Emerging prevalence and clinical features of *Elizabethkingia meningoseptica* infection in Southwest China: A 9-year retrospective study and systematic review

Siyuan Ma, Yali Gong, Xiaoqiang Luo, Yuan Peng, Cheng Zhang, Xiaorong Zhang, Xiaohong Hu, Peng Tang, Zhiqiang Yuan, Gaoxing Luo and Haisheng Li

Supplementary Materials

Supplementary Table S1. Assignment of the collected 18 factors in the Logistic regression analysis of mortality

Risk factors	Variables	Evaluation
Gender	X1	Male=1, Female=0
Ages	X2	
Basic condition	X3	Unhealthy=1, Healthy=0
Operation	X4	Yes=1, No=0
Mechanical ventilation	X5	Yes=1, No=0
CVCs	X6	Yes=1, No=0
Numbers of coinfected pathogens	X7	0=0, 1=1, 2=2, >2=3
Diagnosis days	X8	
Nervous system disease	X9	Yes=1, No=0
Tumor	X10	Yes=1, No=0
Trauma	X11	Yes=1, No=0
Respiratory disease	X12	Yes=1, No=0
Fugal infection	X13	Yes=1, No=0
Abnormal WBC count	X14	Yes=1, No=0
Abnormal neutrophil percentage	X15	Yes=1, No=0
Abnormal Platelet	X16	Yes=1, No=0
Abnormal Lymphocyte percentage	X17	Yes=1, No=0
Abnormal Lymphocyte count	X18	Yes=1, No=0
Death	Y	Yes=1, No=0

Supplementary Table S2. Assignment of the collected 16 factors in the Logistic regression analysis of infection

Risk factors	Variables	Evaluation
Gender	X1	Male=1, Female=0
Ages	X2	
Operation	X3	Yes=1, No=0
Mechanical ventilation	X4	Yes=1, No=0
CVCs	X5	Yes=1, No=0
Numbers of coinfected pathogens	X6	0=0, 1=1, 2=2, >2=3
Nervous system disease	X7	Yes=1, No=0
Tumor	X8	Yes=1, No=0
Trauma	X9	Yes=1, No=0
Respiratory disease	X10	Yes=1, No=0
Fugal infection	X11	Yes=1, No=0
Exposure to β - lactamase inhibitors	X12	Yes=1, No=0
Exposure to Carbapenem	X13	Yes=1, No=0
Exposure to Tigecycline	X14	Yes=1, No=0
Exposure to Fluoroquinolone	X15	Yes=1, No=0
Exposure to antifungal drugs	X16	Yes=1, No=0
Infection	Y	Yes=1, No=0

Supplementary Table S3. The distribution of 150 pathogens co-existed with *E. meningoseptica*

Pathogens	No.	Percentage (%)
Gram positive bacteria	**29**	**19.3**
S. aureus	12	8.0
S.epidermidis	7	4.7
E. faecium	3	2.0
S.hominis	3	2.0
S. haemolyticus	1	0.7
E. faecalis	1	0.7
E. gallinarum	1	0.7
L. mesenteroides	1	0.7
Gram negative bacteria	**109**	**72.7**
K. pneumoniae	23	15.3
A. baumannii	21	14.0
P. aeruginosa	15	10.0
S.maltophilia	8	5.3
E. cloacae	7	4.7
E. coli	7	4.7
H.influenzae	4	2.7
A. loffei	4	2.7
E. aerogenes	2	1.3
M. morgani	2	1.3
S.marcescens	2	1.3
P. mirabilis	2	1.3
Others	12	8.0
Fungi	**12**	**8.0**
C. albicans	5	3.3
C. tropicalis	3	2.0
C. glabrata	2	1.3
C. parapsilosis	1	0.7
A. flavus	1	0.7

Supplementary Table S4. Quality assessment by JBI method

NO.	Author(year)	Was the sample frame appropriate to address the targer population?	Were study participants sampled in an appropriate way?	Was the sample size adequate?	Were the study subjects and the setting described in detail?	Was the data analysis conducted with sufficient coverage of the identified sample?	Were valid methods used for the identification of the condition?	Was the condition measaured in a standard, reliable way for all participants?	Was the appropriate statistical analysis?	Was the response rate adequate, and if not,was the low response rate managed appropriately?	Include
1	Lin, Y.T., et al.(2009)[14]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
2	Hsu, M.S., et al. (2011)[15]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
3	Issack, M.I. , et al. (2011)[23]*	Yes	Yes	No	Yes	No	No	No	No	Yes	No
4	Pereira, G.H., et al.(2013)[24]	Yes	Yes	No	Yes	Yes	Yes	Yes	No	Yes	Yes
5	Ratnamani, M., et al. (2013)[19]	Yes	Yes	No	Yes	Yes	Yes	Yes	No	Yes	Yes
6	Chang, Y.C., et al.(2014)[16]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
7	Ann, S.Y., et al.(2015)[11]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
8	Moore, L.S.P., et al.(2016)[25]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes
9	Rastogi, N., et al.(2016)[20]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes
10	Huang, Y.C., et al. (2017)[8]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
11	Lin, J.N., et al.(2018)[17]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12	Chan, J.C., et al.(2019)[18]	Yes	Yes	No	Yes	Yes	Yes	Yes	No	Yes	Yes
13	Pindi, G., et al.(2019)[21]	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
14	Umair, A. , et al.(2021)[26]	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes
15	Erinmez, M., A. , et al. (2021)[9]	Yes	Yes	No	Yes	Yes	Yes	Yes	No	Yes	Yes

16	Saygılı, N., et al.(2021)[22]	Yes	Yes	No	Yes	Yes	Yes	Yes	No	Yes	Yes

*Excluded studies with a JBI score of less than 7

Supplementary Table S5. Infection features and clinical treatment of included studies reporting E.meningoseptica infection

Author(year)	Identification Methods	Pathogen sources	Antimicrobial susceptibility(sensitivity%)	Treatment
Lin, Y.T., et al.(2009)[14]	VITEK 2 system	Blood (100%)	Levofloxacin (63%), ciprofloxacin (66%), tigecycline(84%), piperacillin-tazobactam (91%), and trimethoprim-sulfamethoxazole (97%). other b-lactam antibiotics(0), colistin(0), vancomycin(0), and aminoglycosides(0).	Not reported
Hsu, M.S., et al. (2011)[15]	VITEK GNI system and/or Phoenix system	Blood(77.8%), Respiratory tract(9.4%), soft tissue and catheter (6.1%)	Piperacillin-tazobactam(79%), fluoroquinolones had low MICs, all anti-pseudomonas cephalosporins, all carbapenems, and aminoglycosides had high MICs	Mono-therapy: Anti-pseudomonal penicillins(28.8%),Fluoroquinolones (25.4%), Anti-pseudomonal Cephalosporins(8.5%), Carbapenems(5.9%), Aminoglycosides (1.7%) Combination therapy:Anti pseudomonal penicillins with fluoroquinolone(59.3%), Carbapenem with aminoglycoside(1.7%)
Issack, M.I. , et al. (2011)[23]	Positive cytochrome oxidase reaction and API 20NE System	Cerebrospinal fluid (100%)	All were susceptible to piperacillin, piperacillin/tazobactam, vancomycin and rifampicin. All were resistant to cefalexin, ceftazidime, cefotaxime, ceftriaxone, gentamicin, amikacin, tetracycline, colistin and meropenem. They had intermediate susceptibility to ciprofloxacin and amoxicillin/clavulanic acid.	All were intravenous piperacillin (100 mg/kg every 8 hours) and oral rifampicin (10 mg/kg every 12 hours)
Pereira, G.H., et al.(2013)[24]	VITEK system , Classical phenotypic	Blood(66.7%), respiratory tract(33.3%)	Not reported	Vancomycin(4/9), vancomycin combined with rifampin or ciprofloxacin(2/9), trimethoprim/sulfamethoxazole and teicoplanin(1/9),none(2/9)

	methods and API 20 NE System			
Ratnamani, M., et al. (2013)[19]	VITEK 2 Compact automated system	Blood(75%), respiratory tract(25%)	Not reported	Piperacillin tazobactam(6/8),Piperacillin tazobactam with Ciprofloxacin(2/8)
Chang, Y.C., et al.(2014)[16]	16S rRNA gene sequencing	Blood (48.7%), sputum (41.0%), urine(5.1%), CVC(2.6%), wound(2.6%)	Minocycline(100%), trimethoprim/sulfamethoxazole(74.4%), ciprofloxacin(35.9%), and cefepime(5.1%) with 100% susceptibility	Not reported
Ann, S.Y., et al.(2015)[11]	VITEK2 system	Sputum (23,76.7%), Catheter (16.7%), Blood (3.3%), Urine (3.3%)	Minocycline (90%) ,levofloxacin (66.7%) , ciprofloxacin (60%),Piperacillin/tazobactam(20%)	Not reported
Moore, L.S.P., et al.(2016)[25]	API and Biotyper MALDI-TOF mass spectroscopy	Respiratory tract(73.3%), blood(3.3%), unknown(23.3%)	Susceptible to piperacillin-tazobactam and trimethoprim-sulfamethoxazole	Trimethoprim/sulfamethoxazole(5/30),tigecycline(6/30),None(19/30)
Rastogi, N., et al.(2016)[20]	Vitek 2 system	Bronchoalveolar lavage fluid (70%) , blood (22%),	Tigecycline(100%), Piperacillin–tazobactam (95.23%) ,Trimethoprim–sulphamethoxazole (14.3%),Ciprofloxacin (19.1%)	Not reported

		cerebrospinal fluid (4%)		
Huang, Y.C., et al. (2017)[8]	VITEK 2 Compact automated system,MALDI-TOF-MS.	Blood (100%)	Minocycline (100%), Piperacillin/tazobatam (95.7%), sulfamethoxazole/trimethoprim (97.8%), tigecycline (90.3%) , ciprofloxacin (34.4%). Cefepime (21.5%), vancomycin(0)	Not reported
Lin, J.N., et al.(2018)[17]	The API/ID32 Phenotyping Kits and VITEK MS System. The species of Elizabethkingia was reidentified using 16S rRNA gene sequencing.	Blood(70%), Cerebrospinal fluid(10%), respiratory tract(5%), catheter(5%), bile(5%), urine(5%)	Minocycline (60%), levofloxacin (30%), piperacillin (15%), and tigecycline (15%)	β-lactams(44.6%), β-lactam/lactamase inhibitors(21.7%),Ciprofloxacin(10.9%), Levofloxacin(26.1%)
Chan, J.C., et al.(2019)[18]	VITEK mass spectrometry system or	Blood (100%), Cerebrospinal fluid (30.8%).	Piperacillin/tazobactam(100%), trimethoprim/sulfamethoxazole (78.6 %), ciprofloxacin(33.3%); moxifloxacin(87.5%), levofloxacin(87.5%)	Piperacillin/tazobactam with trimethoprim/sulfamethoxazole (6/13), piperacillin/tazobactam with a fluroquinolone (4/13). minocycline, clindamycin and rifampicin.

	MALDI-TOF-MS.			
Pindi, G., et al.(2019)[21]	VITEK2 system	Respiratory tract(87.5%), blood (6.25%), CVC(3.12%), bile(3.12%)	Minocycline (100%), cotrimoxazole (65.6 %), Levofloxacin (53.12%), cefoperazone-sulbactum(46.8%), ciprofloxacin(43.75%)	Not reported
Umair, A. , et al.(2021)[26]	VITEK 2 system	Blood(61.5%), Cerebrospinal fluid(15.4%), Respiratory tract(15.4%), urine(7.7%)	Most Susceptible to trimethoprim-sulfamethoxazole,levofloxacin, ciprofloxacin and minocycline	Quinolone(5/13), cotrimoxazole(4/13), minocycline(4/13)
Erinmez, M., A. , et al. (2021)[9]	MALDI-TOF MS	Tracheal aspirates (50%), blood (31%), catheter (12%) , cerebrospinal fluid(6%)	levofloxacin(100%), ciprofloxacin(100%), vancomycin(83.3%), trimethoprim-sulfamethoxazole(50%)	Colistin(4/6), Meropenem(6/6), vancomycin(4/6), amikacin(4/6), clarithromycin(2/6), linezolid(1/6), amphotercin B(1/6), Teicoplanin(1/6)
Saygılı, N., et al.(2021)[22]	VITEK 2 Compact automated system,MALDI-TOF-MS.	Blood(47.1%), endotracheal aspirate(35.3%), cerebrospinal fluid(11.8%), wound swab(5.9%)	Cefoperazone/sulbactam(35.3%), ciprofloxacin(70.6%) , trimethoprim/sulfamethoxazole(58.3%) ,Piperacillintazobactam(8.3%)	Not reported