

Supplementary Table S1. Number of strains isolated from different organs of bats and the positive rate

Items	Lung	Liver	Spleen	Total
Number of strains	0	3	2	5
Positive rate (%)	0	4.69	3.13	2.60

Supplementary Table S2. Details pertaining to the five isolates producing acid from carbohydrates

Details	BF33.1	BF33.2	BF38	BF43	BF45
Glycerol	+	+	+	+	+
L-arabinose	-	+	-	-	+
D-ribose	+	+	+	+	+
D-glucose	+	+	+	+	+
D-fructose	+	+	+	+	+
D-mannose	+	+	+	+	+
Mannitol	+	+	+	-	+
Sorbitol	+	+	+	+	+
Methyl- α D-glucopyranoside	+	+	+	+	+
N-acetylglucosamine	+	+	+	+	+
Amygdalin	+	+	+	+	+
Arbutin	+	+	+	+	+
Salicin	+	+	+	+	+
D-cellobiose	+	+	+	+	+
D-maltose	+	+	+	+	+
D-trehalose	+	+	+	+	+
Starch	+	+	+	+	+
D-gentiobiose	+	+	+	+	+

Supplementary Table S3. General characteristics of the genomes of the five isolates

Characteristics	BF33.1	BF33.2	BF38	BF43	BF45
Genome size (bp)	2,964,643	3,044,263	3,036,912	2,687,751	2,745,235
GC content (%)	32.54	32.65	32.66	32.88	32.75
Gene number	2,356	2,925	2,928	2,685	2,693
Genes of genome (%)	66.48	90.71	90.55	90.12	90.34

Supplementary Table S4. Virulence factors observed in the five strains isolated from bats

Virulence Factors	Gene	Product	Function	BF33.1	BF33.2	BF38	BF43	BF45
(p)ppGpp synthesis and hydrolysis	relA	GTP pyrophosphokinase	Regulation	+	+	+	+	+
ABC transporter	fbpC	iron-uptake permease ATP-binding protein	Iron uptake	+	+	+	+	+
ABC transporter for dispersin	aatC	ABC transporter ATP-binding protein AatC	Adherence	+	+	+	+	+
Accessory secretion factor	secA2	preprotein translocase subunit SecA	Secretion system	+	+	+	+	+
Ace	ace	collagen adhesin protein	Adherence	-	+	+	-	-
Achromobactin	cbrD	ABC transporter	Iron uptake	-	+	+	-	-
Achromobactin biosynthesis and transport	cbrD	achromobactin transport ATP-binding protein CbrD	Iron uptake	-	+	+	-	-
AdsA	adaA	Adenosine synthase A	Protease	-	+	+	-	-
AgrA/AgrC	agrA	hypothetical protein	Adherence	-	+	+	+	+
Anguibactin	fatD	ferric anguibactin transport protein	Iron uptake	-	+	+	+	+
Auto	aut	autolysin	Invasion	+	+	+	+	+
Autoinducer-2	luxS	S-ribosylhomocysteinase	Regulation	-	+	+	-	-
Autolysin (GW protein)	aut	N-acetylmuramoyl-L-alanine amidase family protein	Invasion	-	+	+	-	+
Bcp pili	srtD	Sortase	Adherence	-	+	-	-	-
Bee (biofilm enhancer in enterococci)	srt1	Srt1	Adherence	+	+	+	+	+
BopD	BopD	LacI family transcriptional regulator	Biofilm formation	+	+	+	+	+
Capsular polysaccharide	wbfV/wcvB	Predicted UDP-glucose 6-dehydrogenase	Regulation	+	-	-	-	+
Capsule	Cap, oppF	Transporter biosynthesis protein; oligopeptide ABC transporter, permease component	Adherence	+	+	+	+	+
ClpC	clpC	Endopeptidase Clp ATP-binding chain C	Stress protein	+	+	+	+	+
ClpE	clpE	ATP-dependent protease	Stress protein	-	+	+	+	+
ClpP	clpP	ATP-dependent Clp protease proteolytic subunit	Stress protein	+	+	+	+	+
Colibactin	clbD	Putative 3-hydroxyacyl-CoA dehydrogenase	Toxin	+	+	+	+	+
Copper exporter	ctpV	Cation-transporting ATPase V	Iron uptake	-	+	+	+	+
Cytolysin	cyLR2	Cytolysin regulator R2	Toxin	+	+	+	-	-
D-alanine-polyphosphoribitol ligase	dltA	Putative D-alanine-activating enzyme	Toxin	+	+	+	+	+
Ebp pili	srtC	Sortase	Adherence	+	+	+	-	+
EfaA	efaA	Endocarditis specific antigen	Adherence	+	+	+	+	+
EF-Tu	tuf	Elongation factor Tu	Adherence	-	+	+	+	+
Exopolysaccharide	mrsA/glmM	Phosphoglucosamine mutase		+	+	+	+	+
FbpABC	fbpC	Iron III ABC transporter, ATP-binding protein	Adherence	+	+	+	+	+
Ferrous iron transport	feoA	Ferrous iron transporter A	Iron uptake	-	+	+	+	-
Fibronectin-binding proteins	pavA	Adherence and virulence protein A	Adherence	+	+	+	+	+
Flagella	flgG;fliP	Flagellar biosynthesis protein	Adherence, Invasion	+	+	+	-	+
Glutamine synthesis	glnA1	Glutamine synthetase	Toxin	+	+	+	+	+
GroEL	groEL	Chaperonin GroEL		+	+	+	+	+

Continued

Virulence Factors	Gene	Product	Function	BF33.1	BF33.2	BF38	BF43	BF45
Hcp secretion island-1 encoded type VI secretion system (H-T6SS)	clpV1	Putative ClpA/B-type chaperone	Stress protein	-	+	+	+	+
Heme biosynthesis	hemG	Protoporphyrinogen oxidase	Toxin	-	-	-	+	+
Hemolysin	hlyA	Hemolysin A	Toxin	+	+	+	+	+
Hemolysin III	hlyIII	Hemolysin III	Toxin	+	+	+	+	+
HexNAc	flg; flh; Fli	Flagellar protein	Adherence; Invasion	+	+	+	+	+
Histone-like protein (Hlp)/ laminin-binding protein (LBP)	hlp	Histone-like protein	Adherence	+	+	+	+	+
Hyaluronic acid capsule	hasC	UDP-glucose pyrophosphorylase	Antiphagocytosis	-	+	-	+	-
IlpA	IlpA	Immunogenic lipoprotein A	Adherence	+	+	+	+	+
Laminin-binding protein	lmb	Metal binding lipoprotein	Adherence	-	+	+	+	+
Lipoate protein ligase A1	lplA1	Putative lipoate protein ligase A	Intracellular growth	+	+	+	+	+
Lipoprotein diacylglycerol transferase	lgt	Prolipoprotein diacylglycerol transferase	Adherence	+	+	+	+	+
Lipoprotein-specific signal peptidase II	lspA	Putative signal peptidase II	Adherence	+	+	+	+	+
LisR/LisK	lisR	Two-component response regulator	Regulation	+	+	+	+	+
Listeria adhesion protein	lap	Hypothetical protein	Adherence	+	+	+	+	+
LOS	orfM	Putative deoxyribonucleotide triphosphate pyrophosphatase	Adherence	+	+	+	+	+
LPS	gtrB; Fbphi; fabZ	Bactoprenol glucosyl transferase	Adherence	+	+	+	+	+
Lysine synthesis	lysA	Diaminopimelate decarboxylase		-	+	+	+	+
Mg ²⁺ transport	mgtB	Hypothetical protein	Magnesium uptake	-	+	+	+	+
MOMP	CT396	Molecular chaperone DnaK	Adherence	+	+	+	+	+
MprA/B	mprA	DNA-binding response regulator	Regulation	+	+	+	+	+
ND	fleQ/flrC	FleQ protein	Adherence	-	+	+	-	-
Nucleoside diphosphate kinase	ndk	Nucleoside diphosphate kinase	Protease	-	+	+	+	+
Oligopeptide-binding protein	oppA	Hypothetical protein	Adherence	+	+	+	+	+
PblA	pblA	PblA		-	-	-	+	-
PdgA	pdgA	Polysaccharide deacetylase	Immune evasion	+	+	+	+	+
PDH-B	pdhB	Pyruvate dehydrogenase E1 component subunit beta		+	+	+	+	+
Periplasmic binding protein-dependent ABC transport systems	vctC	ABC-type enterochelin transport system, ATPase component		+	+	+	+	+
Peritrichous flagella	Che; motA; fliQ	Chemotaxis response regulator; flagellar motor protein MotA; flagellar biosynthesis protein	Regulation	+	+	+	+	+
PilB-type pili (PGS3)	ACI49664	Putative pilus-dedicated sortase	Adherence	+	+	+	-	+
Pneumococcal iron uptake	piuA	Iron-compound ABC transporter, iron-compound-binding protein	Iron uptake	+	+	+	+	+
Polar flagella	flmH	3-Oxoacyl-ACP reductase		-	+	+	+	+
Polysaccharide capsule	lytR	Membrane-bound transcriptional regulator LytR	Regulation	+	+	+	+	+
Pse5Ac7Ac	cheA	Chemotaxis histidine kinase	Invasion	+		+	+	
Pse5Ac7Ac, Pse5Ac7Am, Pse8OAc, Pse5Am7AcGlnAc	pseB	UDP-GlcNAc-specific C4,6 dehydratase/C5 epimerase	Motility	-	+	-	-	+
Pyrimidine biosynthesis	carA	Carbamoyl-phosphate synthase small chain	Metabolic adaptation	+	+	+	+	+

Continued

Virulence Factors	Gene	Product	Function	BF33.1	BF33.2	BF38	BF43	BF45
RegX3	regX3	DNA-binding response regulator RegX3	Regulation	+	+	+	+	+
Serine protease	htrA/degP	Serine protease HtrA	Adherence	+	+	+	+	+
Serine-threonine phosphatase	stp	Putative phosphoprotein phosphatase	Adherence	+	+	+	+	+
Sigma A	sigA/rpoV	RNA polymerase sigma factor	Protease	-	+	+	+	+
SodB	sodB	Superoxide dismutase	Stress protein	+	+	+	+	+
Sortase A	srtA	Sortase, putative	Adherence	+	+	+	+	+
Streptococcal enolase	eno	Phosphopyruvate hydratase	Secretion system	+	+	+	+	+
Streptococcal lipoprotein rotamase A	slrA	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type	Secretion system	+	+	+	+	+
Streptococcal plasmin receptor/GAPDH	plr/gapA	Glyceraldehyde-3-phosphate dehydrogenase, type I	Adherence	+	+	+	+	+
T3SS	mlr6326	Putative DNA invertase	Secretion system	+	+	+	+	+
T4SS effectors	CBU_1566	Coxiella Dot/Icm type IVB secretion system translocated effector	Secretion system	+	+	+	+	+
Trehalose-recycling ABC transporter	sugC	Probable sugar ABC transporter, ATP-binding protein SugC	Iron uptake	+	+	+	+	+
Trigger factor	tig/ropA	Trigger factor	Adherence	+	+	+	+	+
Type IV pili	pil	Twitching motility protein	Adherence	-	+	+	+	+
Type IV pili biosynthesis	pilR	Type 4 fimbriae expression regulatory protein pilR	Adherence	+	-	-	-	-
VirR/VirS	virR	Hypothetical protein	Secretion system	+	+	+	+	+

Supplementary Table S5. Comparative genomic analyses of single nucleotide polymorphisms of the five isolates against BH819

Genomic	BF33.1	BF33.2	BF38	BF43	BF45
Synonymous	29,934	29,909	29,910	29,975	29,981
Non-synonymous	11,630	11,589	11,605	11,599	11,613
Total CDS SNPs	41,812	41,742	41,759	41,820	41,845
Total SNPs	44,924	44,838	44,859	44,935	44,959

Note. CDS, coding sequence; SNPs, single nucleotide polymorphisms.

Supplementary Table S6. Comparative genomic analyses of the insertion and deletion (InDel) events of the five isolates against BH819

Items	BF33.1	BF33.2	BF38	BF43	BF45
Frame-shifted	11	7	9	7	8
Start codon	0	0	0	0	1
Stop codon	0	0	0	0	0
Premature stop	0	0	0	0	0
CDS with InDel	24	20	21	20	21
CDS of the reference strain	2,822	2,822	2,822	2,822	2,822

Note. CDS, coding sequence.

Supplementary Table S7. Information about bats

The number of the bat	Bat species	Location of samples collection	Habitat types from where bats captured	Samples type	Isolated strain type	Culture medium used for strains
NO.3	Brown Bat	He Nan	cave dwelling	liver	<i>Vagococcus fluvialis</i>	Chocolate Medium
NO.7	Brown Bat	He Nan	cave dwelling	liver	<i>Vagococcus fluvialis</i>	Chocolate Medium
NO.7	Brown Bat	He Nan	cave dwelling	liver	<i>Enterococcus</i>	Chocolate Medium
NO.7	Brown Bat	He Nan	cave dwelling	liver	<i>Staphylococcus epidermidis</i>	Blood plate
NO.9	Brown Bat	He Nan	cave dwelling	liver	<i>Vagococcus fluvialis</i>	Chocolate Medium
NO.13	Brown Bat	He Nan	cave dwelling	liver	<i>Vagococcus fluvialis</i>	Chocolate Medium
NO.14	Brown Bat	He Nan	cave dwelling	liver	<i>Vagococcus fluvialis</i>	Chocolate Medium
NO.18	Brown Bat	He Nan	cave dwelling	liver	<i>Staphylococcus epidermidis</i>	Blood plate
NO.18	Brown Bat	He Nan	cave dwelling	liver	<i>Actinomyces</i>	Agar medium
NO.22	Brown Bat	He Nan	cave dwelling	liver	<i>Aeromonas veronii</i>	Blood plate
NO.22	Brown Bat	He Nan	cave dwelling	spleen	<i>Enterococcus</i>	Chocolate Medium
NO.22	Brown Bat	He Nan	cave dwelling	spleen	<i>Enterococcus faecalis</i>	Chocolate Medium
NO.25	Brown Bat	He Nan	cave dwelling	spleen	<i>Enterococcus faecalis</i>	Chocolate Medium
NO.26	Brown Bat	He Nan	cave dwelling	liver	<i>Bacillus subtilis</i>	Blood plate
NO.27	Brown Bat	He Nan	cave dwelling	liver	<i>Corynebacterium</i>	Blood plate
NO.28	Brown Bat	He Nan	cave dwelling	liver	<i>Bacillus brevis</i>	Blood plate
NO.28	Brown Bat	He Nan	cave dwelling	liver	<i>Corynebacterium</i>	Blood plate
NO.28	Brown Bat	He Nan	cave dwelling	spleen	<i>Enterococcus</i>	Chocolate Medium
NO.31	Brown Bat	He Nan	cave dwelling	spleen	<i>Aeromonas veronii</i>	Chocolate Medium
NO.32	Brown Bat	He Nan	cave dwelling	spleen	<i>Enterococcus faecalis</i>	Chocolate Medium
NO.33	Brown Bat	He Nan	cave dwelling	spleen	<i>Enterococcus</i>	Chocolate Medium
NO.36	Brown Bat	He Nan	cave dwelling	spleen	<i>staphylococcus</i>	Chocolate Medium
NO.38	Brown Bat	He Nan	cave dwelling	spleen	<i>Klebsiella pneumoniae</i>	Chocolate Medium
NO.38	Brown Bat	He Nan	cave dwelling	liver	<i>Staphylococcus haemolyticus</i>	Chocolate Medium
NO.40	Brown Bat	He Nan	cave dwelling	liver	<i>Staphylococcus haemolyticus</i>	Chocolate Medium
NO.40	Brown Bat	He Nan	cave dwelling	liver	<i>kocuria sp</i>	Chocolate Medium
NO.40	Brown Bat	He Nan	cave dwelling	liver	<i>Enterococcus</i>	Chocolate Medium
NO.41	Brown Bat	He Nan	cave dwelling	liver	<i>Staphylococcus coriolis</i>	Chocolate Medium
NO.42	Brown Bat	He Nan	cave dwelling	liver	<i>Staphylococcus coriolis</i>	Chocolate Medium
NO.44	Brown Bat	He Nan	cave dwelling	liver	<i>Proteus</i>	Chocolate Medium
NO.44	Brown Bat	He Nan	cave dwelling	lung	<i>Bacillus sphaericus</i>	Chocolate Medium
NO.45	Brown Bat	He Nan	cave dwelling	lung	<i>Micrococcus lylae</i>	Chocolate Medium
NO.45	Brown Bat	He Nan	cave dwelling	lung	<i>Enterococcus</i>	Chocolate Medium
NO.46	Brown Bat	He Nan	cave dwelling	lung	<i>Shigella faecalis</i>	Chocolate Medium
NO.47	Brown Bat	He Nan	cave dwelling	lung	<i>Bacillus subtilis</i>	Chocolate Medium
NO.47	Brown Bat	He Nan	cave dwelling	lung	<i>Enterococcus faecalis</i>	Chocolate Medium