

**Genomic Features, Comparative Genomics, and Antimicrobial  
Susceptibility Patterns of *Elizabethkingia brunniana***

Jiun-Nong Lin<sup>1,2,3</sup>, Chung-Hsu Lai<sup>1,2</sup>, Chih-Hui Yang<sup>4</sup>, Yi-Han Huang<sup>1</sup> & Hsi-Hsun  
Lin<sup>5,6</sup>

<sup>1</sup>School of Medicine, College of Medicine, I-Shou University, Kaohsiung, Taiwan

<sup>2</sup>Division of Infectious Diseases, Department of Internal Medicine, E-Da Hospital, I-Shou University, Kaohsiung, Taiwan

<sup>3</sup>Department of Critical Care Medicine, E-Da Hospital, I-Shou University, Kaohsiung, Taiwan

<sup>4</sup>Department of Biological Science and Technology, Meiho University, Pingtung, Taiwan

<sup>5</sup>General Clinical Research Center, Department of Medical Research, Taipei Veterans General Hospital, Taipei, Taiwan

<sup>6</sup>School of Medicine, National Yang-Ming University, Taipei, Taiwan

\*Corresponding author: Jiun-Nong Lin, MD, PhD

Division of Infectious Diseases, Department of Internal Medicine, E-Da Hospital, I-Shou University, Kaohsiung, Taiwan

No. 1, Yida Road, Jiaosu Village, Yanchao District, Kaohsiung, Taiwan

E-mail: jinoli@kmu.edu.tw

Tel: +886-7-6150011-251469

Fax: +886-7-615-0928

**Table S1.** Species, strains, and accession numbers of 16S rRNA used in this study

<b>Species</b>	<b>Strain</b>	<b>GenBank accession number</b>
<i>Elizabethkingia meningoseptica</i>	ATCC 13253	AJ704540
<i>Elizabethkingia anophelis</i>	R26	EF426425
<i>Elizabethkingia anophelis</i>	EM361-97	NZ_KV757122
<i>Elizabethkingia miricola</i>	W3-B1	AB071953
<i>Elizabethkingia bruuniana</i>	G0146	MH789419
<i>Elizabethkingia bruuniana</i>	EM798-26	CP023746
<i>Elizabethkingia ursingii</i>	G4122	MH789420
<i>Elizabethkingia occulta</i>	G4070	MH789418
<i>Chryseobacterium gleum</i>	NBRC 15054	AB680759
<i>Chryseobacterium indologenes</i>	NBRC 14944	AB517708
<i>Escherichia coli</i>	NBRC 102203	AB681728
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i>	LT2	AE006468
<i>Pseudomonas aeruginosa</i>	DSM 50071	HE978271
<i>Klebsiella pneumoniae</i>	DSM 30104	AJ233420
<i>Vibrio cholerae</i>	ATCC 14035	EF032498
<i>Proteus hauseri</i> ( <i>Proteus vulgaris</i> )	NCTC 4175	DQ885262
<i>Aeromonas caviae</i>	ATCC 15467	X60409
<i>Stenotrophomonas maltophilia</i>	CCUG 41684	GU945534
<i>Acinetobacter calcoaceticus</i>	ATCC 23055	HE651903
<i>Acinetobacter baumannii</i>	ATCC 19606	HE651907

<i>Enterobacter cloacae</i>	DSM 30054	HE978272
-----------------------------	-----------	----------

**Table S2.** Information of whole-genome sequences used in this study

<b>Organism/Name</b>	<b>Strain</b>	<b>BioSample</b>	<b>BioProject</b>	<b>Assembly</b>	<b>Size (Mb)</b>	<b>GC%</b>	<b>Genes</b>	<b>Proteins</b>	<b>Level</b>
<i>Elizabethkingia miricola</i> ( <i>Elizabethkingia bruuniana</i> )	BM10	SAMN03398457	PRJNA277897	GCA_000955665.1	4.24252	35.7	3888	3728	Complete Genome
<i>Elizabethkingia miricola</i> ( <i>Elizabethkingia bruuniana</i> )	EM798-26	SAMN07733282	PRJNA412960	GCA_002557775.1	4.39301	35.7	4029	3877	Complete Genome
<i>Elizabethkingia miricola</i> ( <i>Elizabethkingia bruuniana</i> )	ATCC 33958	SAMN02989770	PRJNA259681	GCA_000769445.1	4.57811	35.9	4308	4160	Contig
<i>Elizabethkingia miricola</i>	EM_CHUV	SAMN03998138	PRJNA293155	GCA_001483145.1	4.28605	36.0726	3902	3806	Contig
<i>Elizabethkingia miricola</i>	GTC_862 (type strain)	SAMD00016624	PRJNA301708	GCA_001675285.1	4.29381	35.8	4003	3899	Contig
<i>Elizabethkingia miricola</i>	CSID_3000517120	SAMN05254999	PRJNA301708	GCA_002023335.1	4.4291	35.9	4042	3947	Contig
<i>Elizabethkingia miricola</i>	G4121	SAMN05281843	PRJNA301708	GCA_002023475.1	4.42197	35.9	4104	4010	Contig
<i>Elizabethkingia miricola</i>	CSID_3000516464	SAMN05255998	PRJNA301708	GCA_002023515.1	4.18805	35.8	3853	3765	Contig
<i>Elizabethkingia miricola</i>	CSID_3000516998	SAMN05256599	PRJNA301708	GCA_002023575.1	4.36583	36	4073	3967	Contig
<i>Elizabethkingia miricola</i>	G4074 (type strain)	SAMN05277881	PRJNA301708	GCA_002023685.1	4.27041	35.9	3923	3828	Contig
<i>Elizabethkingia miricola</i>	FL160902	SAMN07139315	PRJNA387126	GCA_002738605.1	4.21902	35.7	-	-	Contig
<i>Elizabethkingia miricola</i>	KCTC 12492	SAMEA4051575	PRJEB13258	GCA_900092045.1	4.29997	35.8	4005	3897	Contig
<i>Elizabethkingia miricola</i>	LDVH-337.01	SAMEA4026803	PRJEB14302	GCA_900157035.1	4.15085	35.9	3816	3676	Contig
<i>Elizabethkingia miricola</i>	CIP111047	SAMEA50780668	PRJEB14302	GCA_900157015.1	4.45145	35.9	4197	4098	Scaffold

<i>Elizabethkingia</i> genomsp. 3 ( <i>Elizabethkingia bruuniana</i> )	G0146	SAMN05277827	PRJNA326741	GCA_002024805.1	4.43352	35.9	4127	4007	Complete Genome
<i>Elizabethkingia</i> genomsp. 3 ( <i>Elizabethkingia bruuniana</i> )	G0146 (type strain)	SAMN05277827	PRJNA301708	GCA_002023205.1	4.38585	35.8	4086	3981	Contig
<i>Elizabethkingia</i> genomsp. 3 ( <i>Elizabethkingia bruuniana</i> )	CSID_3000516589	SAMN05256516	PRJNA301708	GCA_002023545.1	4.21084	35.8	3838	3750	Contig
<i>Elizabethkingia</i> genomsp. 3 ( <i>Elizabethkingia bruuniana</i> )	CSID_3015183685	SAMN05277593	PRJNA301708	GCA_002023765.1	4.3224	35.8	3973	3882	Contig
<i>Elizabethkingia</i> genomsp. 3 ( <i>Elizabethkingia bruuniana</i> )	G0153	SAMN05277862	PRJNA301708	GCA_002023775.1	4.37908	35.8	4073	3965	Contig
<i>Elizabethkingia</i> genomsp. 3 ( <i>Elizabethkingia bruuniana</i> )	G4075	SAMN04254558	PRJNA301708	GCA_001521735.1	4.22977	35.8	3914	3817	Scaffold
<i>Elizabethkingia anophelis</i>	R26 (type strain)	SAMN02470677	PRJNA178189	GCA_000331815.1	4.03272	35.40	3746	3643	Complete Genome
<i>Elizabethkingia meningoseptica</i>	KC1913 (type strain)	SAMN04254555	PRJNA301708	GCA_001521755.1	3.85364	36.40	3462	3383	Scaffold
<i>Elizabethkingia</i> genomsp. 4 ( <i>Elizabethkingia ursingii</i> )	G4122 (type strain)	SAMN04254563	PRJNA301708	GCA_001521765.1	4.3397	35.60	3984	3859	Scaffold
<i>Elizabethkingia</i> genomsp. 4 ( <i>Elizabethkingia occulta</i> )	G4070 (type strain)	SAMN05277871	PRJNA301708	GCA_002023715.1	4.15401	35.60	3751	3645	Contig

**Table S3.** Potential virulence factors predicted using the virulence factor database (VFDB)

Gene id	Identity	E value	Subject id	Protein	Gene description
798_26GL000885	41.32	6.00E-94	VFG0036	LPS	bplC - lipopolysaccharide biosynthesis protein
798_26GL000118	45.83	4.00E-68	VFG0077	ClpP	clpP - ATP-dependent Clp protease proteolytic subunit
798_26GL000516	35.49	4.00E-156	VFG0079	ClpC	clpC - endopeptidase Clp ATP-binding chain C
798_26GL001947	32.82	2.00E-84	VFG0116	Alginate	algB - two-component response regulator AlgB
798_26GL003849	31.4	1.00E-18	VFG0119	Alginate	algR - alginate biosynthesis regulatory protein AlgR
798_26GL002789	30.79	1.00E-56	VFG0122	Alginate	algD - GDP-mannose 6-dehydrogenase AlgD
798_26GL001525	33.16	1.00E-65	VFG0130	Alginate	algI - alginate o-acetyltransferase AlgI
798_26GL003331	30.67	1.00E-28	VFG0246	LOS	lgtF - beta-1,4-glucosyltransferase
798_26GL003803	55.14	2.00E-45	VFG0269	Urease	ureA - urease alpha subunit (ureA) (urea amidohydrolase)
798_26GL003806	32.81	2.00E-27	VFG0272	Urease	ureE - urease accessory protein (ureE)
798_26GL003808	64.14	1.00E-104	VFG0274	Urease	ureG - urease accessory protein (ureG)
798_26GL002571	34.4	2.00E-70	VFG0313	LPS	gluP - glucose/galactose transporter (gluP)
798_26GL002401	37.58	5.00E-33	VFG0320	LPS	kdtB - lipopolysaccharide core biosynthesis protein (kdtB)
798_26GL004066	31.69	3.00E-48	VFG0344	HitABC	hitC - iron(III) ABC transporter, ATP-binding protein
798_26GL001922	44.52	6.00E-160	VFG0431	Vi antigen	tviB - Vi polysaccharide biosynthesis protein, UDP-glucose/GDP-mannose dehydrogenase
798_26GL001231	32.12	2.00E-21	VFG0575	MgtBC	mgtC - Mg <sup>2+</sup> transport protein
798_26GL003027	36.93	9.00E-167	VFG0619	Aerobactin	iutA - receptor-like protein iutA [Shigella flexneri (serotype 2a) 301]
798_26GL001006	33.66	1.00E-76	VFG0670	LPS	gtrB - bactoprenol glucosyl transferase
798_26GL002032	36.15	4.00E-62	VFG0674	SMase	smcL - sphingomyelinase-c

798_26GL000335	32.18	2.00E-52	VFG0679	Capsule	dep/capD - $\gamma$ -glutamyltranspeptidase
798_26GL003341	30.89	9.00E-25	VFG0869	Dispersin	aatC - AatC ATB binding protein of ABC transporter
798_26GL000890	31.07	6.00E-24	VFG0869	Dispersin	aatC - AatC ATB binding protein of ABC transporter
798_26GL002348	36.26	1.00E-36	VFG0869	Dispersin	aatC - AatC ATB binding protein of ABC transporter
798_26GL002829	30	5.00E-21	VFG0872	Type 1 fimbriae	fimE - Type 1 fimbriae Regulatory protein fimE
798_26GL001929	32.34	9.00E-67	VFG0916	Chu	chuS - Putative heme/hemoglobin transport protein
798_26GL001932	34.3	1.00E-59	VFG0922	Chu	chuU - Putative permease of iron compound ABC transport system
798_26GL000108	30.38	5.00E-21	VFG0934	Enterobactin	entA - 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
798_26GL003073	30.68	3.00E-35	VFG0934	Enterobactin	entA - 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
798_26GL001943	31.37	2.00E-32	VFG1206	FbpABC	fbpC - iron(III) ABC transporter, ATP-binding protein
798_26GL000094	32.56	2.00E-92	VFG1214	Type IV pili	pilR - two-component response regulator PilR
798_26GL001361	37.93	2.00E-95	VFG1214	Type IV pili	pilR - two-component response regulator PilR
798_26GL002938	44.35	2.00E-67	VFG1248	Flagella	fleQ - transcriptional regulator FleQ
798_26GL002311	47.31	3.00E-113	VFG1300	Capsule	cap8D - capsular polysaccharide synthesis enzyme Cap8D
798_26GL002308	57.18	4.00E-152	VFG1301	Capsule	cap8E - capsular polysaccharide synthesis enzyme Cap8E
798_26GL003580	30.68	2.00E-10	VFG1310	Capsule	cap8N - capsular polysaccharide synthesis enzyme Cap8N
798_26GL002302	31.86	5.00E-35	VFG1343	Capsule	cpsN - glycosyl transferase CpsN(V)
798_26GL003658	36.32	1.00E-34	VFG1344	Capsule	cpsM - polysaccharide biosynthesis protein CpsM(V)
798_26GL000190	31.98	8.00E-38	VFG1390	MprAB	mprA - hypothetical protein Rv0981
798_26GL003363	32.44	2.00E-53	VFG1390	MprAB	mprA - hypothetical protein Rv0981
798_26GL001772	33.18	8.00E-52	VFG1390	MprAB	mprA - hypothetical protein Rv0981

798_26GL001370	34.22	3.00E-42	VFG1390	MprAB	mprA - hypothetical protein Rv0981
798_26GL001431	35.34	6.00E-60	VFG1390	MprAB	mprA - hypothetical protein Rv0981
798_26GL000086	31.4	2.00E-21	VFG1395	MgtC	mgtC - mgtC
798_26GL001791	36.16	6.00E-48	VFG1395	MgtC	mgtC - mgtC
798_26GL001174	33.74	5.00E-29	VFG1404	AhpC	ahpC - ahpC
798_26GL001165	35.5	6.00E-67	VFG1405	SigA	sigA - sigA
798_26GL003523	50.47	9.00E-38	VFG1416	PanC/PanD	panD - panD
798_26GL002277	40.21	4.00E-47	VFG1417	PanC/PanD	panC - panC
798_26GL001915	30	2.00E-42	VFG1444	AslA	aslA - putative arylsulfatase
798_26GL001526	41.26	2.00E-36	VFG1864	Mip	mip - macrophage infectivity potentiator (Mip)
798_26GL000580	39.18	7.00E-49	VFG1867	SodB	sodB - superoxide dismutase
798_26GL001218	39.59	2.00E-55	VFG1867	SodB	sodB - superoxide dismutase
798_26GL002823	43.88	1.00E-61	VFG1867	SodB	sodB - superoxide dismutase
798_26GL001508	39.48	2.00E-83	VFG1971	Capsule	kpsF - KpsF protein
798_26GL001317	32.14	4.00E-18	VFG2008	Flagella	motB - flagellar motor protein MotB
798_26GL003326	30.6	7.00E-28	VFG2224	LPS	wbkA - mannosyltransferase
798_26GL000886	40.84	1.00E-103	VFG2361	O-antigen	galE - UDP-glucose 4-epimerase
798_26GL002328	45.62	7.00E-115	VFG2364	O-antigen	fcl - GDP-flucose synthetase
798_26GL002327	58.61	5.00E-169	VFG2365	O-antigen	gmd - GDP-mannose 4,6-dehydratase



**Table S4.** Potential antibiotic resistance genes identified using the Antibiotic Resistance Genes Database (ARDB) BLAST Server

<b>Gene id</b>	<b>Identity</b>	<b>E value</b>	<b>Subject id</b>	<b>Antibiotic Resistance</b>	<b>Description</b>
798_26GL001208	30	6.00E-39	ardb_2322	Bacitracin	ABC transporter system, bacitracin efflux pump.
798_26GL001461	30	3.00E-24	ardb_2858	Bacitracin	--
798_26GL001650	30.13	6.00E-37	ardb_115	Vancomycin	VanE type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-serine.
798_26GL003067	30.46	3.00E-53	ardb_2749	Vancomycin	VanG type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-serine.
798_26GL002835	30.51	2.00E-33	ardb_1732	Vancomycin, teicoplanin	VanA type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-lactate.
798_26GL000126	30.95	3.00E-34	ardb_2452	Sulfonamide	Sulfonamide-resistant dihydropteroate synthase, which cannot be inhibited by sulfonamide.
798_26GL000603	31	9.00E-36	ardb_2470	Vancomycin, teicoplanin	VanA type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-lactate.
798_26GL004049	31.09	9.00E-62	ardb_2640	Macrolide	Resistance-nodulation-cell division transporter system. Multidrug resistance efflux pump. Macrolide-specific efflux system.
798_26GL000821	31.3	2.00E-62	ardb_1951	Chloramphenicol	Major facilitator superfamily transporter,

					chloramphenicol efflux pump.
798_26GL002854	31.36	1.00E-06	ardb_2497	Vancomycin, teicoplanin	VanA type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-lactate.
798_26GL002400	31.76	3.00E-51	ardb_2028	Vancomycin	VanG type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-serine.
798_26GL003582	32	2.00E-27	ardb_654	Vancomycin	VanG type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-serine.
798_26GL000111	32.01	2.00E-53	ardb_1853	Bacitracin	ABC transporter system, bacitracin efflux pump.
798_26GL001431	32.63	2.00E-41	ardb_115	Vancomycin	VanE type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine--D-serine.
798_26GL001118	32.82	7.00E-40	ardb_1739	Kasugamycin	Specifically dimethylates two adjacent adenosines in the loop of a conserved hairpin near the 3'-end of 16S rRNA in the 30S particle. Its inactivation leads to kasugamycin resistance.
798_26GL003751	32.98	5.00E-21	ardb_2747	Cephalosporin	Class C beta-lactamase. This enzyme breaks the beta-lactam antibiotic ring open and deactivates the molecule's antibacterial properties.
798_26GL000656	34.05	2.00E-56	ardb_2990	Bacitracin	ABC transporter system, bacitracin efflux pump.

798_26GL002404	34.15	3.00E-40	ardb_13	Trimethoprim	Group A drug-insensitive dihydrofolate reductase, which cannot be inhibited by trimethoprim.
798_26GL000620	34.26	1.00E-16	ardb_1205	Multiple antimicrobials	Small Multidrug Resistance (SMR) protein family. Multidrug resistance efflux pump, which consists of two proteins.
798_26GL001823	34.98	1.00E-49	ardb_998	Penicillin	Class A beta-lactamase. This enzyme breaks the beta-lactam antibiotic ring open and deactivates the molecule's antibacterial properties.
798_26GL001370	35.14	1.00E-39	ardb_1550	Vancomycin	VanB type vancomycin resistance operon genes, which can synthesize peptidoglycan with modified C-terminal D-Ala-D-Ala to D-alanine-D-lactate.
798_26GL001069	35.47	3.00E-82	ardb_1016	Tetracycline	Major facilitator superfamily transporter, tetracycline efflux pump.
798_26GL001517	36.11	1.00E-15	ardb_1267	Multiple antimicrobials	Small Multidrug Resistance (SMR) protein family. Multidrug resistance efflux pump, which consists of two proteins.
798_26GL000702	36.21	2.00E-72	ardb_916	Cephalosporin, penicillin	Class A beta-lactamase. This enzyme breaks the beta-lactam antibiotic ring open and deactivates the molecule's antibacterial properties.
798_26GL000324	38.98	1.00E-69	ardb_916	Cephalosporin, penicillin	Class A beta-lactamase. This enzyme breaks the beta-lactam antibiotic ring open and deactivates the molecule's antibacterial properties.

798_26GL001121	39.43	2.00E-67	ardb_2724	Bacitracin	Undecaprenyl pyrophosphate phosphatase, which consists in the sequestration of undecaprenyl pyrophosphate.
798_26GL000331	40	5.00E-29	ardb_1787	Aminoglycoside	Multidrug resistance efflux pump.
798_26GL000052	55.35	8.00E-160	ardb_2144	Tetracycline	NADP-requiring oxidoreductase, an enzyme that can modify tetracycline. Mechanism detail unknown.
798_26GL002831	63.41	3.00E-108	ardb_2771	Chloramphenicol	Group B chloramphenicol acetyltransferase, which can inactivate chloramphenicol. Also referred to as xenobiotic acetyltransferase.