

Table S1. Susceptibility of the isolate

Antimicrobial agent	Inhibition zone diameter, mm	Interpretation ^a
Ampicillin	6	resistant
Cefuroxime	6	resistant
Cefotaxime	6	resistant
Ceftazidime	6	resistant
Ertapenem	23	sensitive
Imipenem	20	intermediate
Meropenem	23	sensitive
Amoxicillin-clavulanate	6	resistant
Piperacillin-tazobactam	20	intermediate
Amikacin	23	sensitive
Gentamicin	6	resistant
Chloramphenicol	20	sensitive
Ciprofloxacin	29	sensitive
Fosfomycin	6	resistant
Sufisoxazole	25	sensitive
Tetracycline	18	sensitive
Trimethoprim	6	resistant

^a according to the Clinical Laboratory Standards Institute (1).

Table S2. Primers used in the study

Primer	Our primer name	Target	Nucleotide sequence (5' to 3')	Position in GenBank entry for pCRE623
1	pCTX-M3 56725-F	IncL/M scaffold	GGTGAAGACAGGGGAATGTT	2393-2412
2	IS110-942F	Multidrug-resistant region	CAGAGCACAGGTGACGAC	2816-2833*
3	IS5075-340F	Multidrug-resistant region	GTTGATGCTGAAGCTATCTG	c3484-3465*
4	IS110-80R	Multidrug-resistant region	GCCTTCCCACGATGATCCTG	3678-3697
5	IS shell 7154B	Multidrug-resistant region	TCACCGTGCCCTGCTTGA	4318-4335
6	pCRE623 contig14R	Multidrug-resistant region	GCAGCTCTGTTACCTGCGCT	7472-7453
7	pCRE623 contig14F	Multidrug-resistant region	ACGTCAGAAGCCGACTGCAC	8698-8717
8	Int461F	Multidrug-resistant region	GGGTCAAGGATCTGGATTTC	c9425-9406*
9	Int-F	Multidrug-resistant region	GCCACTGCGCCGTTACCACC	c9876-9857*
10	fosC2-F125	Multidrug-resistant region	TGGAGGCTACTTGGATTTG	10168-10186
11	fosC2-R341	Multidrug-resistant region	AGGCTACCGCTATGGATTT	c10384-10366
12	IMP-578R	Multidrug-resistant region	GCT TCTADATTTGCGTCAC	11109-11091
13	TniA5255F	Multidrug-resistant region	CGTGAATCATCTGCATCG	15045-15062
14	pCRE623 Contig13R	Multidrug-resistant region	GGATGACGAAGAACGATTTCG	16340-16359
15	aaCC2-2	Multidrug-resistant region	CTCCGTCAGCGTTTCAGCTA	17825-17842
16	aacC2-1	Multidrug-resistant region	ACTGTGATGGGATACGCGTC	18061-18042
17	pHKU1 tnpA-281F	Multidrug-resistant region	ACAATGGGCATCGTATTGCC	18643-18624
18	IS10-F	Multidrug-resistant region	GACTGGTCTGATATCCGTGA	18651-18670
19	IS10-R	Multidrug-resistant region	CAGGTAAGTTAGTTGCTAGAA	c19179-19159
20	IS10-1034F	Multidrug-resistant region	AGCCGAACGAGCAGCTCA	19290-19307
21	pCRE623 contig18F	Multidrug-resistant region	CATGTGTCAGTCGTCCGT	c20939-20922
22	pCRE623 contig18R	Multidrug-resistant region	TGTTGAAGCTCAAGGCCG	21523-21540
23	uvp130B	Multidrug-resistant region	TGCAAGGCCTGAGCGCGT	22527-22510
24	pHKU1 uvp1 511F	Multidrug-resistant region	TTGCTAAGCGCTTCAACGTT	22637-22656
25	IncN repE 22-F	Multidrug-resistant region	TCCTTGATCCTGCACTCAAG	c23577-23557*
26	N RV	Multidrug-resistant region	GTTTCAACTCTGCCAAGTTC	23584-23603
27	N FW	Multidrug-resistant region	GTCTAACGAGCTTACCGAAG	24143-24124
28	contig11F	Multidrug-resistant region	ACGTTATCAGGCATGGCG	25786-25803

29	IS3-70B	Multidrug-resistant region	ATCTGACGCAACTTGACGGC	26765-26746
30	strA31B	Multidrug-resistant region	ACCGGTTGTGTTCCGGTCTA	c27834-27815
31	Tn3-120F	Multidrug-resistant region	TAAGTTTCGTCGGCTGAGGC	46381-46400
32	IS903 reverse 5'	Multidrug-resistant region	CATCATCCAGCCAGA AAG TT	46706-46725
33	DMT-366F	Multidrug-resistant region	GCTATTTGCGGAACTGCG	50050-50067
34	Int1-285B	Multidrug-resistant region	GCACAGCACCTTGCCGTAGAA	52236-52256
35	pCRE623 dfrA14 41B	Multidrug-resistant region	TTCGCTTTCGCAGCCATC	52707-52690
36	IS6100F	Multidrug-resistant region	CTGCCACGCTCAATACCGA	54170-54188
37	pHKU1-insB-159F	Multidrug-resistant region	AGACAACATCTGGCAAGGCT	57749-57768
38	pKPS30 mphA 236B	Multidrug-resistant region	ATTCTTGAGCATTGCCAGCAC	59248-59228
39	mphR(A) 461F	Multidrug-resistant region	GATGCAGTGGGCCGTCGATC	61625-61644
40	pCRE623 contig6R	Multidrug-resistant region	ACGCGGCCGAGTTCAAGA	c62821-62804
41	merR-303F	Multidrug-resistant region	GACTTGGCGCGCATGGAAAC	68233-68252
42	pCRE623 contig12R	Multidrug-resistant region	GGATCTAGGTGAAGATCC	c69795-69778
43	TEM-R	Multidrug-resistant region	TTATCCGCCTCCATCCAGTC	70083-70102
44	TEM-F	Multidrug-resistant region	TGGGTGCACGAGTGGGTAC	c70608-70589
45	pCRE623 contig12F	Multidrug-resistant region	TGGCAGATTCACCGGTGA	71665-71682
46	trbC_84R	IncL/M scaffold	CTGTACGTTCCGGAGTGAG	78,573-78,590
47	trbB_682F	IncL/M scaffold	CCGCTCCTGTACTCGATA	c78,937-78,920
48	pCTX-M3 trbB 789F	IncL/M scaffold	ACCAGAAAACGTATTGTGCG	79458-79477
49	trbA_156R	IncL/M scaffold	CGGCAGTACACCGTAGAT	80,782-80,799
50	trbN_217F	IncL/M scaffold	CCAGTGCCTACATCCTCA	c81,076-81,059
51	orf92_696R	IncL/M scaffold	GGTGCCATAGCGATTGGT	85,448-85,465
52	orf99_1160R	IncL/M scaffold	AGTTCGTCCGGGGATTCA	88,874-88,891
53	orf99_F	IncL/M scaffold	TCTTCTATCCCTCCGGAG	c89,391-89,374
54	orf103_R	IncL/M scaffold	TGCTGACCAGCACCGATA	92,505-92,522
55	orf104_R	IncL/M scaffold	CAGCATGATGCCGGCAAT	93,061-93,078
56	pCTX-M3 orf27-25888F	IncL/M scaffold	TCCCTCTGTCAGCATTGACG	104719-104738
57	pCTX-M3 rmoA-80R	IncL/M scaffold	TCCAGTGTGTCCGGGTACG	104977-104958
58	orf124_F	IncL/M scaffold	ATCTCGACTATCGCCCTG	105,526-105,543
59	orf125_R	IncL/M scaffold	ACGCCATAACGGCTGTGT	c105,937-105,920

60	traI_23F	IncL/M scaffold	TCTGACGTTACCGCTGCT	113,371-113,379
61	traI_432R	IncL/M scaffold	CCCGGTCAGAAGATAGCT	c113,779-113,762
62	pri_3037F	IncL/M scaffold	ACGGATACGGCCATGTTG	118,613-118,630
63	traL_119R	IncL/M scaffold	TCGTATGCTGCACAGGTC	c118,917-118,900
64	orf141_608F	IncL/M scaffold	CCTGTCCAGGTTATGGAC	c119,566-119,583
65	traM_151R	IncL/M scaffold	GGGCGTTGCTGTCATCAT	c120,055-120,038
66	traP_347F	IncL/M scaffold	GCTGGACGCGATAGAATC	123,567-123,584
67	traP_637R	IncL/M scaffold	CGCCAAGTTGACTACCGA	c123,856-123,839

*These primers can be mapped to more than one location in pIMP-HB623. These include IS110-942F (position c69384-69367); IS5075-340F (68716-68735); Int461F (c52060-52041); IntF (c52511-52492); IncN repE 22-F (43517-43536).

Table S3. Backbone differences between pIMP-HB623, pEL1573 and pCTX-M3

Position in pIMP-HB623 ^a	Nucleotide in pIMP-HB623 (KM877517)	Nucleotide in pEL1573 (JX101693) ^b	Nucleotide in pCTX-M3 (AF550415) ^b
113,651	G	A	G
118,690	C	A	C
123,762	T	G	T
78,796	G	G	T
78,798	G	G	C
80,960	A	A	G
85,538-85,539	1 base deletion	1 base deletion	G
85,551-85,552	2 bases deletion	2 bases deletion	GC
89,195	G	G	T
92,828	C	C	A
105,765	G	G	A
116,878-116,922	ACCCCTGCAGCTGCTGAAGCGGTGGA AGCCGCGCCGGTGGCCAGC	ACCCCTGCAGCTGCTGAAGCGGTGGA AGCCGCGCCGGTGGCCAGC	45 bases deletion
119,808	T	T	C
119,826	G	G	A

^aAccording to numbering in GenBank accession KM877517

^bDifferences with pIMP-HB623 are indicated in boldface.

References

1. **CLSI.** *Performance standards for antimicrobial susceptibility testing: twenty-fourth informational supplement M100-S24.* 2014. CLSI, Wayne, PA, USA, 2014.