Open Forum Infectious Diseases

NOVEL ID CASES

Successful Treatment of Recurrent Extensively Drug-Resistant *Elizabethkingia anophelis* Bacteremia Secondary to Ventricular Assist Device–Associated Infection

Madeleine B. Vessely,[1,a] Marrium Siddiqui,[1,a] Kendall Kling,[1,2] Alexis Guenette,[1] and Kelly E. R. Bachta[1]

[1]Division of Infectious Diseases, Department of Medicine, Northwestern University, Chicago, Illinois, USA, and [2]Department of Pathology, Northwestern University Feinberg School of Medicine, Chicago, Illinois, USA

Elizabethkingia anophelis is an emerging pathogen increasingly implicated in health care–associated infections. Here, we report a case of recurrent ventricular assist device–associated infection caused by multidrug-resistant *Elizabethkingia anophelis* and describe the clinical course, treatment challenges, and ultimate case resolution. Our results demonstrate that standard clinical methodologies for determining trimethoprim-sulfamethoxazole minimum inhibitory concentration, including VITEK2 and gradient diffusion tests, may be unsuitable for *Elizabethkingia anophelis* as they result in false-negative susceptibility results. The discrepancy between antimicrobial susceptibility testing reported here highlights the importance of investigating and validating the applicability of standard clinical antimicrobial susceptibility testing and interpretation when treating emerging pathogens such as *Elizabethkingia anophelis*.

Keywords. antimicrobial resistance; bacteremia; *Elizabethkingia anophelis*; left ventricular assist device; trimethoprim-sulfamethoxazole.

The gram-negative bacterium *Elizabethkingia anophelis* is widely distributed in natural environments. *Elizabethkingia* spp. were originally considered part of the genus *Chryseobacterium* until 2005 when 16S rRNA sequencing identified them as part of a new genus [1]. This genus was initially thought to contain only 2 species, *E miricola* and *E meningoseptica*; however, *E anophelis* was identified as a separate species in 2011 after its isolation from the midgut of a mosquito [2]. All members of the *Elizabethkingia* genus besides *E ursingii* have been reported to cause infections in humans [3, 4], though species-level identification is problematic due to a high degree of sequence similarity, lack of species-distinguishing biochemical tests, and poor genomic annotations in commercial databases [5–7]. Of all members of the *Elizabethkingia* genus, *E anophelis* is the most prevalent nosocomial pathogen and an important emerging cause of health care–associated outbreaks [4, 6, 8–12]. While *Elizabethkingia* spp. rarely cause disease in healthy individuals, they have been shown to cause infections in neonates, the elderly, and in immunocompromised hosts, often manifesting as meningitis or bloodstream infection [13]. Though rare, invasive *E anophelis* infections have high mortality rates ranging from 20% to 45% [11, 12, 14, 15]. Treatment of *E anophelis* infections is challenging as isolates exhibit intrinsic multidrug resistance to several common antibiotic classes including aminoglycosides, third-generation cephalosporins, carbapenems, and polymyxins [9, 14, 16, 17]; however, rates of resistance to fluroquinolones and piperacillin-tazobactam are more variable [4, 9, 11, 14]. Though prior studies have reported that minocycline is the most effective antimicrobial for treating *E anophelis* [4, 9, 18, 19], doxycycline, rifampin, and trimethoprim (TMP)-sulfamethoxazole (SMX) are other effective treatment options [4, 9, 14, 18].

Patients with end-stage heart failure who are poorly responsive to medical management are offered mechanical circulatory support in the form of ventricular assist devices (VADs) as either a bridge to transplant or long-term destination treatment [20]. While VAD placement can be life-prolonging, successful long-term outcomes are limited largely by infectious complications. Within 3 months of placement, up to 25% of all VAD patients experience a major infectious episode [21]. Additionally, bloodstream infections are the most common VAD-associated infection, and VAD-related sepsis is the second most common cause of death in the early postimplantation period [22]. Unsurprisingly, the most prevalent bacterial species reported in VAD-related infections are gram-positive (typically *Staphyloccocus aureus* and coagulase-negative staphylococci); however, gram-negative bacteria are implicated in 15% of all infections. *Pseudomonas* species are the most common, followed closely by *Klebsiella* and *Enterobacter* [22]. Though extremely rare, catheter-associated and cardiac device–associated infections secondary to *Elizabethkingia* species have been reported [11, 23]. Here, we report a case of recurrent multidrug-resistant *E anophelis* bacteremia associated with a left ventricular assist

Received 07 August 2024; editorial decision 30 September 2024; accepted 09 October 2024; published online 11 October 2024

[a]Equal contribution

Correspondence: Kelly E. R. Bachta, MD, PhD, Division of Infectious Diseases, Department of Medicine, Northwestern University, 645 N. Michigan Avenue, Suite 900, Chicago, IL 60611 (kelly.bachta@northwestern.edu).

Open Forum Infectious Diseases®

https://doi.org/10.1093/ofid/ofae611

device (LVAD) and describe the clinical course, treatment challenges, and ultimate case resolution.

CASE PRESENTATION

A 56-year-old male initially presented to the hospital in shock with acute altered mental status, hypoglycemia, and diarrhea. His medical history was notable for a transcatheter aortic valve replacement, ischemic cardiomyopathy requiring an LVAD implantation, recurrent complicated chronic driveline infections with *Pseudomonas aeruginosa* and *Providencia stuartii*, and recent severe *Clostridiodes difficile* infection for which he was on oral vancomycin therapy. On admission, his temperature was 36.4°C (97.5°F), blood pressure was 71/66 mmHg, heart rate was 104 beats per minute (bpm), and respiratory rate was 23 with an oxygen saturation of 92% on room air. Physical exam was notable for mild encephalopathy. His driveline site was clean, dry, and intact, and he had no abdominal pain. A transthoracic echocardiogram (TTE) revealed a left ventricular ejection fraction of 17%, a well-seated aortic valve replacement, and no evidence of vegetations. Laboratory investigations were notable for a white blood cell (WBC) count of 25.3×10^3 cells/μL (reference range, $3.5–10.5 \times 10^3$ cells/μL), aspartate aminotransferase (AST) of 66 units/L (reference range, 0–39 units/L), alanine aminotransferase (ALT) of 62 units/L (reference range, 0–39 units/L), and creatinine of 1.95 mg/dL (reference range, 0.6–1.3 mg/dL). He was admitted, given intravenous (IV) fluid resuscitation, and started on empiric IV vancomycin and cefepime. His altered mental status rapidly improved with resolution of his hypoglycemia and the administration of intravenous fluids and antibiotics. He was briefly started on vasopressors, which were quickly weaned off. Repeat *C difficile* polymerase chain reaction and toxin testing were again positive, but his blood and urine cultures were negative. His IV antibiotics were discontinued when blood cultures were negative for 48 hours, and the patient was restarted on oral vancomycin with plans for a prolonged taper. It was felt that his initial presentation of sepsis was secondary to dehydration in the setting of *C difficile*–associated colitis and diarrhea. The patient remained admitted on the advanced heart failure service as it was challenging to titrate his cardiovascular medications to optimize both his blood pressure and volume status.

On hospital day 18 (HD 18), the patient developed tachycardia with a heart rate of 125 bpm and a new fever to 38.3°C (100.9°F). At that time, his WBC count was normal (9.8×10^3 cells/μL), and his creatinine had returned to his baseline of 0.8 mg/dL. Repeat peripheral blood cultures were obtained, and 1 of 2 bottles was positive for gram-negative bacilli that produced large, creamy white colonies on a 5% sheep blood agar plate (Figure 1). The patient was initially restarted on IV cefepime. Shortly thereafter, the organism was identified as *E anophelis* using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS; VITEK MS, bioMérieux, Marcy-l'Étoile, France). Additional workup included a TTE, which was negative, a chest x-ray, which showed pulmonary congestion, urinalysis, which was negative, and a computer assisted tomography (CT) scan of the abdomen and pelvis, which was unremarkable. In the absence of a clear focus of infection, his LVAD was presumed to be the source. Given that *E anophelis* is very rarely a part of the human microbiome and that the patient developed infection 18 days into his admission, his bacteremia was deemed hospital-associated. His *E anophelis* isolate (isolate 1) underwent susceptibility testing on the VITEK2 (bioMérieux, Marcy-l'Étoile, France) platform, which revealed that it was only susceptible to minocycline and trimethoprim-sulfamethoxazole (SXT). On HD 21, cefepime

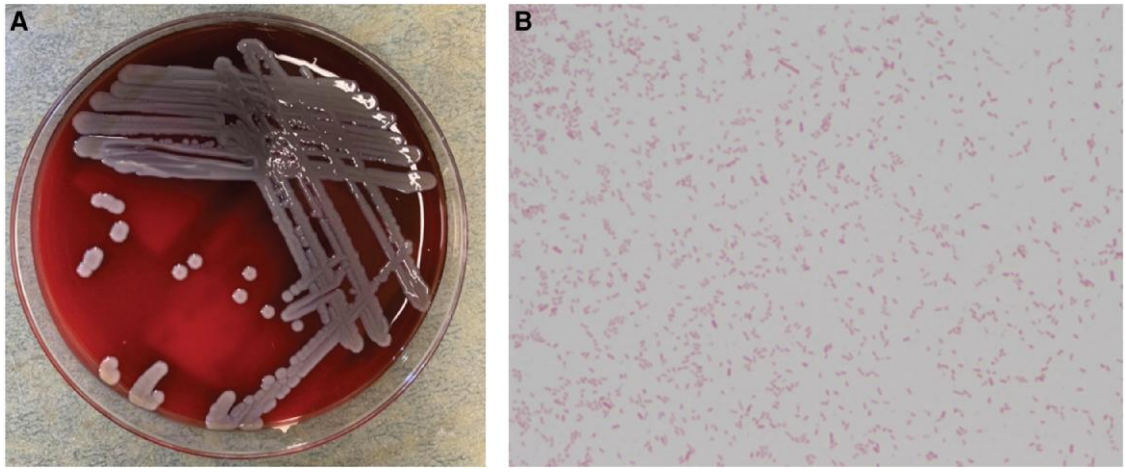

Figure 1. Colony morphology (*A*) and Gram stain (*B*) of the patient's first *Elizabethkingia anophelis* bloodstream isolate.

was discontinued, and trimethoprim-sulfamethoxazole (dosed at 6 mg/kg of the TMP component due to the patient's impaired renal function) was started. Given the fact that his repeat blood cultures cleared and he improved rapidly, the patient was discharged with 21 days of trimethoprim-sulfamethoxazole therapy.

One day after completing his course of trimethoprim-sulfamethoxazole, the patient returned to the hospital with hypotension. Upon admission, his vital signs were notable for a temperature of 98.7°F, mean arterial pressure of 52 mmHg, heart rate of 83 bpm, respiratory rate of 16, and an oxygen saturation of 97% on room air. Laboratory investigations were notable for a WBC count of 7.7×10^3 cells/μL and an elevated creatinine of 1.49 mg/dL. A repeat CT of the abdomen and pelvis was again unremarkable. On HD 1, his blood cultures were again positive for a gram-negative bacillus identified by VITEK MS as recurrent *E anophelis* (isolate 2). He was restarted on oral trimethoprim-sulfamethoxazole, and twice-daily minocycline (100 mg) was added. VITEK2 antimicrobial susceptibility testing (AST) identified this second *E anophelis* isolate as newly resistant to trimethoprim-sulfamethoxazole. Trimethoprim-sulfamethoxazole was discontinued, and the dose of oral minocycline was increased to 200 mg twice daily. Given the recurrence of his bacteremia, he underwent a transesophageal echocardiogram (TEE), which demonstrated a 0.3 × 0.3-cm mobile echodensity in the aorta at the level of the sinotubular junction. This echodensity was hypothesized to represent either a mobile atheroma or vegetation. The Infectious Disease consulting team recommended that the patient be evaluated for an LVAD explant; however, he was not a favorable surgical candidate. Five days into his second hospitalization, his blood cultures cleared. Based on synergistic activity of minocycline and rifampin and reported in vitro efficacy against *Elizabethkingia* biofilms, the patient was discharged on high-dose minocycline and oral rifabutin given retention of his original LVAD device [24]. He completed 6 weeks of dual therapy without recurrence of his bacteremia and remains on chronic antibiotic suppressive therapy with both agents.

Given the rapid recurrence of the patient's bacteremia despite initial therapy with trimethoprim-sulfamethoxazole, we sought a more extensive evaluation of the antimicrobial susceptibility profile of both *E anophelis* isolates. Expanded antimicrobial susceptibility testing was undertaken using the standard broth microdilution (BMD) method. The minimal inhibitory concentrations (MICs) of 8 antibiotics were determined for isolates 1 and 2 in triplicate (Table 1). Isolate 1 was susceptible to doxycycline, minocycline, and rifampicin and resistant to aztreonam, aztreonam-avibactam, trimethoprim-sulfamethoxazole, and vancomycin. Isolate 2 was only susceptible to minocycline and rifampin. Omadacycline BMD revealed MICs of 4 and 8 μg/mL for isolates 1 and 2, respectively; however, no guidelines exist to interpret these results. To our surprise and contrary to the initial VITEK2 results, isolate 1 was resistant to trimethoprim-sulfamethoxazole by BMD (MIC of 320/16 μg/mL) (Table 2). Given this discordance, VITEK2 analysis was repeated for isolate 1 and again resulted in a susceptible result (MIC of <20 μg/mL). The VITEK2 and BMD methods were concordant for isolate 2, which was resistant to trimethoprim-sulfamethoxazole by both methods. We also conducted trimethoprim-sulfamethoxazole gradient diffusion tests (E-test) on both isolates. Intriguingly, both were susceptible to trimethoprim-sulfamethoxazole by gradient diffusion testing with MICs of 15 and 30 μg/mL, respectively (Table 2). *Escherichia coli* ATCC 25922 was used as a control strain to validate trimethoprim-sulfamethoxazole testing and resulted in MIC values that agreed with published standards (Table 2) [25, 26]. We also obtained an additional *E anophelis* isolate, OC5467, that had previously been identified by VITEK2 as resistant to trimethoprim-sulfamethoxazole (MIC of 160 μg/mL). *E anophelis* OC5467 was resistant to trimethoprim-sulfamethoxazole by BMD with an MIC of 640 μg/mL; however, gradient diffusion testing resulted in a susceptible MIC of 20 μg/mL.

Table 1. Broth Microdilution Minimal Inhibitory Concentrations for Select Antimicrobial Agents for Isolates of *Elizabethkingia anophelis*

Antibiotic	Isolate 1 MIC, μg/mL	Isolate 2 MIC, μg/mL
Aztreonam (ATM)	>128 (ns)	>128 (ns)
Aztreonam + avibactam (ATM + AVI)	>128/4 (ns)	>128/4 (ns)
Doxycycline (DOX)	4	8 (ns)
Minocycline (MNO)	0.25	1
Omadacycline (OMC)[a]	4	8
Rifampin (RIF)	0.25	0.5
Trimethoprim/sulfamethoxazole, 1:19 (SXT)	320 (ns)	1280 (ns)
Vancomycin (VAN)	64 (ns)	64 (ns)

Each reported MIC is the result of 3 independent replicates.

Abbreviations: CLSI, Clinical and Laboratory Standards Institute; MIC, minimal inhibitory concentration; ns, nonsusceptible according to CLSI guidelines for other gram-negative, non-Enterobacterales.

[a]No susceptibility guidelines exist for this antibiotic.

Table 2. Trimethoprim/Sulfamethoxazole Minimal Inhibitory Concentrations as Determined by Indicated Methods

	Trimethoprim/Sulfamethoxazole MIC, μg/mL		
Strain	BMD	VITEK2	E-test
E coli ATCC 25922	≤10	n.d.	2
E anophelis OC 5467	640 (ns)	160 (ns)	20
E anophelis isolate 1	320 (ns)	≤20	15
E anophelis isolate 2	1280 (ns)	≥320 (ns)	30

Abbreviations: BMD, broth microdilution; CLSI, Clinical and Laboratory Standards Institute; MIC, minimal inhibitory concentration; n.d., no data obtained; ns, nonsusceptible according to CLSI guidelines for other gram-negative, non-Enterobacterales.

DISCUSSION

Here we present an unusual case of recurrent multidrug-resistant *E anophelis* bacteremia and presumed endocarditis in a patient with an LVAD. This case presented several management and treatment challenges. Diagnosing *E anophelis* infections is problematic given its relatively recent designation as a new species and rarity as a cause of infections in immunocompetent hosts [13]. Additionally, there is extremely limited information on *E anophelis* cardiac device–associated infections and routes of transmission [17, 23, 27]. Given that positive blood cultures were not documented until 18 days into his hospital stay, we believe that our patient suffered from a health care–associated bloodstream infection, whereby *E anophelis* was acquired from the health care environment. Despite its clinical rarity, *E anophelis* is now recognized as an emerging nosocomial pathogen [10, 12–14]. There are 2 major, well-described outbreaks of *E anophelis*–associated infections. The first was reported in Singapore in 2012 involving 5 medically complex patients in an intensive care unit. All were ventilated, most received multiple antecedent courses of broad-spectrum antibiotics, and 2 ultimately died due to *E anophelis* sepsis. A post hoc investigation isolated *E anophelis* from the intensive care unit rooms in which the patients resided, suggesting that the origin of the outbreak was the health care environment. Interestingly, these infections were originally designated as *E meningoseptica* and were only identified as *E anophelis* after additional sequencing [28]. The second well-documented outbreak occurred in late 2015 in the United States. Sixty-five cases were identified across the Midwest in Wisconsin, Illinois, and Michigan. The majority of cases in this outbreak presented as bloodstream infections in persons with significant comorbidities, resulting in a case fatality rate of 30% [12, 29]. Given the challenges in identifying *E anophelis*, it is likely that additional outbreaks have been either misidentified or underreported. The deployment of MALDI-TOF MS and improved reference standards allowed for rapid identification of *E anophelis* in our patient. No additional cases of *E anophelis* infection were identified; thus we suspect that this was an isolated incident. Though *E anophelis* bloodstream infections are well documented, we were able to identify only 1 prior case of *E anophelis* bacteremia attributed to an implanted cardiac device, a dual-chamber cardiac pacemaker [23], highlighting the uniqueness of this case.

Despite adequate antimicrobial therapy with trimethoprim-sulfamethoxazole, our patient rapidly relapsed with bacteremia following antibiotic discontinuation. We hypothesized that relapse could be attributed to (1) the relatively short duration of initial antimicrobial therapy, (2) the retention of the implanted cardiac device, or (3) a small, undetected subpopulation of trimethoprim-sulfamethoxazole-resistant *E anophelis* present at the time of the initial infection. To address the third possibility, we revisited susceptibility testing using BMD as a gold standard. Much to our surprise, isolate 1 was resistant to trimethoprim-sulfamethoxazole by BMD despite repeatedly testing susceptible by VITEK2. The discordance between trimethoprim-sulfamethoxazole MICs across 3 testing methods, in conjunction with the rapid clinical failure of trimethoprim-sulfamethoxazole, suggests that his initial therapy may have been inadequate and that reliance on VITEK2 AST testing in this case was problematic. Prior groups have reported discordance between various methods of AST for *E anophelis* [30, 31]. In contrast to our findings, Chiu et al. found that, in 84 *E anophelis* isolates, the gradient diffusion method (E-test) tended to overestimate the trimethoprim-sulfamethoxazole MIC compared with gold standard agar dilution, resulting in a false-positive major error (ME) [30]. Kuo et al. reported that the VITEK2 similarly overestimated the trimethoprim-sulfamethoxazole MIC compared with BMD methods, also resulting in ME [31]. While these studies observed false-positive results by 2 methods compared with a gold standard, our case demonstrates that a more concerning issue may be false-negative susceptibility (also known as very major error [VME]). Using BMD, we demonstrated VME between gradient diffusion testing and BMD for isolates 1 and 2 and VME between VITEK2 and BMD for isolate 1. Our results call into question the reliability of AST methodologies for *E anophelis*. Given our discordant MIC results and multiple reports in the literature of *E anophelis* trimethoprim-sulfamethoxazole MICs varying greatly between methodologies, we encourage caution when utilizing trimethoprim-sulfamethoxazole as a backbone for the treatment of invasive *E anophelis* infections.

This case highlights the need for continued development and deployment of diagnostics to rapidly identify emerging pathogens such as *E anophelis*. Additionally, it raises concerns about relying on trimethoprim-sulfamethoxazole MICs to guide treatment of *E anophelis*. Despite numerous studies investigating susceptibilities of *E anophelis*, the lack of interpretive criteria unique to *Elizabethkingia* from the Clinical and Laboratory Standards Institute (CLSI) and the European Committee for Antimicrobial Susceptibility Testing (EUCAST) makes interpretation of susceptibility results challenging. The relative paucity of studies comparing methodologies for AST in emerging pathogens contributes to difficulties in deciding upon appropriate clinical therapeutic regimens. To make accurate clinical decisions, it is critical that we validate gold standard AST methods and develop a deeper appreciation for the limitations of AST testing and interpretation for emerging pathogens such as *E anophelis*.

METHODS

Determination of Clinical Minimal Inhibitory Concentrations

Blood cultures were collected and incubated with the BacT/ALERT system (bioMérieux, Marcy-l'Étoile, France). At 24 hours, the aerobic bottle flagged positive and Gram stain showed gram-negative bacilli. A Rapid BioFire Blood Culture Identification Panel 2 (BCID2, bioMérieux, Marcy-l'Étoile, France) was negative for all pathogens. The blood culture was plated, and growth was observed at 24 hours on blood and chocolate, but not MacConkey agar (Figure 1A). Colonies were large, white, and nonhemolytic, and biochemical testing revealed that the colonies produced oxidase and catalase. Gram stain showed gram-negative coccobacilli (Figure 1B). MALDI-TOF MS from the VITEK MS platform utilizing library Knowledge Base 3.2, version 3.0, with Myla, version 4.7.1 (bioMérieux, Marcy-l'Étoile, France), revealed a 99.9% match to *Elizabethkingia anophelis*. Susceptibility testing was performed via the VITEK2 using the gram-negative susceptibilities card AST-GN95 and extension card XN09 (bioMérieux, Marcy-l'Étoile, France).

Laboratory Broth Microdilution and Gradient Diffusion (E-test) Determination of MICs

The following antibiotics were prepared from commercially available sources and were used to assess MICs by BMD: avibactam (AVI), aztreonam (ATM), doxycycline (DOX), minocycline (MNO), omadacycline (OMC), rifampin (RIF), trimethoprim-sulfamethoxazole (SXT 1:19), and vancomycin (VAN). MNO, OMC, and AVI were obtained from MedChemExpress (Monmouth Junction, NJ, USA). DOX, RIF, TMP, and VAN were obtained from Thermo Fisher (Waltham, MA, USA), ATM was obtained from Sigma-Aldrich (St. Louis, MO, USA), and SMX was obtained from Research Products International (Mt. Prospect, IL, USA). All BMD MICs were conducted in cation-adjusted Mueller Hinton Broth as outlined by the Clinical and Laboratory Standards Institute (M100-Ed33). *E coli* ATCC 25922 was used as the quality control strain for DOX, MNO, OMC, RIF, and SXT. *S aureus* ATCC 29213 was used as the quality control strain for VAN, and *K pneumoniae* strain ATCC 700603 was used as the quality control strain for ATM and ATM/AVI. For SXT, the MIC was recorded as the lowest concentration of antibiotic that reduced the growth by ≥80% compared with the growth control, and all MICs were determined in triplicate in compliance with the CLSI BMD protocol (M07-Ed12). The MICs for ATM, ATM/AVI, DOX, MNO, RIF, and SXT were interpreted based on the CLSI criteria for other non-Enterobacterales. The MICs for RIF and VAN were interpreted according to the CLSI criteria for *Enterococcus* species because the CLSI does not provide breakpoints for non-Enterobacterales. The MICs for OMC were not interpreted due to a lack of standardized interpretation criteria from the CLSI. Gradient diffusion MIC test strips for SXT (1:19) were purchased from Liofilchem (Roseto degli Abruzzi, Italy) and utilized according to the manufacturer's instructions. Gradient diffusion testing was carried out on cation-adjusted Mueller Hinton agar, and *E coli* ATCC 25922 was used as the quality control strain.

Acknowledgments

Author contributions. The authors confirm contributions to the paper as follows: clinical case identification and treatment M.S., K.K., and A.G., data collection M.V. and K.K., analysis and interpretation of results M.V. and K.B., draft manuscript preparation M.V., M.S., K.K., A.G., and K.B., and manuscript editing M.V., M.S., K.K., A.G., and K.B. All authors reviewed the results and approved the final version of the manuscript.

Patient consent. Patient consent was not required due to anonymization of the case.

Financial support. This study was funded in part by the National Institute of Allergy and Infectious Disease (NIAID) through a training grant (grant number T32 AI007476, awarded to M.B.V.) and by the American Cancer Society (ACS) through a Clinician Scientist Development Grant (grant number 134251-CSDG-20-053-01-MPC, awarded to K.E.R.B.).

Potential conflicts of interest. All authors: no reported conflicts.

References

1. Kim KK, Kim MK, Lim JH, Park HY, Lee ST. Transfer of *Chryseobacterium meningosepticum* and *Chryseobacterium miricola* to *Elizabethkingia* gen. nov. as *Elizabethkingia meningoseptica* comb. nov. and *Elizabethkingia miricola* comb. nov. Int J Syst Evol Microbiol **2005;** 55(Pt 3):1287–93.
2. Kampfer P, Matthews H, Glaeser SP, Martin K, Lodders N, Faye I. *Elizabethkingia anophelis* sp. nov., isolated from the midgut of the mosquito *Anopheles gambiae*. Int J Syst Evol Microbiol **2011;** 61(Pt 11):2670–5.
3. Lin JN, Lai CH, Yang CH, Huang YH, Lin HH. *Elizabethkingia bruuniana* infections in humans, Taiwan, 2005-2017. Emerg Infect Dis **2019;** 25:1412–4.
4. Cheng YH, Perng CL, Jian MJ, et al. Multicentre study evaluating matrix-assisted laser desorption ionization-time of flight mass spectrometry for identification of clinically isolated *Elizabethkingia* species and analysis of antimicrobial susceptibility. Clin Microbiol Infect **2019;** 25:340–5.
5. Bai F, Liu J. A complication of lower respiratory tract infection caused by *Elizabethkingia anophelis* of patient with severe craniocerebral injury. Int J Infect Dis **2020;** 101:174.
6. Han MS, Kim H, Lee Y, et al. Relative prevalence and antimicrobial susceptibility of clinical isolates of *Elizabethkingia* species based on 16S rRNA gene sequencing. J Clin Microbiol **2017;** 55:274–80.
7. Frank T, Gody JC, Nguyen LB, et al. First case of *Elizabethkingia anophelis* meningitis in the Central African Republic. Lancet **2013;** 381:1876.
8. Yang C, Liu Z, Yu S, Ye K, Li X, Shen D. Comparison of three species of *Elizabethkingia* genus by whole-genome sequence analysis. FEMS Microbiol Lett **2021;** 368:fnab018.
9. Chew KL, Cheng B, Lin RTP, Teo JWP. *Elizabethkingia anophelis* is the dominant *Elizabethkingia* species found in blood cultures in Singapore. J Clin Microbiol **2018;** 56:e01445-17.
10. Choi MH, Kim M, Jeong SJ, et al. Risk factors for *Elizabethkingia* acquisition and clinical characteristics of patients, South Korea. Emerg Infect Dis **2019;** 25:42–51.
11. Lau SK, Chow WN, Foo CH, et al. *Elizabethkingia anophelis* bacteremia is associated with clinically significant infections and high mortality. Sci Rep **2016;** 6:26045.
12. Perrin A, Larsonneur E, Nicholson AC, et al. Evolutionary dynamics and genomic features of the *Elizabethkingia anophelis* 2015 to 2016 Wisconsin outbreak strain. Nat Commun **2017;** 8:15483.
13. Janda JM, Lopez DL. Mini review: new pathogen profiles: *Elizabethkingia anophelis*. Diagn Microbiol Infect Dis **2017;** 88:201–5.
14. Guerpillon B, Fangous MS, Le Breton E, et al. *Elizabethkingia anophelis* outbreak in France. Infect Dis Now **2022;** 52:299–303.
15. Nielsen HL, Tarpgaard IH, Fuglsang-Damgaard D, Thomsen PK, Brisse S, Dalager-Pedersen M. Rare *Elizabethkingia anophelis* meningitis case in a Danish male. JMM Case Rep **2018;** 5:e005163.
16. Comba IY, Schuetz AN, Misra A, et al. Antimicrobial susceptibility of *Elizabethkingia* species: report from a reference laboratory. J Clin Microbiol **2022;** 60:e0254121.
17. Burnard D, Gore L, Henderson A, et al. Comparative genomics and antimicrobial resistance profiling of *Elizabethkingia* isolates reveal nosocomial transmission and

in vitro susceptibility to fluoroquinolones, tetracyclines, and trimethoprim-sulfamethoxazole. J Clin Microbiol **2020;** 58:e00730-20.
18. Yasmin M, Rojas LJ, Marshall SH, et al. Characterization of a novel pathogen in immunocompromised patients: *Elizabethkingia anophelis*—exploring the scope of resistance to contemporary antimicrobial agents and beta-lactamase inhibitors. Open Forum Infect Dis **2023;** 10:XXX–XX.
19. Lin JN, Lai CH, Yang CH, Huang YH, Lin HH. Clinical manifestations, molecular characteristics, antimicrobial susceptibility patterns and contributions of target gene mutation to fluoroquinolone resistance in *Elizabethkingia anophelis*. J Antimicrob Chemother **2018;** 73:2497–502.
20. Rose EA, Gelijns AC, Moskowitz AJ, et al. Long-term use of a left ventricular assist device for end-stage heart failure. N Engl J Med **2001;** 345:1435–43.
21. Molina EJ, Shah P, Kiernan MS, et al. The Society of Thoracic Surgeons Intermacs 2020 annual report. Ann Thorac Surg **2021;** 111:778–92.
22. Blanco-Guzman MO, Wang X, Vader JM, Olsen MA, Dubberke ER. Epidemiology of left ventricular assist device infections: findings from a large nonregistry cohort. Clin Infect Dis **2021;** 72:190–7.
23. Arora Y, D'Angelo-Piaggio L, Llaneras N, Carrillo R. A unique case of *Elizabethkingia* associated cardiac device infection. Cureus **2021;** 13:e20028.
24. Tang HJ, Lin YT, Chen CC, et al. Molecular characteristics and in vitro effects of antimicrobial combinations on planktonic and biofilm forms of *Elizabethkingia anophelis*. J Antimicrob Chemother **2021;** 76:1205–14.
25. Humphries RM, Ambler J, Mitchell SL, et al. CLSI methods development and standardization working group best practices for evaluation of antimicrobial susceptibility tests. J Clin Microbiol **2018;** 56:e01934-17.
26. Humphries RM, Ambler J, Mitchell SL, et al. Erratum for Humphries et al., "CLSI methods development and standardization working group best practices for evaluation of antimicrobial susceptibility tests". J Clin Microbiol **2023**; 61:e0073923.
27. Lau SK, Wu AK, Teng JL, et al. Evidence for *Elizabethkingia anophelis* transmission from mother to infant, Hong Kong. Emerg Infect Dis **2015;** 21:232–41.
28. Teo J, Tan SY, Tay M, et al. First case of *E anophelis* outbreak in an intensive-care unit. Lancet **2013;** 382:855–6.
29. Navon L, Clegg WJ, Morgan J, et al. Notes from the field: investigation of *Elizabethkingia anophelis* cluster—Illinois, 2014-2016. MMWR Morb Mortal Wkly Rep **2016;** 65:1380–1.
30. Chiu CT, Lai CH, Huang YH, Yang CH, Lin JN. Comparative analysis of gradient diffusion and disk diffusion with agar dilution for susceptibility testing of *Elizabethkingia anophelis*. Antibiotics (Basel) **2021;** 10:450.
31. Kuo SC, Tan MC, Huang WC, et al. Susceptibility of *Elizabethkingia* spp. to commonly tested and novel antibiotics and concordance between broth microdilution and automated testing methods. J Antimicrob Chemother **2021;** 76:653–8.