Epidemiology of *Elizabethkingia* spp. Infections in Southeast Asia

Subjects: Infectious Diseases | Microbiology

Contributor: Asdren Zajmi, Jeanette Teo, Chew Chieng Yeo

Elizabethkingia spp. is a ubiquitous pathogenic bacterium that has been identified as the causal agent for a variety of conditions such as meningitis, pneumonia, necrotizing fasciitis, endophthalmitis, and sepsis and is emerging as a global threat including in Southeast Asia. *Elizabethkingia* infections tend to be associated with high mortality rates (18.2–41%) and are mostly observed in neonates and immunocompromised patients. Difficulties in precisely identifying *Elizabethkingia* at the species level by traditional methods have hampered the understanding of this genus in human infections. In Southeast Asian countries, hospital outbreaks have usually been ascribed to *E. meningoseptica*, whereas in Singapore, *E. anophelis* was reported as the main *Elizabethkingia* spp. associated with hospital settings. Misidentification of *Elizabethkingia* spp. could, however, underestimate the number of cases attributed to the bacterium, as precise identification requires tools such as MALDI-TOF MS, and particularly whole-genome sequencing, which are not available in most hospital laboratories. *Elizabethkingia* spp. has an unusual antibiotic resistance pattern for a Gram-negative bacterium with a limited number of horizontal gene transfers, which suggests an intrinsic origin for its multidrug resistance.

Keywords: Elizabethkingia spp. ; antibiotic resistance ; multidrug resistance ; meningitis ; bacteremia ; outbreak ; Southeast Asia

1. Introduction

The Gram-negative bacteria of the genus *Elizabethkingia* have recently emerged as an important pathogen in hospital-acquired infections and are generally associated with high mortality [1]. Recent literature has reported several cases of severe infection in humans owing to this organism, with neonatal meningitis most commonly presented in children [2], accompanied by a range of other clinical manifestations such as septicemia and bacteremia [3][4], osteomyelitis [5], urinary tract infections [6][7], endogenous endophthalmitis [8], endocarditis [9], epididymo-orchitis [10], pulmonary abscess [11], necrotizing fasciitis [12][13], cystic fibrosis [14], hydrocephalus [15], and secondary infections with a high mortality rate, particularly in immunocompromised patients [16]. *Elizabethkingia meningoseptica* infections have also been associated with COVID-19 patients [17]. *Elizabethkingia* spp. infects not only immunocompromised patients but also immunocompetent ones [18][19][20].

Historically, the first report of human infection due to *Elizabethkingia* was that of 19 cases of meningitis in infants in the United States of America [21]. Even in its earliest description, the isolates were demonstrated to be multidrug-resistant. Not long after King's (1959) report, an outbreak of meningitis infection with *E. meningoseptica* was reported among neonates in the Congo [22] with varying sensitivities to chloramphenicol, carbomycin, magnamycin, and erythromycin.

Worldwide infections caused by *E. meningoseptica* were reportedly high amongst immunocompetent neonates as well as hospitalized patients with existing underlying infections, and in a comprehensive review, Dzuiban et al. [2] showed that from 283 cases reported from 28 countries from 1944 to 2017, 76% of them were neonates aged 0–1 month. From the 283 cases that were reviewed, 209 of the patients were diagnosed with meningitis [2]. Infections by this pathogen have been reported in many parts of the world, including in Southeast Asian countries such as Malaysia [2], Singapore [23], Thailand [24], Indonesia [25], and Cambodia [26]. However, until now, there have been no published reports from other Southeast Asian countries such as the Philippines, Brunei, Myanmar, Laos, and Timor-Leste.

2. Identification

When first discovered in 1959, the suggested name for the bacterium was *Flavobacterium meningosepticum*, which was later recommended to be changed to *Chryseobacterium meningosepticum* (in 1994) [27]. In 2005, it was assigned to the genus *Elizabethkingia* (named after the first scientist to report its' discovery, Elizabeth King) under the Flavobacteriaceae family based on 16S rRNA phylogenetic studies [28]. Recently, whole-genome sequence analysis along with optical

mapping and MALDI-TOF mass spectrometry led to the revision of the genus *Elizabethkingia* into eight species, namely *E. meningoseptica*, *E. miricola*, *E. anophelis*, *E. bruuniana*, *E. ursingii*, *E. occulta* [29], *E. argenteiflava* sp. nov. [30], and the latest *E. umeracha* [31].

Since correct identification of *Elizabethkingia* is difficult using traditional microbiological methods and misidentification of *E. anophelis* with *E. meningoseptica* has been found to be common (Lau et al., 2016), it is therefore highly likely for this pathogen to be underreported. Correct identification of the organism is crucial for the diagnosis and management strategies, as *E. anophelis* is a nososcomial pathogen [32]. Hence, differentiation between *E. anophelis* and *E. meningoseptica* requires accurate microbial identification, but the phenotypic similarities between *E. anophelis* and *E. meningoseptica* present a challenge to accurate identification, particularly for clinically derived isolates; 16S rRNA gene analysis had identified a 98.6% similarity between *E. meningoseptica* and *E. anophelis*, which has often led to the misidentification of these bacteria [32].

The four automated bacterial identification systems that are commonly used in diagnostic laboratories are: (1) API/ID32 Phenotyping Kits (bioMérieux, Marcy l'Etoile, France); (2) Phoenix 100 ID/AST Automated Microbiology System (Becton Dickinson Co., Sparks, MD, USA); (3) VITEK 2 Automated Identification System [33]; and (4) MALDI-TOF MS System (bioMérieux, Marcy l'Etoile, France) [34]. At the time of writing this research, the four microbial identification systems that are listed above do not, however, contain all eight species of *Elizabethkingia* in their reference spectra database. Studies have also shown that misidentification of *Elizabethkingia* was rife using these automated identification systems, with *E. anophelis* commonly misidentified as *E. meningoseptica* [1][33][35]. When the accuracy of the API/ID32, Phoenix 100 ID/AST, Vitek 2, and Vitek MS *Elizabethkingia,* clinical isolate identifications were compared with 16S rRNA gene sequencing; it was reported that species identification concordance between these identification systems and 16S rRNA gene sequencing was low at only 24.5–26.5% [33]. Nevertheless, MALDI-TOF MS systems with amended databases (labeled as "research-use only" system) either in the Vitek MS Knowledge Base v3.2 and Bruker MALDI Biotyper Library (Bruker Daltonics GmbH, Bremen, Germany) are now able to reliably differentiate *E. meningoseptica* from *E. anophelis*, but not the remaining species of the genus *Elizabethkingia* [33]. In a recent report of 22 clinical and 6 environmental hospital isolates from Queensland, Australia, Burnard et al. (2020) showed that the VITEK MS Knowledge Base v3.2 had a 96.2% accuracy in identifying *Elizabethkingia*, with a solitary isolate of *E. bruuniana* being the only species that was misidentified. Whole-genome sequencing confirmed that the majority of the isolates were *E. anophelis* (*n* = 22), with the rest being *E. miricola* (*n* = 3), *E. meningoseptica* (*n* = 2), and *E. bruuniana* (*n* = 1) [36].

In the near future, the inclusion of novel *Elizabethkingia* species spectra into the databases should ensure highly accurate identification using MALDI-TOF MS systems, making it a reliable identification tool in lieu of whole-genome sequencing.

3. Antibiotic Resistance

Elizabethkingia are intrinsically resistant to most β-lactams, β-lactam/lactamase inhibitors, and carbapenems due to the presence of two unique class B metallo-β-lactamases (MBLs), namely bla_{BlaB} and bla_{GOB}, along with a class A extended-spectrum β-lactamase (ESBL), bla_{CME} [37][38][39]. *Elizabethkingia* are the only known bacteria thus far with multiple chromosomally encoded MBLs [40]. Reports of subclasses of MBL genes such as $bla_{\text{BlaB-1}}$ [38], bla_{BlaB}, and bla_{GOB} in both *E. meningoseptica* and *E. anophelis* [39], as well as $bla_{\text{BlaB-16}}$ and $bla_{\text{GOB-19}}$ in *E. miricola* isolated from a black-spotted frog in China [41], make *Elizabethkingia* spp. a possible environmental reservoir for β-lactam resistance.

Elizabethkingia isolates are frequently resistant to aminoglycosides, macrolides, tetracycline, and vancomycin but show variable susceptibility to piperacillin, piperacillin-tazobactam, fluoroquinolones, minocycline, tigecycline, and trimethoprim-sulfamethoxazole [3][36][39][42][43][44]; cephalosporins, monobactams, and moderate susceptibilities to piperacillin [45][46][47], ceftazidime, colistin, and meropenem [48]; and levofloxacin [49]. There are currently no established MIC breakpoints for *Elizabethkingia*, and susceptibilities are largely reported based on *Enterobacteriaceae* breakpoints of the Clinical and Laboratory Standards Institute (CLSI) M100 guidelines and/or the European Committee on Antimicrobial Susceptibility Testing (EUCAST) pharmacokinetic–pharmacodynamic (PK–PD) "non-species" breakpoints [35][36]. It has been pointed out that susceptibilities, especially for vancomycin and piperacillin-tazobactam as determined by disk diffusion and E-test, are deemed unreliable and inaccurate for *Elizabethkingia*, and broth microdilution is instead recommended for susceptibility determination [43][50]. Although successful therapy has been attributed to rifampicin, there has been a report of bacterial resistance after three days of starting treatment [51]. A similar case was reported for an *E. meningoseptica* isolate in the Kuala Lumpur General Hospital, which developed resistance during treatment to cefepime, a cephalosporin antibiotic that is normally highly active against both Gram-positive and Gram-negative organisms [52].

Using disk diffusion, Lau, Chow [1] reported 21 *Elizabethkingia* isolates from Hong Kong as susceptible to vancomycin. However, studies using broth microdilution tests on isolates from Taiwan [43][53] and Australia [36] indicated that the isolates are likely non-susceptible based on the high MICs obtained (that ranged between 8 and 256 µg/mL). Similar ranges of vancomycin MICs were obtained by Han et al. [35], who investigated *Elizabethkingia* isolates from South Korea using the agar dilution method and concluded that all isolates were non-susceptible based on the interpretive criteria used for *Staphylococcus* spp. The vancomycin resistance gene, *vanW*, was reported in the majority of *Elizabethkingia* genomes, although the exact function of *vanW* is currently unknown [36][44]. However, mutations in *vanW* have been identified in microorganisms with VanB-type glycopeptide resistance [44][54]. In view of these facts and despite some anecdotal reports of success in using intravenous vancomycin alone to treat *Elizabethkingia* infections [55][56], it was recommended that even if intravenous vancomycin is the favored therapy for *Elizabethkingia* meningitis, ciprofloxacin, linezolid, or rifampicin should also be included until future clinical studies could be carried out to conclusively determine the clinical efficacy of these vancomycin-combination regiments for treatment [50].

One of the earliest reports of the whole-genome sequences of *Elizabethkingia* spp. strains from Southeast Asia was from Singapore, whereby sputum isolates obtained from three patients (NUHP1, NUHP2, and NUHP3) and four from the hospital's sink (NUH1, NUH4, NUH6, and NUH11) at the National University Hospital, Singapore, were compared against five previously sequenced *E. anophelis* strains Ag1 (PRJNA80705) and R26 (PRJNA178189), *E. meningoseptica* ATCC 12535 (NITE) (PRJNA199489), *E. meningoseptica* ATCC 12535 (OSU) (PRJNA198814), and *E. meningoseptica* 502 (PRJNA176121). This led to the discovery of 16 antibiotic resistance genes from the core genomes and 19 antibiotic resistance genes from the accessory genomes of *Elizabethkingia* spp., and this included genes that confer resistance to aminoglycosides, β-lactams, fluoroquinolones, glycopeptides, macrolide-lincosamide-streptogramins, tetracyclines, trimethoprim, and rifampicin [38]. A later study on two African isolates, E27017 and E18064, that compared their genomes with the genomes of 18 strains belonging to the genus *Elizabethkingia* from many different regions, including Malaysian and Singaporean genomic sequences that were available at that time, identified that all *Elizabethkingia* genomes contained at least 17 antimicrobial resistance genes [39].

A whole-genome sequencing study on three isolates of *E. meningoseptica* collected from an outbreak from three separate patients living in different counties in the Midwest regions of Michigan led to the identification of 22 resistance genes and 18 multidrug resistance efflux pump-encoded genes in all samples [57]. While *Elizabethkingia* spp. genomes shared many antibiotic-resistance genes with each other, minor differences have been reported [3][58]. Hence, genomic investigations of *Elizabethkingia* spp. offers invaluable novel information on the species, but unfortunately, there have not been any reports of the whole-genome sequence of *Elizabethkingia* spp. isolates from Southeast Asia besides those from Singapore.

4. Virulence Factors

The mechanisms of pathogenesis of *Elizabethkingia* spp. are still being studied [57]. When the virulence factor database (VFDB, http://www.mgc.ac.cn/VFs/, accessed on 12 December 2021) was used to predict their presence from the genome sequences of various *Elizabethkingia* spp., this led to the prediction of a total of 270 putative virulence factor genes. More than fourteen virulence factor classes for *Elizabethkingia* spp. were identified with the following defined virulence-associated functions: adherence, antimicrobial activity, biofilm, cellular metabolism, effector delivery system, exoenzyme, exotoxin, immune modulation, invasion, motility, nutritional/metabolic factor, post-translational modification, regulation, stress survival, and others. Different species of *Elizabethkingia* shared the same virulence factors (**Figure 1**).

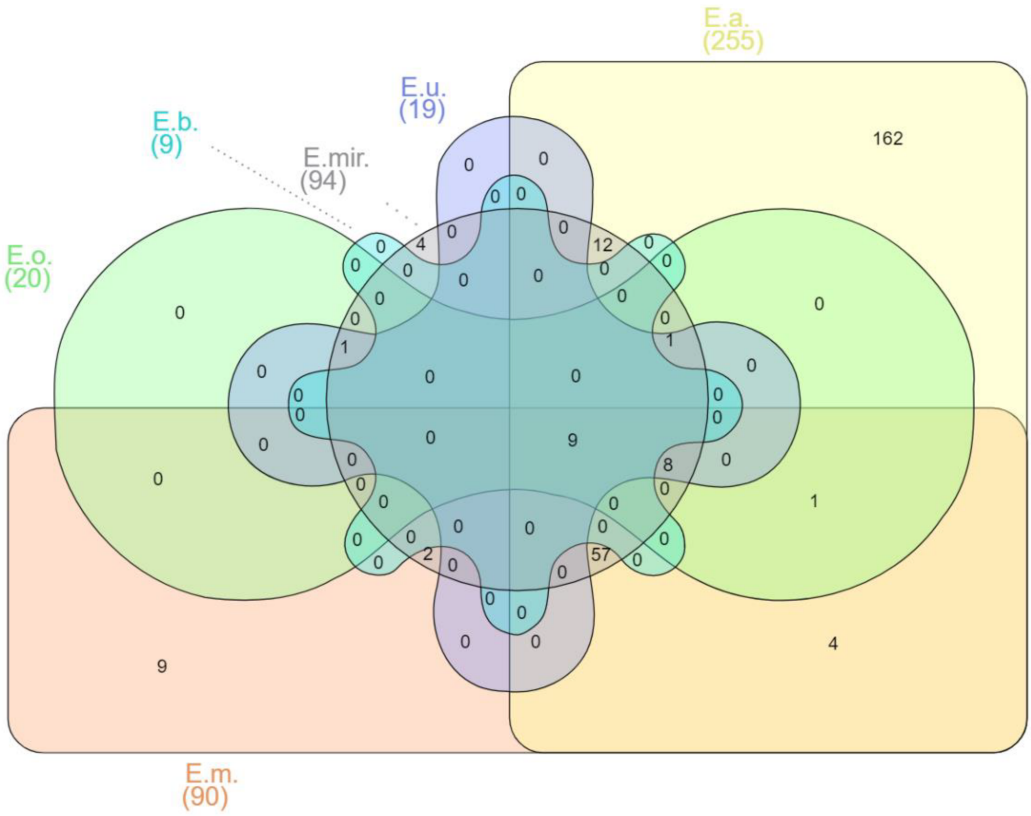

Figure 1. Venn diagram of shared virulence factor genes of *Elizabethkingia* spp. E.m.—*E. meningoseptica*; E.a.—*E. anophelis*; E.mir.—*E. miricola*; E.o.—*E. occulta*; E.u.—*E. ursingii*; E.b.—*E. bruuniana.* Edwards mode was used to process virulence factor gene outputs for Venn diagram visualization with InteractiVenn [59].

Among the 270 predicted genes for virulence factors, 162 have been reported as unique in *E. anophelis*. *E. meningoseptica* carried six unique genes involved in adherence that encode curli nucleator protein (*csgB*), curli assembly proteins (*curEm1, curEm2*, *curEm3*, *curEm4*), a curli production assembly protein (*csgG*), and two genes involved in immune modulation encoding a capsular polysaccharide synthesis enzyme (*cap8O*), a gene encoding Rab2-interacting conserved protein A (*ricA*) and a putative carbonic anhydrase-encoded gene (*mig-5*). Four of the *E. miricola* unique virulence genes were predicted to be involved with urease accessory protein (*ureE*), urease alpha subunit (*ureA*), twitching motility protein (*pilG*), and sphingomyelinase-c (*smcL*).

Identification of 6880 gene families in *E. anophelis* highlighted the genomic heterogeneity of *Elizabethkingia* species [39]. Genes homologous to heme iron acquisition, oxidative stress resistance proteins, and hemolysins were reported in earlier studies [32][60][61]. Extensive variations of capsular polysaccharide synthesis genes in *E. anopheles* were first reported by Breurec, Criscuolo [39], with variable *cps* clusters observed amongst the different lineages suggesting virulence heterogeneity among *Elizabethkingia* strains [39]. Identification of the capsule biosynthesis gene, *capD* [57], and the *adeG* gene for the AdeFGH efflux pump [20] in all *Elizabethkingia* species leads to possible biofilm formation [42][62], which empowers the bacteria with the ability to persist on various surfaces [57][63]. Thirty clinical isolates from Malaysia, which comprised *E. anophelis*, *E. meningoseptica,* and *E. miricola,* were recently shown to produce biofilms on polystyrene microtiter plates [64].

Nine virulence factor genes were shared between six of the *Elizabethkingia* spp., including the *E. argenteiflava*-encoded *adeFGH* efflux pump, isocitrate lyase (*icl*), catalase/(hydro)peroxidase (*katA*), 60K heat shock protein (*htpB*), phospholipase C (*plc*), phosphopyruvate hydratase (*eno*), translation elongation factor (*tuf*), catalase/peroxidase HPI (*katG*), and aspartate 1-decarboxylase precursor (*panD*), which is involved with adherence, biofilm formation, cellular metabolism, exotoxin production, and stress survival. Isocitrate lyase (*icl*) plays an important role in the glyoxylate cycle [65], and its presence in *Elizabethkingia* spp. can predict its essential role in stationary-phase survival. An early report had shown that the presence of *icl* in *Mycobacterium tuberculosis* promoted the tenacity of infection by helping the pathogen to survive inside macrophages [66].

However, the specific role of bacterial enzymes in pathogenesis varies with infection. The presence of phospholipases C (*plc*) in all *Elizabethkingia* spp. [44] suggest its crucial role in downregulating host immunity [67]. In *L. monocytogenes*, *plc* aided bacterial escape toward the cytosol and cell-to-cell propagation, whereas, in *C. perfringens,* it helped bacteria induce endothelial damage and platelet aggregation, and in *P. aeruginosa*, it led to the triggering of signaling pathways that lead to inflammation [68].

The catalase-peroxidase genes, *katA* and *katG* (encoding hydroperoxidase I), are crucial against oxidative stress [69]. An earlier report showed that strains with *katA* were resistant to dodecyl sulfate, proteinase K, pepsin, trypsin, chymotrypsin, and the neutrophil protease cathepsin G, and they could survive for a long period once released from lysed cells [70]. Presence of *katA* [38][39][42][44][58][60][71][72] and *katG* [42][44][71][72] could also support *Elizabethkingia* species' resistance to aminoglycosides.

5. Sources of Isolation and Transmission

The genera *Elizabethkingia* are aerobic, non-fermenting, non-motile, catalase-positive, oxidase-positive, indole-positive, and Gram-negative bacilli widely distributed in soil, mosquitoes, plants, fresh and marine fish [28][73], food products [74], hospital settings [75], stagnant water, inland wetlands, and rivers [31]. Due to their biofilm-forming ability [62], they have been isolated from sinks and taps where they colonize the most, leading to nosocomial and community infections [76] (**Table 1**).

Table 1. Various sources of isolation of *Elizabethkingia* spp. in Southeast Asia.

Source of Isolation	Country of Origin	Citation
Blood	Malaysia, Singapore, Thailand, Indonesia, Cambodia	[8][13][15][23][24][25][26][34][64][77][78][79][80][81][82]
Peritoneal fluid	Malaysia	[77]
Cerebrospinal fluid (CSF)	Malaysia, Singapore	[15][23][77][83][84][85][86]
Contact lens	Malaysia	[87]
Hospital environment (aerators, sink drains and traps at ICUs, pediatric wards, surgical wards, orthopedic wards)	Singapore	[8][88][89][90]
Catheter tips	Singapore	[8]
Respiratory specimens	Singapore Malaysia	[8][64]
Rectal swabs	Singapore	[91]
Urine	Malaysia	[64]
Wound swabs	Malaysia	[64]
Nasal swabs	Malaysia	[64]

Source of Isolation	Country of Origin	Citation
Vitreous culture	Singapore	[8]
Frogs (*Rana catesbeiana* (American bullfrogs) and *Theloderma bicolor* Chapa bug-eyed frogs, Warty toads (*Bombina microdeladigitora*), and Northern leopard frogs (*Lithobates pipiens*)	Malaysia Vietnam	[92][93][94]
Mosquitoes (*Anopheles minimus, Anopheles dirus, Anopheles maculatus, Anopheles sawadwongporni,* and *Anopheles dravidicus*)	Thailand	[95][96]
Fish (*Clarias gariepinus* (African sharptooth catfish) and *Pangasius hypophthalmus* (Tra catfish)	Malaysia, Vietnam	[73][97][98]
Retail sausages	Malaysia	[74]
Gnetum gnemon (Tree)	Malaysia	[99][100]

Vector-borne transmission of the bacterial pathogen via mosquito bites has been suggested ever since the discovery of *E. anophelis* in the midgut of the *Anopheles gambiae* mosquito [101][102] and, more recently, in the salivary glands and saliva of *Aedes albopictus* [103]. The microbiome of *Anopheles* mosquitoes has evidently revealed the strong symbiotic nature of *E. meningoseptica* [104], which has been isolated from various independent sources, including *Anopheles stephensi*, the vector for the malarial parasite *Plasmodium vivax* [76][105][106], semi-field *Anopheles gambiae* females [104][106][107][108], field sampled mosquitoes in Cameroon [109][110], and laboratory-reared mosquitoes where *Anopheles* were the predominant species [109][111]. Another comparative study on bacterial microbiota isolated from the midgut of various *Anopheles* spp., which were obtained in the same region of Mae Sot District and Sop Moei District in Thailand, reported on the findings of *Elizabethkingia* spp. from *Anopheles minimus*, *Anopheles dirus, Anopheles maculatus, Anopheles sawadwongporni,* and *Anopheles dravidicus* mosquitoes [95]. However, sequences associated with the genus *Elizabethkingia* could not be definitively assigned to either *E. anophelis* or *E. meningoseptica* as the V3–V4 region of the 16S rRNA gene used for microbiome profiling could not differentiate between the two species [95]. Despite these multiple discoveries of *Elizabethkingia* spp. in the midgut and salivary glands of various mosquito species, there is currently a lack of strong direct evidence that supports *Elizabethkingia* infection, particularly *E. anophelis*, as a mosquito-borne disease [43], although this should not be ruled out with the current level of knowledge. A comparative genomics study of three cases of *E. anophelis* also provided evidence of vertical transmission from mother to her baby [61].

Zainuri et al. (2013) reported on the isolation of *E. meningoseptica* from American bullfrogs (*Lithobates catesbeianus* or *Rana catesbeiana*) suffering from red leg syndrome and cataract in Sabah, Malaysia [93]. Isolation of *E. meningoseptica* from bullfrogs was also described in an earlier study, in which the isolates obtained were found to be resistant to multiple antibiotics [94]. *E. miricola*, which had been implicated in acute infections in humans, caused a disease outbreak associated involving the internal organs of different anuran species, including northern leopard frogs (*Lithobates pipiens*), Chapa bug-eyed frogs (*Theloderma bicolor*), and Vietnamese warty toads (*Bombina microdeladigitora*) captured in Vietnam. The presence of β-lactamases and putative virulence genes in the *E. miricola isolates* were detected in silico [92].

E. miricola was also reportedly isolated from Tra catfish (*Pangasius hypophthalmus*) fillets in the industrial processing lines in Vietnam [98]. Tra catfish is a type of freshwater fish, which is one of the major fish species in the Mekong River, and its processed fillets are exported to more than 80 different countries worldwide [97]. Other scientists have also reported the isolation of *E. meningoseptica* from retail sausages in Kampar, Malaysia, although the identification was performed by traditional biochemical methods and identified as *Chryseobacterium meningosepticum* [74].

Furthermore, 454 pyrosequencing of the 16S rRNA gene from the bacterial community of the root of the gnetalean gymnosperm *Gnetum gnemon* and nearby bulk soils of a tropical forest arboretum at the Forest Research Institute of Malaysia (FRIM) at Kepong, near Kuala Lumpur, identified the mutualistic presence of *E. meningoseptica* and *E. miricola* [99]. *Elizabethkingia* spp. was surprisingly found in relative abundance (4.9%) on the leaves of *Gnetum gnemon* in

comparison with rhizoplane (1.4%) [100]. These reports indicate the ubiquity of *Elizabethkingia* spp. in the environment and, thus, the difficulty in tracing an outbreak should one occur in the community and outside of hospital settings.

References

1. Lau, S.K.; Chow, W.-N.; Foo, C.-H.; Curreem, S.O.; Lo, G.C.-S.; Teng, J.L.; Chen, J.H.; Ng, R.H.; Wu, A.K.; Cheung, I.Y.; et al. Elizabethkingia anophelis bacteremia is associated with clinically significant infections and high mortality. Sci. Rep. 2016, 6, 26045.
2. Dziuban, E.J.; Franks, J.L.; So, M.; Peacock, G.; Blaney, D.D. Elizabethkingia in children: A comprehensive review of symptomatic cases reported from 1944 to 2017. Clin. Infect. Dis. 2018, 67, 144–149.
3. Opota, O.; Diene, S.M.; Bertelli, C.; Prod'hom, G.; Eckert, P.; Greub, G. Genome of the carbapenemase-producing clinical isolate Elizabethkingia miricola EM_CHUV and comparative genomics with Elizabethkingia meningoseptica and Elizabethkingia anophelis: Evidence for intrinsic multidrug resistance trait of emerging pathogens. Int. J. Antimicrob. Agents 2017, 49, 93–97.
4. Swain, B.; Rout, S.; Otta, S.; Rakshit, A. Elizabethkingia meningoseptica: An unusual cause for septicaemia. JMM Case Rep. 2015, 2, e000005.
5. Lee, C.-H.; Lin, W.-C.; Chia, J.-H.; Su, L.-H.; Chien, C.-C.; Mao, A.-H.; Liu, J.-W. Community-acquired osteomyelitis caused by Chryseobacterium meningosepticum: Case report and literature review. Diagn. Microbiol. Infect. Dis. 2008, 60, 89–93.
6. Gupta, P.; Zaman, K.; Mohan, B.; Taneja, N. Elizabethkingia miricola: A rare non-fermenter causing urinary tract infection. World J. Clin. Cases 2017, 5, 187.
7. Raghavan, S.; Thomas, B.; Shastry, B. Elizabethkingia meningoseptica: Emerging multidrug resistance in a nosocomial pathogen. Case Rep. 2017, 2017, bcr-2017-221076.
8. Young, S.M.; Lingam, G.; Tambyah, P.A. Elizabethkingia meningoseptica Engodenous Endophthalmitis—A Case Report. Antimicrob. Resist. Infect. Control 2014, 3, 35.
9. Yang, J.; Xue, W.; Yu, X. Elizabethkingia meningosepticum endocarditis: A rare case and special therapy. Anatol. J. Cardiol. 2015, 15, 427.
10. Chi, S.; Fekete, T. Epididymo-orchitis. In Clinical Infectious Disease, 2nd ed.; Schlossberg, D., Ed.; Cambridge University Press: Cambridge, UK, 2015; pp. 401–405.
11. Gonzalez, C.; Coolen-Allou, N.; Allyn, J.; Esteve, J.; Belmonte, O.; Allou, N. Severe sepsis and pulmonary abscess with bacteremia due to Elizabethkingia miricola. Med. Mal. Infect. 2015, 46, 49–51.
12. Lee, C.-C.; Chen, P.-L.; Wang, L.-R.; Lee, H.-C.; Chang, C.-M.; Lee, N.-Y.; Wu, C.-J.; Shih, H.-I.; Ko, W.-C. Fatal case of community-acquired bacteremia and necrotizing fasciitis caused by Chryseobacterium meningosepticum: Case report and review of the literature. J. Clin. Microbiol. 2006, 44, 1181–1183.
13. Taufiq Kadafi, K.; Yuliarto, S.; Aji Cahyono, H.; Ratridewi, I.; Khalasha, T. Cerebral Salt Wasting Due to Bacteremia Caused by Elizabethkingia meningoseptica: A Case Report. Arch. Pediatr. Infect. Dis. 2020, 8, e44832.
14. Kenna, D.T.; Fuller, A.; Martin, K.; Perry, C.; Pike, R.; Burns, P.J.; Narayan, O.; Wilkinson, S.; Hill, R.; Woodford, N.; et al. rpoB gene sequencing highlights the prevalence of an E. miricola cluster over other Elizabethkingia species among UK cystic fibrosis patients. Diagn. Microbiol. Infect. Dis. 2018, 90, 109–114.
15. Amir, A.; IC Sam, J.; Nawi, S. Elizabethkingia meningoseptica neonatal meningitis in a premature infant. Asian J. Med. Biomed. 2018, 2 (Suppl. 1), 22.
16. Seong, H.; Kim, J.H.; Kim, J.H.; Lee, W.J.; Ahn, J.Y.; Ku, N.S.; Choi, J.Y.; Yeom, J.S.; Song, Y.G.; Jeong, S.J. Risk factors for mortality in patients with elizabethkingia infection and the clinical impact of the antimicrobial susceptibility patterns of elizabethkingia species. J. Clin. Med. 2020, 9, 1431.
17. Nori, P.; Cowman, K.; Chen, V.; Bartash, R.; Szymczak, W.; Madaline, T.; Katiyar, C.P.; Jain, R.; Aldrich, M.; Weston, G.; et al. Bacterial and fungal coinfections in COVID-19 patients hospitalized during the New York City pandemic surge. Infect. Control Hosp. Epidemiol. 2021, 42, 84–88.
18. Hayek, S.S.; Abd, T.T.; Cribbs, S.K.; Anderson, A.M.; Melendez, A.; Kobayashi, M.; Polito, C.; Wang, Y.F.W. Rare Elizabethkingia meningosepticum meningitis case in an immunocompetent adult. Emerg. Microbes Infect. 2013, 2, 1–4.
19. Sebastiampillai, B.S.; Luke, N.V.; Silva, S.; De Silva, S.T.; Premaratna, R. Septicaemia caused by Elizabethkingia-sp in a 'healthy'Sri Lankan man. Trop. Dr. 2018, 48, 62–63.

20. 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.

21. King, E.O. Studies on a group of previously unclassified bacteria associated with meningitis in infants. Am. J. Clin. Pathol. 1959, 31, 241–247.

22. Buttiaux, R.; Vandepitte, J. Flavobacterium in Epidemic Meningitis of New-Born Infants. Ann. Inst. Pasteur 1960, 98, 398–404.

23. Chan, J.; Chong, C.; Thoon, K.; Tee, N.; Maiwald, M.; Lam, J.; Bhattacharya, R.; Chandran, S.; Yung, C.; Tan, N. Invasive paediatric Elizabethkingia meningoseptica infections are best treated with a combination of piperacillin/tazobactam and trimethoprim/sulfamethoxazole or fluoroquinolone. J. Med. Microbiol. 2019, 68, 1167–1172.

24. Saetiew, N.; Nilkate, S.; Suankratay, C. Elizabethkingia meningoseptica Infection: The First Case Series in Thailand. Presented at the 26th European Congress of Clinical Microbiology and Infectious Diseases, Bangkok, Thailand, 9–12 April 2016.

25. Agustini, N.M.A.; Wati, D.K.; Suparyatha, I.; Hartawan, I.N.B.; Utama, I.M.G.D.L.; Budayanti, N.N.S.; Tunas, I.K. The relationship between bacterial types and antibiotic resistance with the clinical outcomes of sepsis patients in Pediatric Intensive Care Unit at Sanglah Hospital Denpasar, Bali-Indonesia. Indones. J. Biomed. Sci. 2018, 12, 13–18.

26. Reed, T.A.; Watson, G.; Kheng, C.; Tan, P.; Roberts, T.; Ling, C.L.; Miliya, T.; Turner, P. Elizabethkingia anophelis Infection in Infants, Cambodia, 2012–2018. Emerg. Infect. Dis. 2020, 26, 320.

27. Frederiksen, W.; Ursing, J. Proposed new bacterial taxa and proposed changes of bacterial names published during 1994 and considered to be of interest to medical or veterinary bacteriology. APMIS 1995, 103, 651–654.

28. Kim, K.; Kim, M.; Lim, J.; Park, H.; Lee, S. 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, 1287–1293.

29. Nicholson, A.C.; Gulvik, C.A.; Whitney, A.M.; Humrighouse, B.W.; Graziano, J.; Emery, B.; Bell, M.; Loparev, V.; Juieng, P.; Gartin, J.; et al. Revisiting the taxonomy of the genus Elizabethkingia using whole-genome sequencing, optical mapping, and MALDI-TOF, along with proposal of three novel Elizabethkingia species: Elizabethkingia bruuniana sp. nov., Elizabethkingia ursingii sp. nov., and Elizabethkingia occulta sp. nov. Antonie Van Leeuwenhoek 2018, 111, 55–72.

30. Hwang, J.-H.; Kim, J.; Kim, J.-H.; Mo, S. Elizabethkingia argenteiflava sp. nov., isolated from the pod of soybean, Glycine max. Int. J. Syst. Evol. Microbiol. 2021, 71, 004767.

31. Hem, S.; Jarocki, V.M.; Baker, D.J.; Charles, I.G.; Drigo, B.; Aucote, S.; Donner, E.; Burnard, D.; Bauer, M.J.; Harris, P.N.; et al. Genomic analysis of Elizabethkingia species from aquatic environments: Evidence for potential clinical transmission. Curr. Res. Microb. Sci. 2022, 3, 100083.

32. Kukutla, P.; Lindberg, B.G.; Pei, D.; Rayl, M.; Yu, W.; Steritz, M.; Faye, I.; Xu, J. Insights from the genome annotation of Elizabethkingia anophelis from the malaria vector Anopheles gambiae. PLoS ONE 2014, 9, e97715.

33. Lin, J.-N.; Lai, C.-H.; Yang, C.-H.; Huang, Y.-H.; Lin, H.-F.; Lin, H.-H. Comparison of four automated microbiology systems with 16S rRNA gene sequencing for identification of Chryseobacterium and Elizabethkingia species. Sci. Rep. 2017, 7, 13824.

34. Ekcharoenkul, K.; Ngamskulrungroj, P.; Joyjamras, K.; Leelaporn, A.; Harun, A.; Kiratisin, P. Identification of Uncommon Pathogenic Bacteria by MALDI-TOF Mass Spectrometry Using a Custom Library of Siriraj Hospital. Siriraj Med. J. 2018, 70, 127–130.

35. Han, M.-S.; Kim, H.; Lee, Y.; Kim, M.; Ku, N.S.; Choi, J.Y.; Yong, D.; Jeong, S.H.; Lee, K.; Chong, Y. Relative prevalence and antimicrobial susceptibility of clinical isolates of Elizabethkingia species based on 16S rRNA gene sequencing. J. Clin. Microbiol. 2017, 55, 274–280.

36. Burnard, D.; Gore, L.; Henderson, A.; Ranasinghe, A.; Bergh, H.; Cottrell, K.; Sarovich, D.S.; Price, E.P.; Paterson, D.L.; Harris, P.N. 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.

37. González, L.J.; Vila, A.J. Carbapenem resistance in Elizabethkingia meningoseptica is mediated by metallo-β-lactamase BlaB. Antimicrob. Agents Chemother. 2012, 56, 1686–1692.

38. Teo, J.; Tan, S.Y.-Y.; Liu, Y.; Tay, M.; Ding, Y.; Li, Y.; Kjelleberg, S.; Givskov, M.; Lin, R.T.P.; Yang, L. Comparative Genomic Analysis of Malaria Mosquito Vector-Associated Novel Pathogen Elizabethkingia anophelis. Genome Biol. Evol. 2014, 6, 1158–1165.

39. Breurec, S.; Criscuolo, A.; Diancourt, L.; Rendueles, O.; Vandenbogaert, M.; Passet, V.; Caro, V.; Rocha, E.P.; Touchon, M.; Brisse, S. Genomic epidemiology and global diversity of the emerging bacterial pathogen Elizabethkingia anophelis. Sci. Rep. 2016, 6, 30379.

40. Hu, R.; Zhang, Q.; Gu, Z. Molecular diversity of chromosomal metallo-β-lactamase genes in Elizabethkingia genus. Int. J. Antimicrob. Agents 2020, 56, 105978.

41. Hu, R.; Zhang, Q.; Gu, Z. Whole-genome analysis of the potentially zoonotic Elizabethkingia miricola FL160902 with two new chromosomal MBL gene variants. J. Antimicrob. Chemother. 2020, 75, 526–530.

42. Perrin, A.; Larsonneur, E.; Nicholson, A.C.; Edwards, D.J.; Gundlach, K.M.; Whitney, A.M.; Gulvik, C.A.; Bell, M.E.; Rendueles, O.; Cury, J.; et al. Evolutionary dynamics and genomic features of the Elizabethkingia anophelis 2015 to 2016 Wisconsin outbreak strain. Nat. Commun. 2017, 8, 15483.

43. Lin, J.-N.; Lai, C.-H.; Yang, C.-H.; Huang, Y.-H. Elizabethkingia infections in humans: From genomics to clinics. Microorganisms 2019, 7, 295.

44. Liang, C.-Y.; Yang, C.-H.; Lai, C.-H.; Huang, Y.-H.; Lin, J.-N. Comparative Genomics of 86 Whole-Genome Sequences in the Six Species of the Elizabethkingia Genus Reveals Intraspecific and Interspecific Divergence. Sci. Rep. 2019, 9, 19167.

45. Bellais, S.; Poirel, L.; Naas, T.; Girlich, D.; Nordmann, P. Genetic-Biochemical Analysis and Distribution of the Ambler Class A β-Lactamase CME-2, Responsible for Extended-Spectrum Cephalosporin Resistance in Chryseobacterium (Flavobacterium) meningosepticum. Antimicrob. Agents Chemother. 2000, 44, 1–9.

46. Chang, J.; Hsueh, P.; Wu, J.; Ho, S.; Hsieh, W.; Luh, K. Antimicrobial susceptibility of flavobacteria as determined by agar dilution and disk diffusion methods. Antimicrob. Agents Chemother. 1997, 41, 1301–1306.

47. Moulin, V.; Freney, J.; Hansen, W.; Philippon, A. Comportement phénotypique des Flavobacterium vis-à-vis de 39 antibiotiques. Méd. Mal. Infect. 1992, 22, 902–907.

48. Kwambana-Adams, B.; Laxton, C.; Foster-Nyarko, E.; Weinstock, G.; Antonio, M. Isolation of Methicillin-resistant Staphylococcus aureus and Multidrug-resistant Elizabethkingia meningoseptica from Neonates within Minutes of Birth. Pediatric Infect. Dis. J. 2017, 36, 123–124.

49. Huang, Y.; Huang, Y.; Lin, Y.; Wang, F.; Chan, Y.; Yang, T. Risk factors and outcome of levofloxacin-resistant Elizabethkingia meningoseptica bacteraemia in adult patients in Taiwan. Eur. J. Clin. Microbiol. Infect. Dis. 2017, 36, 1–8.

50. Jean, S.-S.; Hsieh, T.-C.; Ning, Y.-Z.; Hsueh, P.-R. Role of vancomycin in the treatment of bacteraemia and meningitis caused by Elizabethkingia meningoseptica. Int. J. Antimicrob. Agents 2017, 50, 507–511.

51. Lee, E.; Robinson, M.; Thong, M.; Puthucheary, S.; Ong, T.; Ng, K. Intraventricular chemotherapy in neonatal meningitis. J. Pediatr. 1977, 91, 991–995.

52. Lim, V.; Halijah, M. A comparative study of the in-vitro activity of cefepime and other cephalosporins. Malays. J. Pathol. 1993, 15, 65–68.

53. Chang, T.-Y.; Chen, H.-Y.; Chou, Y.-C.; Cheng, Y.-H.; Sun, J.-R. In vitro activities of imipenem, vancomycin, and rifampicin against clinical Elizabethkingia species producing BlaB and GOB metallo-beta-lactamases. Eur. J. Clin. Microbiol. Infect. Dis. 2019, 38, 2045–2052.

54. Santona, A.; Paglietti, B.; Al-Qahtani, A.A.; Bohol, M.F.F.; Senok, A.; Deligios, M.; Rubino, S.; Al-Ahdal, M.N. Novel type of VanB2 teicoplanin-resistant hospital-associated Enterococcus faecium. Int. J. Antimicrob. Agents 2014, 44, 156–159.

55. Sader, H.S.; Jones, R.N.; Pfaller, M.A. Relapse of catheter-related Flavobacterium meningosepticum bacteremia demonstrated by DNA macrorestriction analysis. Clin. Infect. Dis. 1995, 21, 997–1000.

56. Ozkalay, N.; Anil, M.; Agus, N.; Helvaci, M.; Sirti, S. Community-acquired meningitis and sepsis caused by Chryseobacterium meningosepticum in a patient diagnosed with thalassemia major. J. Clin. Microbiol. 2006, 44, 3037–3039.

57. Chen, S.; Soehnlen, M.; Blom, J.; Terrapon, N.; Henrissat, B.; Walker, E.D. Comparative genomic analyses reveal diverse virulence factors and antimicrobial resistance mechanisms in clinical Elizabethkingia meningoseptica strains. PLoS ONE 2019, 14, e0222648.

58. Lin, J.-N.; Lai, C.-H.; Yang, C.-H.; Huang, Y.-H.; Lin, H.-H. Genomic features, phylogenetic relationships, and comparative genomics of Elizabethkingia anophelis strain EM361-97 isolated in Taiwan. Sci. Rep. 2017, 7, 14317.

59. Heberle, H.; Meirelles, G.V.; da Silva, F.R.; Telles, G.P.; Minghim, R. InteractiVenn: A web-based tool for the analysis of sets through Venn diagrams. BMC Bioinform. 2015, 16, 169.

60. Li, Y.; Liu, Y.; Chew, S.C.; Tay, M.; Salido, M.M.S.; Teo, J.; Lauro, F.M.; Givskov, M.; Yang, L. Complete genome sequence and transcriptomic analysis of the novel pathogen Elizabethkingia anophelis in response to oxidative stress. Genome Biol. Evol. 2015, 7, 1676–1685.

61. Lau, S.K.; Wu, A.K.; Teng, J.L.; Tse, H.; Curreem, S.O.; Tsui, S.K.; Huang, Y.; Chen, J.H.; Lee, R.A.; Yuen, K.-Y.; et al. Evidence for Elizabethkingia anophelis transmission from mother to infant, Hong Kong. Emerg. Infect. Dis. 2015, 21, 232.

62. Jacobs, A.; Chenia, H.Y. Biofilm formation and adherence characteristics of an Elizabethkingia meningoseptica isolate from Oreochromis mossambicus. Ann. Clin. Microbiol. Antimicrob. 2011, 10, 16.

63. Alav, I.; Sutton, J.M.; Rahman, K.M. Role of bacterial efflux pumps in biofilm formation. J. Antimicrob. Chemother. 2018, 73, 2003–2020.

64. Puah, S.M.; Fong, S.P.; Kee, B.P.; Puthucheary, S.; Chua, K.H. Molecular identification and biofilm-forming ability of Elizabethkingia species. Microb. Pathog. 2022, 162, 105345.

65. Dunn, M.; Ramirez-Trujillo, J.; Hernández-Lucas, I. Major roles of isocitrate lyase and malate synthase in bacterial and fungal pathogenesis. Microbiology 2009, 155, 3166–3175.

66. McKinney, J.D.; Zu Bentrup, K.H.; Muñoz-Elías, E.J.; Miczak, A.; Chen, B.; Chan, W.-T.; Swenson, D.; Sacchettini, J.C.; Jacobs, W.R.; Russell, D.G. Persistence of Mycobacterium tuberculosis in macrophages and mice requires the glyoxylate shunt enzyme isocitrate lyase. Nature 2000, 406, 735–738.

67. Roberts, M.F.; Khan, H.M.; Goldstein, R.; Reuter, N.; Gershenson, A. Search and subvert: Minimalist bacterial phosphatidylinositol-specific phospholipase C enzymes. Chem. Rev. 2018, 118, 8435–8473.

68. Monturiol-Gross, L.; Villalta-Romero, F.; Flores-Díaz, M.; Alape-Girón, A. Bacterial phospholipases C with dual activity: Phosphatidylcholinesterase and sphingomyelinase. FEBS Open Bio 2021, 11, 3262–3275.

69. Vicente, C.S.; Nascimento, F.X.; Ikuyo, Y.; Cock, P.J.; Mota, M.; Hasegawa, K. The genome and genetics of a high oxidative stress tolerant Serratia sp. LCN16 isolated from the plant parasitic nematode Bursaphelenchus xylophilus. BMC Genom. 2016, 17, 301.

70. Hassett, D.J.; Alsabbagh, E.; Parvatiyar, K.; Howell, M.L.; Wilmott, R.W.; Ochsner, U.A. A protease-resistant catalase, KatA, released upon cell lysis during stationary phase is essential for aerobic survival of a Pseudomonas aeruginosa oxyR mutant at low cell densities. J. Bacteriol. 2000, 182, 4557–4563.

71. Wang, M.; Gao, H.; Lin, N.; Zhang, Y.; Huang, N.; Walker, E.D.; Ming, D.; Chen, S.; Hu, S. The antibiotic resistance and pathogenicity of a multidrug-resistant Elizabethkingia anophelis isolate. Microbiologyopen 2019, 8, e804.

72. Yang, C.; Liu, Z.; Yu, S.; Ye, K.; Li, X.; Shen, D. Comparison of Whole-Genome Sequences for Three Species of the Elizabethkingia Genus. 2020. Available online: https://www.researchsquare.com/article/rs-61004/v1 (accessed on 21 April 2022).

73. Laith, A.; Mazlan, A.; Ambak, M.; Jabar, A.; Najiah, M. Isolation and Identification of Elizabethkingia meningoseptica from Diseased African Catfish Clarias gariepinus. J. Microbiol. Biotechnol. Food Sci. 2017, 6, 1070–1076.

74. Tew, L.-S.; She, L.-Y.; Chew, C.-H. Isolation, Antimicrobial Susceptibility Profile and Detection of Sul1, blaTEM, and blaSHV in Amoxicillin-Clavulanate-Resistant Bacteria Isolated From Retail Sausages in Kampar, Malaysia. Jundishapur J. Microbiol. 2016, 9, e37897.

75. Chen, C.; Chen, Y.; Wang, F. Risk factors of healthcare-associated Elizabethkingia meningoseptica infections in Taiwan medical center. Int. J. Antimicrob. Agents 2017, 50, S141.

76. Khan, I.; Lall, M.; Sen, S.; Ninawe, S.; Chandola, P. Multiresistant Elizabethkingia meningoseptica infections in tertiary care. Med. J. Armed Forces India 2015, 71, 282.

77. Thong, M.; Puthucheary, S.; Lee, E. Flavobacterium meningosepticum infection: An epidemiological study in a newborn nursery. J. Clin. Pathol. 1981, 34, 429–433.

78. Chew, K.L.; Cheng, B.; Lin, R.T.; Teo, J.W. Elizabethkingia anophelis is the dominant Elizabethkingia species found in blood cultures in Singapore. J. Clin. Microbiol. 2018, 56, e01445-17.

79. Yung, C.-F.; Maiwald, M.; Loo, L.H.; Soong, H.Y.; Tan, C.B.; Lim, P.K.; Li, L.; Tan, N.W.; Chong, C.-Y.; Tee, N.; et al. Elizabethkingia anophelis and association with tap water and handwashing, Singapore. Emerg. Infect. Dis. 2018, 24, 1730.

80. Loo, L.W.; Liew, Y.X.; Choong, H.L.L.; Tan, A.L.; Chlebicki, P. Microbiology and audit of vascular access-associated bloodstream infections in multi-ethnic Asian hemodialysis patients in a tertiary hospital. Infect. Dis. 2015, 47, 225–230.

81. Sooklin, L.; Anand, A.J.; Rajadurai, V.S.; Chandran, S. Management of large congenital chylous ascites in a preterm infant: Fetal and neonatal interventions. BMJ Case Rep. CP 2020, 13, e235849.

82. Liestiadi, D.E.F.; Azlin, E.; Nafianti, S. A hematologic scoring system and C-reactive protein compared to blood cultures for diagnosing bacterial neonatal sepsis. Paediatr. Indones 2017, 57, 71.

83. Lee, E.; Robinson, M.; Thong, M.; Puthucheary, S. Rifamycin in Neonatal Flavobacteria meningitis. Arch. Dis. Child. 1976, 51, 209–213.

84. Raimondi, A.; Moosdeen, F.; Williams, J. Antibiotic resistance pattern of Flavobacterium meningosepticum. Eur. J. Clin. Microbiol. Infect. Dis. 1986, 5, 461–463.

85. Zakaria, Z.; Idris, B. Intraoperative Cerebrospinal Fluid Sample from First Ventriculoperitoneal Shunt Operation: Is it Indicated? Malays. J. Med. Sci. MJMS 2013, 20, 102.

86. Wan Hassan, W.M.N.; Paramasivam, R.P.; Kandasamy, R.; Hassan, M.H.; Zaini, R.H.M. An uncommon Elizabethkingia meningoseptica septicemia in hemorrhagic stroke with septic shock patient during prolonged neuro-intensive care management. Anaesth. Pain Intensive Care 2017, 21, 268–271.

87. Ali, N.A.M.; Reddy, S.C. Bilateral simultaneous infectious keratitis secondary to contact lens wear: An unusual case report with rare organisms. Eye Contact Lens 2007, 33, 338–340.

88. Phoon, H.Y.; Hussin, H.; Hussain, B.M.; Lim, S.Y.; Woon, J.J.; Er, Y.X.; Thong, K.L. Distribution, genetic diversity and antibiotic resistance of clinically important bacteria from the environment of a tertiary hospital. J. Glob. Antimicrob. Resist. 2018, 14, 132–140.

89. Haller, L.; Chen, H.; Ng, C.; Le, T.H.; Koh, T.H.; Barkham, T.; Sobsey, M.; Gin, K.Y.-H. Occurrence and characteristics of extended-spectrum β-lactamase-and carbapenemase-producing bacteria from hospital effluents in Singapore. Sci. Total Environ. 2018, 615, 1119–1125.

90. Balm, M.; Salmon, S.; Jureen, R.; Teo, C.; Mahdi, R.; Seetoh, T.; Teo, J.; Lin, R.; Fisher, D. Bad design, bad practices, bad bugs: Frustrations in controlling an outbreak of Elizabethkingia meningoseptica in intensive care units. J. Hosp. Infect. 2013, 85, 134–140.

91. Venkatachalam, I.; Teo, J.; Balm, M.N.; Fisher, D.A.; Jureen, R.; Lin, R.T. Klebsiella pneumoniae carbapenemase-producing enterobacteria in hospital, Singapore. Emerg. Infect. Dis. 2012, 18, 1381.

92. Trimpert, J.; Eichhorn, I.; Vladimirova, D.; Haake, A.; Schink, A.K.; Klopfleisch, R.; Lübke-Becker, A. Elizabethkingia miricola infection in multiple anuran species. Transbound. Emerg. Dis. 2020, 68, 931–940.

93. Zainuri, N.; Ransangan, J.; Lal, T.; Jintoni, B.; Chung, V. Identification of Elizabethkingia meningoseptica from American bullfrog (Rana catesbeiana) farmed in Sabah, Malaysia using PCR method and future management of outbreak. Malays. J. Microbiol. 2013, 9, 13–23.

94. Tee, L.; Najiah, M. Antibiogram and heavy metal tolerance of bullfrog bacteria in Malaysia. Open Vet. J. 2011, 1, 39–45.

95. Tainchum, K.; Dupont, C.; Chareonviriyaphap, T.; Jumas-Bilak, E.; Bangs, M.J.; Manguin, S. Bacterial microbiome in wild-caught Anopheles mosquitoes in western Thailand. Front. Microbiol. 2020, 11, 965.

96. Surat, W.; Mhuantong, W.; Sangsrakru, D.; Chareonviriyaphap, T.; Arunyawat, U.; Kubera, A.; Sittivicharpinyo, T.; Siripan, O.; Pootakham, W. Gut Bacterial Diversity in Plasmodium-infected and Plasmodium-uninfected Anopheles minimus. Chiang Mai J. Sci. 2016, 43, 427–440.

97. Karl, H.; Lehmann, I.; Rehbein, H.; Schubring, R. Composition and quality attributes of conventionally and organically farmed Pangasius fillets (Pangasius hypophthalmus) on the German market. Int. J. Food Sci. Technol. 2010, 45, 56–66.

98. Thi, A.N.T.; Noseda, B.; Samapundo, S.; Nguyen, B.L.; Broekaert, K.; Rasschaert, G.; Heyndrickx, M.; Devlieghere, F. Microbial ecology of Vietnamese Tra fish (Pangasius hypophthalmus) fillets during processing. Int. J. Food Microbiol. 2013, 167, 144–152.

99. Kim, M.; Singh, D.; Lai-Hoe, A.; Go, R.; Rahim, R.A.; Ainuddin, A.; Chun, J.; Adams, J.M. Distinctive phyllosphere bacterial communities in tropical trees. Microb. Ecol. 2012, 63, 674–681.

100. Oh, Y.M.; Kim, M.; Lee-Cruz, L.; Lai-Hoe, A.; Go, R.; Ainuddin, N.; Rahim, R.A.; Shukor, N.; Adams, J.M. Distinctive bacterial communities in the rhizoplane of four tropical tree species. Microb. Ecol. 2012, 64, 1018–1027.

101. Kämpfer, P.; Matthews, H.; Glaeser, S.P.; 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, 2670–2675.

102. Chen, S.; Johnson, B.K.; Yu, T.; Nelson, B.N.; Walker, E.D. Elizabethkingia anophelis: Physiologic and transcriptomic responses to iron stress. Front. Microbiol. 2020, 11, 804.

103. Onyango, M.; Payne, A.; Stout, J.; Dieme, C.; Kuo, L.; Kramer, L.; Ciota, A. Potential for transmission of Elizabethkingia anophelis by Aedes albopictus and the role of microbial interactions in Zika virus competence. bioRxiv 2020, 702464.

104. Akhouayri, I.; Habtewold, T.; Christophides, G. Melanotic pathology and vertical transmission of the gut commensal Elizabethkingia meningoseptica in the major malaria vector Anopheles gambiae. PLoS ONE 2013, 8, e77619.
105. Rani, A.; Sharma, A.; Rajagopal, R.; Adak, T.; Bhatnagar, R.K. Bacterial diversity analysis of larvae and adult midgut microflora using culture-dependent and culture-independent methods in lab-reared and field-collected Anopheles stephensi-an Asian malarial vector. BMC Microbiol. 2009, 9, 96.
106. Ngwa, C.; Glöckner, V.; Abdelmohsen, U.R.; Scheuermayer, M.; Fischer, R.; Hentschel, U.; Pradel, G. 16S rRNA gene-based identification of Elizabethkingia meningoseptica (Flavobacteriales: Flavobacteriaceae) as a dominant midgut bacterium of the Asian malaria vector Anopheles stephensi (Dipteria: Culicidae) with antimicrobial activities. J. Med. Entomol. 2013, 50, 404–414.
107. Lindh, J.; Borg-Karlson, A.; Faye, I. Transstadial and horizontal transfer of bacteria within a colony of Anopheles gambiae (Diptera: Culicidae) and oviposition response to bacteria-containing water. Acta Trop. 2008, 107, 242–250.
108. Wang, Y.; Gilbreath, T.M., III; Kukutla, P.; Yan, G.; Xu, J. Dynamic gut microbiome across life history of the malaria mosquito Anopheles gambiae in Kenya. PLoS ONE 2011, 6, e24767.
109. Boissière, A.; Tchioffo, M.; Bachar, D.; Abate, L.; Marie, A.; Nsango, S.; Shahbazkia, H.; Awono-Ambene, P.; Levashina, E.; Christen, R.; et al. Midgut microbiota of the malaria mosquito vector Anopheles gambiae and interactions with Plasmodium falciparum infection. PLoS Pathog. 2012, 8, e1002742.
110. Wang, S.; Ghosh, A.K.; Bongio, N.; Stebbings, K.A.; Lampe, D.J.; Jacobs-Lorena, M. Fighting malaria with engineered symbiotic bacteria from vector mosquitoes. Proc. Natl. Acad. Sci. USA 2012, 109, 12734–12739.
111. Dong, Y.; Manfredini, F.; Dimopoulos, G. Implication of the mosquito midgut microbiota in the defense against malaria parasites. PLoS Pathog. 2009, 5, e1000423.