Table S1. Strains used in this study

Year of isolation	Number of strains/Strain	Accession	Serogroup	Country/Province(s)(n)	Source	*ctxB**
This study						
2001	1	-	Non-O1/O139	Guangdong(1)	Water	-
2002	1	-	Non-O1/O139	Fujian(1)	Water	-
2003	2	-	Non-O1/O139	Chongqing(2)	Water	-
2005	1	-	Non-O1/O139	Guangdong(1)	Water	-
2006	51	-	Non-O1/O139	Fujian(7),Liaoning(2),Guangdong(41),Jiangxi(1)	Water	-
2007	57	-	Non-O1/O139	Fujian(7),Liaoning(10),Guangdong(40)	Water	-
2008	102	-	Non-O1/O139	Fujian(4),Liaoning(40),Guangdong(55),Hainan(3)	Water	-
2008	1	-	Non-O1/O139	Sichuan(1)	Water	+
2009	76	-	Non-O1/O139	Guangdong(76)	Water	-
2010	3	-	Non-O1/O139	Zhejiang(2),Shandong(1)	Water	-
2001	1	-	O139	Jiangxi(1)	Water	-
2002	1	-	O139	Guangdong(1)	Water	-
2005	2	-	O139	Jiangxi(1),Jiangsu(1)	Water	-
2006	2	-	O139	Jiangxi(1),Guangdong(1)	Water	-
2008	2	-	O139	Jiangxi(2)	Water	-
Reference strains						
1910	NCTC_8457(ATCC14033)	AAWD00000000	O1	Saudi Arabia	Unknown	-
1937	M66-2	NC_012578	O1	Indonesia	Unknown	-
1965	O395	NC_012582	O1	India	Unknown	+
1968	V52	AAKJ00000000	O37	Sudan	Patient	+
1975	N16961	NC_002505	O1	Bangladesh	Unknown	+

1978	116063	NZ_APFK00000000	O1	Brazil	Patient	-
1980	2740-80	AAUT00000000	O1	United States	Water	-
1980	TM_11079-80	ACHW00000000	O1 Ogawa	Brazil	Sewage	-
1985	12129(1)	ACFQ00000000	O1 Inaba	Australia	Water	-
1987	V51	AAKI00000000	O141	USA	Patient	+
1991	Amazonia	AFSV00000000	O1	Brazil	Patient	-
1993	4260B	NZ_AMVL00000000	O139	Bangladesh	Patient	+
2001	G4222	NZ_ANNB00000000	O1	South Africa: Gauteng	Patient	-
2001	MZO-2	AAWF00000000	O14	Bangladesh	Patient	-
2001	AM-19226	AATY00000000	O39	Bangladesh	Patient	-
2001	MZO-3	AAUU00000000	O37	Bangladesh	Patient	-
2004	VC35	AMBR00000000	O1	Malaysia	Patient	-
2010	NHCC-008D	NZ_APGC00000000	O1	Bangladesh	Patient	-
2011	EM-1676A	NZ_APFY00000000	O1	Bangladesh	Water	-
Unknown	LMA3984-4	NC_017270	O1	Brazil	Water	-
Unknown	PS15	AIJR00000000	O106	USA	Sediment in Puget Sound, WA	-

* +, positive; -, negative

Table S2. PCR primers used in this study

Primer	Nucleotide sequence (5' to 3')	Amplicon size (bp)	Reference
ctxB-F	GCCGGGTTGTGGGAATGCTCCAAG	536	1
ctxB-R	CATGCGATTGCCGCAATTAGTATGGC		
rstR$^{\mathrm{ET}}$-F	GAGCTAAAATACAGCAACCAATGC	487	2
rstR$^{\mathrm{ET}}$-R	ACTCACCTTGTATTCG		
rstR$^{\mathrm{class}}$-F	TATTGGGATTGTAAACAGCTGTCC	480	3
rstR$^{\mathrm{class}}$-R	ACTCACCTTGTATTCG		
rstR$^{\mathrm{calc}}$-F	TAGCGCGCCATGTTTGAGCG	456	4
rstR$^{\mathrm{calc}}$-R	GGACTCAAGGGGAGCTAGCCGAA		
rstR-4**-F	GCGGAAACTTTAAATACTTAG	339	5
rstR-4**-R	CTGTTTTGTCGCTGAAAAACTTTG		
rstR-5-F	CATGCTGTAAATACACATGCACGC	312	5
rstR-5-R	GCGAGTTTCACTCTAAC		
*rstR*6-F	CCGATTTGAATTCAAGTATGCAA	362	6
rstR6-R	GCACTCACCTTGTATTCG		
*rstR*232-F	CACTTTTTGACCGCGAAGCG	649	7
*rstR*232-R	ATGCGTCCCAACGAATGGAA		
rstR-18F	TAGCGTGCGGAGTCGCGTTG	557	8
rstR-18R	CCGTTCAAACGCCATGCACCA		
*tcpA*72F	CACGATAAGAAA ACCGGTCAAGAG		
tcpA 477R	CGAAAGCACCTTCTTTCACGTTG	451 (El Tor)	9
*tcpA*647R	TTA CCAAATGCA ACGCCGAATG	620 (Classical)	
*tcpA*1185-F	TGCTGTCCGTGTCGCACCAG	1185	this study
*tcpA*1185-R	CGGCAGAGGCCAAAATCGCCT		
VSP-I			
VC0175F	TGGATGCTCTCTTCTTCA	2834	10
VC0175R	CGCTCACTCACTAATACCGAG		
VC0178F	AGAGGCTTGTTTACTATCAG	2053	
VC0178R	ATCGGTACTGTCAGGGCT		
VC0180F	GGATGAGCAAATACAGCTAAC	2283	
VC0180R	CTAGGAAGAATTTTATCGGC		
VC0183F	CAGTAAGAGTGTAGCGTGCC	3389	
VC0183R	CCTGCACATCGAGATGC		

VC0185F	AGGAGGCGTGTAAGTCATAGC	1110	
VC0185R	AGACCACGAATACCTGCTCC		
VSP-II			
VC0490F	CGTGAAGGGATATAGGAG	2337	10
VC0490R	TGCAGTTGTTGAATGGAC		
VC0493F	AATGCTTCTCAGGGGGGTCTT	3600	
VC0493R	CGCTCTTCTTTCCACGCTTCA		
VC0498F	AGGTGGTATCGGGCTGGT	4140	
VC0498R	TGCGGCTGGAATGGAGTCTG		
VC0502F	TCATCAGTTAGCACACGAAC	476	
VC0502R	GCTATCGTTATACTTGGCG		
VC0504F	CAGCAAAGGCGGAAGAGGTAG	3240	
VC0504R	AGCCCGAAATGAATCCCAAAA		
VC0512F	CAGTGGCTTCGCAGAGGA	3900	
VC0512R	CCCTCCACTGCTATTCCG		
VC0514F	TTATGATCCAAGGAGTAGGG	2089	
VC0514R	AGGCTGAAAAACAACTTGAG		
VC0516F	GTTTTCTGCGTTGTTCGAG	965	
VC0516R	TCCTGATGTCTCTCTTGCCG		
VC0517F	CCCACTTCTTCCAGAGTATG	1753	
VC0517R	CGCAGTCACAGCTTAAACAAC		
Putative accessory virulence genes			
TTSS(vcsV2)-F	ATGCAGATCTTTTGGCTCACTTGATGGG	742	11
TTSS(vcsV2)-R	ATGCGTCGACGCCACATCATTGCTTGCT		
IS1004-F	ATTGTCATCCCTAAACCACC	603	
IS1004-R	AGGCGGTTTTAATATAAGCC		
ST-F	TATTATTTTCTTCAATCGCATTTAGC	206	12
ST-R	ATTTAAACATCCAAAGCAAGCTGG		
hlyA-CL-F	GAGCCGGCATTCATCTGAAT	738	9
hlyA-CL-R	CTCAGCGGGCTAATACGGTTTA		
hlyA-ET-F	GGCAAACAGCGAAACAAATACC	481	
hlyA-ET-R	CTCAGCGGGCTAATACGGTTTA		
mshA-F	CGCACAATGAGGTTCGCCAAG	512	13
mshA-R	CCGAAAATTGACCGCCATTATC		
chxA-F	TGTGTGATGATGCTTCTGG	2000	14

chxA-R	TTATTTCAGTTCATCTTTTCGC		
rtxA-F	GGGATACAATGCCCTCTGGCA	977	15
rtxA-R	TGGGTTGGCGGTTGGATTTTAC		
rtxC-F	CGACGAAGATCATTGACGAC	265	
rtxC-R	CATCGTCGTTATGTGGTTGC		
SXT-F	TCGGGTATCGCCCAAGGGCA	986	16
SXT-R	GCGAAGATCATGCATAGACC		
MLST			
adk-F	CATCATTCTTCTCGGTGCTC	572	17
adk-R	AGTGCCGTCAAACTTCAGGTA		
gyrB-F	GTACGTTTCTGGCCTAGTGC	730	
gyrB-R	GGGTCTTTTTCCTGACAATC		
metE-F	CGGGTGACTTTGCTTGGT	802	
metE-R	CAGATCGACTGGGCTGTG		
mdh-F	ATGAAAGTCGCTGTTATTGG	794	
mdh-R	TAGCTTGATAGGTTGGG		
pntA-F	GGCCAGCCCAAAATCCT	739	
pntA-R	GATATTGCCGTCTTTTTCTT		
purM-F	GGTGTCGATATTGATGCAGG	715	
purM-R	GGAATGTTTTCCCAGAAGCC		
pyrC-F	ATCATGCCTAACACGGTTCC	709	
pyrC-R	TTCAAACACTTCGGCATA		

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Table S3. Characterization of VSP-I/II clusters and their relationship with elements of CTX prophage and TCP genes

No. of strain(s)	CTX prophage		TCP		VSP-I					VSP-II							
	ctxB	*rstR*	*tcpA*	*tcpI*	VC0175	VC0178	VC0180	VC0183	VC0185	VC0490	VC0493	VC0498	VC0502	VC0504	VC0512	VC0514	VC0516
3	−	+	+	+	−	−	−	−	−	−	−	−	−	+	−	−	−
5	−	+	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−
1	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
1	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
1	−	−	−	−	−	+	−	+	+	−	−	−	−	+	−	−	−
1	−	−	−	−	−	−	−	−	+	−	−	−	−	+	−	−	+
1	−	−	−	−	−	+	−	+	+	−	−	−	−	−	−	−	−
1	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−
3	−	−	−	−	−	−	−	−	−	+	+	+	+	+	+	+	+
2	−	−	−	−	−	−	−	−	−	+	+	+	+	+	−	+	+
1	−	−	−	−	−	−	−	−	−	+	+	−	−	+	−	−	+
1	−	−	−	−	−	−	−	−	−	+	+	−	+	−	−	+	+
1	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−
1	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	+

Table S4. Correlations of putative virulence genes and CTX prophage/TCP/VSP-I,II genes.

	tcpA	*ctxB*	*rstR*	VSP-I	VSP-II	*rtxC*	TTSS	SXT	*chxA*	*mshA*	*rtxA*	ST	IS1004	*hlyA*
tcpA	1	-0.01	.891**	-0.02	.257**	0.056	-0.024	0.103	-0.019	-0.066	0.076	-0.033	-0.051	0.037
	.	0.868	0	0.738	0	0.336	0.684	0.076	0.748	0.26	0.191	0.574	0.379	0.524
ctxB	-0.01	1	.311**	-0.007	-0.013	0.02	-0.027	-0.025	-0.038	0.013	0.027	-0.011	0.055	0.013
	0.868	.	0	0.907	0.824	0.737	0.641	0.672	0.512	0.83	0.648	0.844	0.346	0.824
rstR	.891**	.311**	1	-0.022	.222**	0.001	-0.039	0.077	-0.042	-.142*	0.036	-0.037	-0.048	-0.046
	0	0	.	0.707	0	0.986	0.506	0.188	0.478	0.014	0.537	0.528	0.408	0.428
VSP-I	-0.02	-0.007	-0.022	1	.250**	0.039	0.098	0.032	0.051	0.025	-0.024	-0.023	0.052	0.026
	0.738	0.907	0.707	.	0	0.5	0.094	0.587	0.386	0.667	0.683	0.693	0.374	0.654
VSP-II	.257**	-0.013	.222**	.250**	1	0.022	.228**	.127*	-0.043	-0.03	0.06	-0.044	.147*	0.05
	0	0.824	0	0	.	0.702	0	0.029	0.467	0.611	0.305	0.452	0.012	0.394
rtxC	0.056	0.02	0.001	0.039	0.022	1	-0.018	0.08	0.075	.256**	.350**	0.066	0.087	.558**
	0.336	0.737	0.986	0.5	0.702	.	0.76	0.169	0.202	0	0	0.257	0.137	0
TTSS	-0.024	-0.027	-0.039	0.098	.228**	-0.018	1	-0.076	-0.038	0.057	.167**	0.001	.176**	0.104
	0.684	0.641	0.506	0.094	0	0.76	.	0.194	0.513	0.325	0.004	0.985	0.002	0.073
SXT	0.103	-0.025	0.077	0.032	.127*	0.08	-0.076	1	-0.032	0.045	-0.005	-0.083	0.004	0.095
	0.076	0.672	0.188	0.587	0.029	0.169	0.194	.	0.58	0.44	0.925	0.153	0.948	0.105
chxA	-0.019	-0.038	-0.042	0.051	-0.043	0.075	-0.038	-0.032	1	.141*	.261**	-0.051	.132*	.147*
	0.748	0.512	0.478	0.386	0.467	0.202	0.513	0.58	.	0.015	0	0.379	0.023	0.012
mshA	-0.066	0.013	-.142*	0.025	-0.03	.256**	0.057	0.045	.141*	1	.208**	0.042	0.095	.496**
	0.26	0.83	0.014	0.667	0.611	0	0.325	0.44	0.015	.	0	0.47	0.103	0
rtxA	0.076	0.027	0.036	-0.024	0.06	.350**	.167**	-0.005	.261**	.208**	1	0.09	.395**	.488**
	0.191	0.648	0.537	0.683	0.305	0	0.004	0.925	0	0	.	0.123	0	0
ST	-0.033	-0.011	-0.037	-0.023	-0.044	0.066	0.001	-0.083	-0.051	0.042	0.09	1	-0.101	0.044
	0.574	0.844	0.528	0.693	0.452	0.257	0.985	0.153	0.379	0.47	0.123	.	0.083	0.452
IS1004	-0.051	0.055	-0.048	0.052	.147*	0.087	.176**	0.004	.132*	0.095	.395**	-0.101	1	.236**
	0.379	0.346	0.408	0.374	0.012	0.137	0.002	0.948	0.023	0.103	0	0.083	.	0
hlyA	0.037	0.013	-0.046	0.026	0.05	.558**	0.104	0.095	.147*	.496**	.488**	0.044	.236**	1
	0.524	0.824	0.428	0.654	0.394	0	0.073	0.105	0.012	0	0	0.452	0	.

Correlations (Spearman's rho,N=295); **. Correlation is significant at the 0.01 level (2-tailed); *. Correlation is significant at the 0.05 level (2-tailed).

Table S5 Characterization of putative accessory virulence genes and relationships with CTX prophage/TCP genes

No. of strain(s)	*tcpA*	*ctxB*	*rstR*	VSP-I	VSP-II	*rtxC*	TTSS(vcsC2)	SXT	*chxA*	*mshA*	*rtxA*	ST	IS1004	*hlyA*
1	+	-	+	-	+	+	-	-	+	+	+	-	+	+
1	+	-	+	-	+	+	-	-	-	-	+	-	+	+
1	+	-	+	-	+	+	-	+	-	+	+	-	-	+
1	+	-	+	-	-	+	+	-	+	+	+	-	-	+
2	+	-	+	-	-	+	-	+	-	+	+	-	-	+
1	+	-	+	-	-	+	-	-	-	+	+	-	-	+
1	+	-	+	-	-	+	-	-	-	+	+	-	+	+
1	-	+	+	-	-	+	-	-	-	+	+	-	+	+
1	-	-	+	-	-	-	-	-	-	-	-	-	-	-
1	-	-	-	+	+	+	+	-	-	+	+	-	+	+
1	-	-	-	+	+	+	-	+	-	+	-	-	-	+
1	-	-	-	+	-	+	+	-	+	+	+	-	+	+
1	-	-	-	+	-	+	-	-	+	+	+	-	+	+
2	-	-	-	-	+	+	+	+	-	+	+	-	+	+
1	-	-	-	-	+	+	+	-	+	+	+	-	+	+
3	-	-	-	-	+	+	+	-	-	+	+	-	+	+
1	-	-	-	-	+	+	-	-	-	+	+	-	+	+
1	-	-	-	-	+	+	-	-	+	+	+	-	+	+
1	-	-	-	-	+	-	+	+	-	+	+	-	+	+
1	-	-	-	-	-	-	+	+	-	+	+	-	+	+
1	-	-	-	-	-	-	+	-	+	+	+	-	-	+
1	-	-	-	-	-	-	+	-	-	+	+	-	-	+
2	-	-	-	-	-	-	+	-	-	+	-	-	+	+
4	-	-	-	-	-	-	-	-	+	+	+	-	+	+
1	-	-	-	-	-	-	-	-	+	+	+	-	-	+
2	-	-	-	-	-	-	-	-	-	+	+	-	+	+
2	-	-	-	-	-	-	-	-	-	+	+	-	-	+
2	-	-	-	-	-	-	-	-	-	+	-	-	+	+
1	-	-	-	-	-	-	-	-	-	+	-	-	-	+
6	-	-	-	-	-	-	-	-	-	+	-	-	-	-
5	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1	-	-	-	-	-	+	+	+	-	+	+	-	+	+
1	-	-	-	-	-	+	+	-	+	+	+	+	+	+
6	-	-	-	-	-	+	+	-	+	+	+	-	+	+
3	-	-	-	-	-	+	+	-	+	+	+	-	-	+
1	-	-	-	-	-	+	+	-	-	+	+	+	-	+
17	-	-	-	-	-	+	+	-	-	+	+	-	+	+
8	-	-	-	-	-	+	+	-	-	+	+	-	-	+
1	-	-	-	-	-	+	+	-	-	-	+	-	+	+
8	-	-	-	-	-	+	-	+	+	+	+	-	+	+
3	-	-	-	-	-	+	-	+	+	+	+	-	-	+
1	-	-	-	-	-	+	-	+	+	+	-	-	-	+
10	-	-	-	-	-	+	-	+	-	+	+	-	+	+
7	-	-	-	-	-	+	-	+	-	+	+	-	-	+
1	-	-	-	-	-	+	-	+	-	+	-	-	+	+
5	-	-	-	-	-	+	-	+	-	+	-	-	-	+
1	-	-	-	-	-	+	-	+	-	-	+	-	-	+
1	-	-	-	-	-	+	-	-	+	+	+	+	-	+

32	–	–	–	–	–	+	–	–	+	+	+	–	+	+
1	–	–	–	–	–	+	–	–	+	+	–	–	–	+
21	–	–	–	–	–	+	–	–	+	+	+	–	–	+
2	–	–	–	–	–	+	–	–	–	+	+	+	+	+
6	–	–	–	–	–	+	–	–	–	+	+	+	–	+
48	–	–	–	–	–	+	–	–	–	+	+	–	+	+
31	–	–	–	–	–	+	–	–	–	+	+	–	–	+
23	–	–	–	–	–	+	–	–	–	+	–	–	–	+
1	–	–	–	–	–	+	–	–	–	+	–	–	–	–
2	–	–	–	–	–	+	–	–	–	–	+	–	+	+
1	–	–	–	–	–	+	–	–	–	–	+	–	–	+
1	–	–	–	–	–	+	–	–	–	–	–	–	–	–

Table S6. Characteristics of virulence-associated genes and housekeeping genes from non-O1/O139 strains in this study

Strain	Serogroup	*tcpA*	*ctxB*	*rstR*	VSP-I	VSP-II	*rtxC*	TTSS	SXT	*chxA*	*mshA*	*rtxA*	ST	IS1004	*hlyA*	*adk*	*gyrB*	*mdh*	*metE*	*pntA*	*purM*	*pyrC*
ZJ193-1	unknow	-	-	-	-	-	+	-	+	+	+	+	-	+	+	5	1	32	30	1	1	6
ZJ194-1	unknow	-	-	-	-	-	+	-	-	+	+	+	-	+	+	5	1	32	30	2	1	6
ZJ197-1	unknow	-	-	-	-	-	+	-	+	-	+	-	-	+	+	11	1	23	14	2	24	1
ZJ198-2	unknow	-	-	-	-	-	+	-	+	+	+	+	-	+	+	25	1	23	14	5	1	1
ZJ199-1	unknow	-	-	-	-	+	+	+	-	+	+	+	-	+	+	11	1	23	18	1	24	3
ZJ203-1	unknow	-	-	-	-	-	+	-	-	-	+	+	-	+	+	16	28	23	18	10	18	2
ZJ205-1	unknow	-	-	-	-	-	+	-	-	+	+	+	-	-	+	20	28	23	20	10	1	30
ZJ209-1	unknow	-	-	-	-	-	+	-	-	-	+	+	-	-	+	20	28	13	20	28	21	15
ZJ217-2	unknow	+	-	+	-	-	+	+	-	+	+	+	-	-	+	20	28	13	20	28	21	10
ZJ221-1	unknow	-	-	-	-	-	+	+	-	-	+	+	-	+	+	5	20	6	15	6	21	41
ZJ227-3	unknow	+	-	+	-	+	+	-	-	+	+	+	-	+	+	5	20	6	12	13	21	7
ZJ229-1	unknow	-	-	-	-	-	+	-	-	+	+	+	-	+	+	5	33	6	29	13	21	8
ZJ231-1	unknow	-	-	-	-	-	+	-	-	+	+	+	-	+	+	23	32	27	42	3	21	38
ZJ234-1	unknow	+	-	+	-	+	+	-	-	-	-	+	-	+	+	33	20	34	31	25	21	1
ZJ341-1	unknow	-	-	-	-	-	+	+	-	+	+	+	+	+	+	26	26	2	4	16	21	10
ZJ345-1	unknow	-	-	-	-	+	+	-	-	-	+	+	-	+	+	1	7	8	17	34	1	27
ZJ349-1	unknow	-	-	-	-	-	-	-	-	+	+	+	-	-	+	1	36	28	34	31	1	20
ZJ351-2	unknow	-	-	-	-	-	-	+	-	+	+	+	-	-	+	26	18	2	36	31	3	7
ZJ356-1	unknow	-	-	-	-	-	+	-	-	+	+	+	+	-	+	1	24	28	4	10	8	32
ZJ419-1	unknow	-	-	-	-	-	+	-	+	+	+	+	-	-	+	34	10	1	22	18	25	40
ZJ421-1	unknow	-	-	-	-	+	+	-	-	+	+	+	-	+	+	4	22	37	8	21	6	21
ZJ186-3	unknow	-	-	-	-	-	+	-	-	-	-	+	-	-	+	24	22	17	38	24	3	12
ZJ191-1	unknow	-	-	-	-	-	+	-	-	-	+	+	-	+	+	26	22	11	19	34	1	27
ZJ269-2	unknow	-	-	-	+	+	+	+	-	-	+	+	-	+	+	26	22	18	23	4	1	28

ZJ278-1	unknow	-	-	-	-	-	+	-	-	-	+	-	-	-	+	2	40	28	23	28	8	15
ZJ278-2	unknow	-	-	-	+	+	+	-	+	-	+	-	-	-	+	10	40	39	44	38	15	17
ZJ279-1	unknow	-	-	-	-	-	+	+	+	-	+	+	-	+	+	32	40	35	14	5	18	1
ZJ280-1	unknow	-	-	-	+	-	+	+	-	+	+	+	-	+	+	26	20	18	14	6	18	41
ZJ282-1	unknow	-	-	-	-	-	+	+	-	-	-	+	-	+	+	15	6	18	14	15	8	12
ZJ283-2	unknow	-	-	-	-	-	+	-	-	-	+	+	-	-	+	20	1	18	30	1	2	6
ZJ287-2	unknow	-	-	-	-	-	-	-	-	-	+	-	-	-	-	1	28	18	28	10	2	2
ZJ180-1	unknow	-	-	-	-	-	+	-	-	-	+	+	+	+	+	1	5	18	2	13	7	10
ZJ184-1	unknow	-	-	-	-	-	+	+	-	-	+	+	+	-	+	1	1	18	30	1	19	5
ZJ242-1	unknow	-	-	-	-	-	+	-	-	+	+	+	-	+	+	18	1	18	41	1	19	42
ZJ243-1	unknow	-	-	-	-	-	-	+	-	-	+	-	-	+	+	24	1	9	41	1	19	42
ZJ245-1	unknow	-	-	-	-	-	+	-	-	-	+	+	-	+	+	27	3	9	27	22	20	4
ZJ247-1	unknow	-	-	-	-	-	+	+	-	+	+	+	-	+	+	27	3	9	28	10	20	2
ZJ251-1	unknow	-	-	-	-	-	+	-	-	-	+	+	+	-	+	13	3	20	28	10	20	2
ZJ252-1	unknow	-	-	-	-	-	+	-	-	-	+	+	+	-	+	14	19	1	37	9	20	38
ZJ259-1	unknow	+	-	+	-	+	+	-	+	-	+	+	-	-	+	1	12	23	46	12	19	43
ZJ260-2	unknow	+	-	+	-	-	+	-	+	-	+	+	-	-	+	13	20	16	31	25	19	1
ZJ146-1	unknow	-	-	-	-	-	+	-	-	-	-	+	-	+	+	6	13	1	32	27	19	1
ZJ147-1	unknow	-	-	-	-	-	+	-	-	-	-	+	-	+	+	29	4	7	35	17	19	36
ZJ149-1	unknow	-	-	-	-	-	+	-	-	+	+	+	-	+	+	29	4	3	43	38	23	18
ZJ150-1	unknow	-	-	-	-	-	+	-	+	+	+	-	-	-	+	32	38	35	43	36	18	24
ZJ157-1	unknow	-	-	-	-	-	-	-	-	-	+	+	-	-	+	32	20	38	18	25	18	25
ZJ158-2	unknow	-	-	-	-	-	+	-	+	-	-	+	-	-	+	31	4	38	18	17	18	36
ZJ163-1	unknow	-	-	-	-	-	+	-	+	-	+	+	-	-	+	1	4	23	13	17	18	36
ZJ172-1	unknow	-	-	-	-	-	+	-	-	+	+	+	-	+	+	28	16	23	21	16	4	36
ZJ172-2	unknow	-	-	-	-	-	-	-	-	-	+	-	-	-	-	9	2	23	21	22	4	32
ZJ301-1	unknow	-	-	-	-	-	+	-	-	-	+	+	-	+	+	13	9	23	33	1	12	36

ZJ302-2	unknow	-	-	-	-	-	+	-	-	-	+	+	-	+	+	1	41	1	33	39	17	19
ZJ258-1	unknow	-	-	-	-	-	-	-	-	-	-	-	-	-	-	17	27	29	32	27	11	1
MJ-34	unknow	-	-	+	-	-	-	-	-	-	-	-	-	-	-	4	34	1	33	23	9	11
MJ-36	unknow	-	-	-	-	-	+	-	-	-	+	+	-	+	+	26	27	22	33	27	10	1
MJ-50	unknow	-	-	-	-	-	+	-	-	+	+	+	-	+	+	28	27	23	33	14	13	16
MJ-51	unknow	+	-	+	-	-	+	-	-	-	+	+	-	+	+	21	34	23	33	23	12	11
YL823006	unknow	-	-	-	-	-	+	-	-	-	+	+	-	-	+	20	37	15	47	37	2	23
YL823014	unknow	-	-	-	-	-	+	+	-	-	+	+	-	+	+	8	21	23	6	7	9	11
YL823016	unknow	-	-	-	-	-	+	-	-	-	+	+	+	-	+	26	21	24	15	7	5	39
YL823018	unknow	-	-	-	-	-	+	-	-	-	+	+	+	-	+	11	8	18	15	11	9	39
YL823019	unknow	-	-	-	-	-	+	-	-	-	+	+	+	-	+	22	8	9	15	11	2	39
YL823033	unknow	-	-	+	-	+	+	+	-	-	+	+	-	+	+	1	13	30	40	11	1	9
YL823034	unknow	-	-	-	-	+	+	+	-	-	+	+	-	+	+	32	13	38	40	8	1	9
YL714013	unknow	-	-	-	-	-	+	+	-	+	+	+	-	-	+	32	4	9	7	8	1	41
YL0882807	unknow	-	-	-	-	-	+	-	+	-	+	-	-	-	+	1	39	23	43	35	19	18
YL0882811	unknow	-	-	-	-	+	+	+	+	-	+	+	-	+	+	26	25	14	45	1	19	18
YL0882828	unknow	-	-	-	-	-	-	+	-	-	+	-	-	+	+	29	13	3	24	25	23	1
YL0882830	unknow	-	-	-	-	+	+	+	+	-	+	+	-	+	+	29	25	3	45	1	23	11
SC2008	unknow	-	+	+	-	-	+	-	-	-	+	+	-	+	+	13	31	3	3	19	3	43
2740-80	O1	+	-	-	-	-	+	+	-	-	+	-	+	-	+	5	30	32	1	19	1	43
NCTC_8457(ATCC14033)	O1	-	-	-	-	-	+	+	+	-	+	-	+	-	+	5	31	32	1	19	1	43
12129(1)	O1 Inaba	-	-	-	-	-	+	+	-	-	+	-	+	-	+	26	35	33	11	23	1	13
TM_11079-80	O1 Ogawa	-	-	-	-	-	+	+	-	-	+	-	+	-	+	1	13	5	39	26	8	1
Amazonia	O1	-	-	-	-	-	+	+	+	+	+	-	+	-	+	1	13	5	39	26	8	1
VC35	O1	-	-	-	-	-	+	+	-	-	-	-	+	-	+	1	13	5	32	27	8	13
AM-19226	O39	-	-	-	-	-	+	-	-	-	+	-	+	-	+	20	13	10	25	8	19	11
G4222	O1	+	-	-	-	-	+	-	-	-	+	-	+	-	+	5	30	32	1	19	1	43

LMA3984-4	O1	+	-	-	-	-	+	-	-	-	+	-	+	-	+	26	11	4	12	33	3	13
M66-2	O1	+	-	-	-	-	+	-	-	-	+	-	+	-	+	5	31	32	1	19	1	43
MZO-2	O14	-	-	-	-	-	+	-	-	-	+	-	+	-	+	20	26	21	9	34	22	26
MZO-3	O37	-	-	-	-	+	+	-	-	-	+	-	+	-	+	7	27	25	21	13	3	31
N16961	O1	+	+	+	+	+	+	-	-	-	-	-	+	-	+	5	31	32	1	19	1	36
4260B	O139	+	+	+	+	+	+	-	-	-	+	-	+	+	+	5	31	32	1	19	1	36
116063	O1	-	-	-	-	-	-	-	-	-	-	-	+	-	+	1	13	5	39	26	8	1
EM-1676A	O1	-	-	-	-	-	+	-	-	-	-	-	+	-	+	1	15	31	16	16	12	22
NHCC-008D	O1	-	-	-	-	-	+	-	+	-	-	-	+	-	+	3	15	19	24	32	16	29
O395	O1	+	+	-	+	+	-	-	-	-	+	-	+	+	+	5	31	32	4	19	1	43
PS15	O106	-	-	-	-	+	+	-	+	+	-	-	+	-	+	12	17	12	5	30	12	14
V51	O141	-	+	-	-	-	+	-	-	-	+	-	+	-	+	19	23	36	26	29	12	33
V52	O37	-	+	+	-	-	+	-	-	-	+	-	+	-	+	5	31	32	10	20	1	10
JS2005001	O139	-	-	-	-	-	+	-	-	-	+	-	-	-	-	32	40	40	48	38	14	34
JX2006101	O139	-	-	-	-	-	+	-	-	-	+	+	-	+	+	1	13	26	32	27	8	1
GD2002005	O139	+	-	-	+	+	+	-	+	-	+	+	-	+	+	5	31	32	1	19	1	37
GD2006058	O139	-	-	-	-	-	+	-	-	-	+	-	-	-	-	32	40	40	48	38	14	15
JX2001016	O139	-	-	-	-	-	+	-	-	-	+	-	-	-	-	32	40	40	48	38	14	35
JX2008029	O139	+	-	+	-	-	+	-	-	-	+	-	-	-	-	32	29	40	48	38	14	35
JX2008031	O139	-	-	-	-	-	+	-	-	-	+	-	-	-	-	30	40	40	48	38	14	35
JX2005004	O139	-	-	-	-	-	+	-	-	-	+	-	-	-	-	32	31	40	48	38	15	35