marcescens* bacteremia was reported to the infection prevention team during multidisciplinary microbiology rounds at a large, pediatric, tertiary-care hospital in Colorado. Six days later, the infection prevention team was notified by the microbiology laboratory of a second case of *S. marcescens* bacteremia. The hospital identifies only 1–4 cases of *Serratia* bacteremia annually, so the hospital infection prevention team initiated an investigation and reported a possible outbreak to the public health department.

A case was defined as a *S. marcescens* bloodstream infection between January 1 and April 5, 2018. Epidemiologic classifications were assigned to cases based on the definitions established by the National Healthcare Safety Network (NHSN). To determine whether a common source was responsible for the outbreak, the infection preventionist reviewed medical records of all patients with blood cultures positive for *S. marcescens*, including a review of common products, medications, procedures, shared staff, and hospital locations. Clinical nursing staff worked on the units where the cases occurred were interviewed. An environmental assessment of hospital rooms and shared areas was conducted. Line lists were created to discover common exposures and epidemiological links between patients and to generate possible hypotheses. Shared product lot numbers were located and tracked. A national children's hospital infection prevention listserv and distribution of a notification through the Centers for Disease Control and Prevention Epidemic Information Exchange (EpiX) solicited reports of cases outside of Colorado.

From January 1 to April 3, 2018, 5 cases among 5 patients were identified at our facility. All patients were male, 2–10 years of age, and had central venous catheters: 1 peripherally inserted central catheter [PICC], 2 implantable ports, 1 hemodialysis catheter, 2 Hickman broviac catheters. Two patients (40%) were immunocompromised. Three patients were admitted to the pediatric intensive care unit (PICU). Two patients (40%) were receiving outpatient therapies (radiation therapy or hemophilia treatment) and had positive blood cultures upon admission to the hospital. Two patients with central venous ports had repeat *S. marcescens* bloodstream infections within 2 weeks following completion of a treatment course of antimicrobial therapy and subsequently required removal of their ports.

Common exposures among the 3 initial patients generated initial hypotheses including environmental contamination, product contamination, and drug diversion. The identification of a fourth case in the outpatient setting narrowed our investigation to a possible contaminated product. Common products shared among all 5 patients included prefilled, sterile-field, ready, normal saline flushes and prefilled heparin flushes from the same manufacturer; antiseptic skin preparation; and sterile alcohol prep pads. Discussion with public health officials and other facilities in the United States identified another pediatric institution outside Colorado with patients who had *S. marcescens* bacteremia. This collaboration narrowed the concern to potentially contaminated prefilled heparin flushes.

All 5 *S. marcescens* isolates were genetically indistinguishable by PFGE and matched those from the other pediatric institution. In total, 165 prefilled heparin syringes from 10 lots were cultured in the hospital's microbiology laboratory. None were positive for *S. marcescens*, but 9 cultures grew *Bacillus* spp. On April 13, 2018, our facility removed all prefilled heparin flushes of 2 concentrations (10:1 units/mL and 100:1 units/mL) and replaced them with product from a different manufacturer. No additional cases were identified following the removal of the prefilled heparin flushes.

Outbreaks of *S. marcescens* bacteremia have been reported in the healthcare setting and have been linked to a variety of contaminated products.[1–7] However, this outbreak might have been overlooked if our surveillance and investigation had been limited to strictly defined hospital-associated infections because several of the cases in this outbreak occurred in outpatients who were receiving care with the same product as hospitalized patients. This finding underscores the need to investigate all clusters of bloodstream infections regardless of patient location.

Timely communication with other pediatric institutions and close collaboration with public health colleagues were critical to the success of this investigation. A national infection prevention listserv was key to uncovering the epidemiological link between cases and to revealing a multistate outbreak. Close collaboration with public health colleagues afforded rapid identification of a matching organism strain, aided dialogue regarding potential hypotheses, and facilitated communication with other state and national authorities.

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Although we were unable to culture *S. marcescens* from any products, based on the strength of the epidemiological data and molecular results, we concluded that the outbreak of *S. marcescens* bacteremia was most likely associated with contaminated prefilled heparin flushes. Prefilled heparin syringes were a common product shared by all cases at our institution, and this was also the only product shared by other institutions. Additionally, none of the cases were in the neonates or adult patient populations, which have limited use of prefilled heparin flushes at the concentrations used in pediatric patients. Although *S. marcescens* was not found in any cultures from any prefilled heparin flushes, *Bacillus* spp were identified from several different lots, suggesting a problem with sterility during manufacturing.[2,8]

In conclusion, our experience highlights key features of a successful epidemiologic outbreak investigation including rapid identification and reporting to public health of a suspected outbreak, investigation of all inpatient and outpatient clusters of bacteremia by infection preventionists, the essential role of molecular typing, and timely communication via a pediatric national network listserv. Furthermore, this investigation underscores the importance of pursuing product-associated outbreaks supported by strong epidemiologic data despite the lack of culture-proven product contamination.

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A phylogenetic study of *Elizabethkingia anophelis* bloodstream isolates obtained from inpatients at a single medical center

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To the Editor—Elizabethkingia anophelis is a rapidly emerging nosocomial pathogen reported to cause bacteremia in immune-compromised elderly people and neonates.[1,2] The unknown pathogenesis and unclear resistance mechanism of *E. anophelis* and their phenotypic similarity to *E. meningoseptica* mislead and complicate the infection management of this pathogen, resulting in treatment failure. Inherent resistance to multiple classes of drugs and absence of an antibiotic sensitivity profile standard for this bacterium makes empirical treatment nearly impossible. *Elizabethkingia anophelis* bacteremia has recently been considered clinically significant, leading to high morbidity and mortality that has been mistakenly attributed to *E. meningoseptica* because of their phenotypic similarity.[2] Molecular epidemiological analyses of recent *Elizabethkingia* bacteremia infections and outbreaks have been conducted in United States, Singapore, China, and Korea. These outbreaks were predominated by *E. anopheles*.[3–6] This finding warrants the implementation of molecular typing for an accurate diagnosis to guide appropriate antibiotic regimen instead of relying solely on conventional phenotypic identification with a compact automated VITEK-2 system, which uses a factory default database and lacks timely amendments.[3,5]

In the first report of an outbreak in a tertiary healthcare center of Eastern India, the clinical and molecular epidemiology of 9 bacteremia episodes during 2 months of surveillance from August to September 2017 were identified as *E. meningoseptica* by the VITEK-2 system. These findings were genetically validated by species-specific markers, such as lipid-A disaccharide synthase

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