SUPPLEMENTAL MATERIAL

PCR assay title	PCR assay code (genetic target)	Oligo Name	Oligo features	5'-3' sequence	Expected amplicon size(bp)
Genetic	PCR1 (ADC upstream)	folE/ADC-F	External, inwards	GCTGAACGCGATAAACTTCG	814 / 1902 / 2003
context of bla_{ADC}		ADC-R	Internal, outwards	TCGAATCGGCTGATTTTCTT	
	PCR2 (ADC downstream)	ADC-F	Internal, outwards	CTGGCTCAACTACCGGTTTC	2360 / 3551
		ADC/orf-R	External, inwards	GCTGTAGGCCAAGGTGAAAG	
Genetic	PCR3 (OXA-51-like	fxsA-F	External, inwards	TTTGCGAGTGTTCTCATTGC	1706 / 2895
context of bla _{OXA-51-like}	upstream)	N-Acyltransferase-R	External, inwards	GGCTTGACGCTGCTTTTTAC	
Genetic	PCR4 (Tn2006	Tn6022-sup-F	External, inwards	CCTTGCCCTTTACATTCTCG	3309
bla _{OXA-23}	downstream)	ΔDEAD-R	Internal, outwards	ATGGGCTTCGTCATTCATTG	
	PCR5 (Tn2006 upstream)	ΔDEAD-F	Internal, outwards	GTGCCGCCTATCAGTTCTCT	2688
		Tn6022-orf4-R	External, inwards	GAAAATGCCAAGGGAATAAAAA	
	PCR6 (Tn2009	fimC-F	External, inwards	TTTTGTCGCTTCAACACGAG	1610
	downstream)	Tn2009-orf-R	Internal, outwards	ATCGCCACGGAAGTATGAAC	
	PCR7 (Tn2009, OXA-23	Tn2009-T5orf172-F		CTTTCTTTGGTGAGGCTTGC	2484
	downstream)	ΔDEAD-R		ATGGGCTTCGTCATTCATTG	
	PCR8 (Tn2009 upstream)	ΔDEAD-F	Internal, outwards	GTGCCGCCTATCAGTTCTCT	2441
		fimA-R	External, inwards	TCAATGGGTTGACGTAGCTG	
Genetic	PCR9 (OXA-72-positive	pAB0057-orf-F		AATACGATCGGCTTGCTGTT	1609
context of bla _{OXA-24-like}	Acil plasmid)	pAB0057-repB-R		GACGCGCGAATAAATCCTTA	
	PCR10 (OXA-24-positive	pABVA01-orf-F		ATACGATCTGCCTGCTGCTT	1732
	Acil plasmid)	pABVA01-repB-R		CTATGGCTGGGGGCAAAGATA	
	PCR11 (OXA-24-like	repA-F	External, inwards	TACCACACCCAAACGCTACA	635
	downstream)	oxa-24-R	Internal, outwards	CAAAAAGTGGATGGGGAATG	
	PCR12 (OXA-24-like	oxa-24-F	Internal, outwards	GCTTTTTCATGTTGCTGAGAA	1438 / 2298
	upstream)	tonB-R	External, inwards	CCTGCCCACGAATAATAGGA	
	PCR13 (OXA-72-positive	pA100-F-1		CGAGGGCGAAATTTTAATGA	445
	Acil plasmid - isolate A100)	pA100-emrE-R		ACCATCACGCTTGGAAAAAG	
	PCR14 (OXA-72-positive	pA100-F-2		GCTTGCAAAGCAAGTGGATA	1011
	Aci1 plasmid - isolate A100)	pA100-mobA-R		GTGGTTTAAGCCGTGTCGAT	
	PCR15 (OXA-72-positive	pA100-F-1		CGAGGGCGAAATTTTAATGA	3240
	Aci1 plasmid - isolate A100)	pAB0057-repB-R		GACGCGCGAATAAATCCTTA	
	For additional sequencing	ISAba31-F		AACGAATAGCCAATCGAACAA	

PCR assay title	PCR assay code (genetic target)	Oligo Name	Oligo features	5'-3' sequence	Expected amplicon size(bp)
Genetic	PCR16 (OXA-58	hsdS-F	External, inwards	CGTGGAGCTACATGTGGTGA	2428
context of bla_{OXA-58}	downstream)	oxa-58-R	Internal, outwards	GGGTTGGTATGTGGGTTTTG	
0111700	PCR17 (OXA-58 upstream)	oxa-58-F	Internal, outwards	AAAAGCGCTTGAACATTCTGA	2242
		cinH-R	External, inwards	GGATTTTTGTTGACCGTGCT	
	For additional sequencing	ISAba3-R		AGAGGCAGCGGTATACGAGA	
Genetic	PCR18 (Ab-ST3-aadB1	MMPL-F	External, inwards	TCTTGGCATCGAACCCTTCT	1332
context of aadB1	upstream)	TnST3-IS6100-R	Internal, outwards	GGCTTTTCCCAGTGCTTCAG	
	PCR19 (Ab-ST3-aadB1	TnST3-IS6100-F	Internal, outwards	AGGGTGATGTGATCCTGTGG	1150
	downstream)	MMPL-R	External, inwards	AGGACCCTTTCACTACACCG	
	PCR20 (Ab-ST3-aadB1	TnST3-IS6100-F	Internal, outwards	AGGGTGATGTGATCCTGTGG	1192
	circular form)	TnST3-IS6100-R	Internal, outwards	GGCTTTTCCCAGTGCTTCAG	
	PCR21 (Ab-ST3-aadB1	TnST3-F	Internal, outwards	TCAGAAGACGACTGCACCAG	2008
	circular form)	TnST3-ssb-R	Internal, outwards	ATCTTGCCCTGCACGAATAC	
	PCR22 (Ab-ST3-aadB1	MMPL-F	External, inwards	TCTTGGCATCGAACCCTTCT	1290
	insertion site)	MMPL-R	External, inwards	AGGACCCTTTCACTACACCG	
	PCR23 (<i>aadB1</i> -positive	mobA-F		GCTGTACTTCGTTCTAGCTCG	1228
	plasmid pKA Y^{*-V1}	mobA-R		TGTGATTCCCAATGTTGAGC	
Genetic	PCR24 (Tn6279 upstream,	HPA2-F	External, inwards	GCTGCACAGTGGTTTTCTGA	1967
context of armA	linkage between host chromosome and Tn6020b)	aphA1b-F (R)	Internal, outwards	CGACTGAATCCGGTGAGAAT	
	PCR25 (Tn6279 upstream,	araC-F	External, inwards	AATGCCAATGGGGATCATAA	1801
	linkage between host chromosome and Tn6020b)	aphA1b-F (R)	Internal, outwards	CGACTGAATCCGGTGAGAAT	
	PCR26 (Tn6279 upstream,	HPA2-F	External, inwards	GCTGCACAGTGGTTTTCTGA	3214
	linkage between host chromosome and Tn1548- like_1)	catB8-R	Internal, outwards	GCACCGTCTCCAATTTTGAT	
	PCR27 (Tn6279 upstream,	araC-F	External, inwards	AATGCCAATGGGGATCATAA	3208
	linkage between host chromosome and Tn1548- like_1)	catB8-R	Internal, outwards	GCACCGTCTCCAATTTTGAT	
	PCR28 (ΔTn6279	sig-pep-F	External, inwards	AAAGTGACTCCGGTCTCGAA	507
	upstream, linkage between host chromosome and ATn6279)	tnpU-R	Internal, outwards	GTGGCATCAATGACCAAGTG	
	PCR29 (Tn6020b)	IS26-F		TGGTACTGGCGTAACCCTTC	1180 / 1349
		aphA1b-F (R)		CGACTGAATCCGGTGAGAAT	
	PCR30 (Tn6020b)	aphA1b-R (F)		GGTTGCATTCGATTCCTGTT	931
		IS26-R1		TCTGCCACTTCTTCACGTTG	
	PCR31 (linkage between	aphA1b-R (F)		GGTTGCATTCGATTCCTGTT	3325
	Tn6020b and Tn1548-like- 1)	catB8-R		GCACCGTCTCCAATTTTGAT	
	PCR32 (Tn1548-like-1)	catB8-F		ATGACTGGGCATCATCCTTC	3114
		CR1-R		GCTTTGAAGGCTGGGTAGTG	

PCR assay title	PCR assay code (genetic target)	Oligo Name	Oligo features	5'-3' sequence	Expected amplicon size(bp)
Genetic	PCR33 (Tn1548-like-1)	catB8-F		ATGACTGGGCATCATCCTTC	886
context of <i>armA</i>		aadA1-R		ACCAAGGCAACGCTATGTTC	
	PCR34 (Tn1548-like-1)	aadA1-F		TGATTTGCTGGTTACGGTGA	2522
		CR1-R		GCTTTGAAGGCTGGGTAGTG	
	PCR35 (Tn1548-like-1)	aadA1-F		TGATTTGCTGGTTACGGTGA	4462
		tnpU-R		GTGGCATCAATGACCAAGTG	
	PCR36 (host plasmid,	CR2-F		ATCAAAATGCTGCGTTCACA	1044
	adjacent to Tn1548-like-2, - $\Delta 1$ and - $\Delta 2$)	sulI2-R		GATATTCGCGGTTTTCCAGA	
	PCR37 (host plasmid,	CR2-F		ATCAAAATGCTGCGTTCACA	2338
	adjacent to Tn1548-like-2, - $\Delta 1$ and - $\Delta 2$)	parA-R		ATGGGCTCGTAGTCACCATC	
	PCR38 (linkage between the	Tnsul2-F		GAATTGCCTTTTGGCGTTTA	3546
	host plasmid and Tn1548- like-2)	arr2-R		GCTCCATCAAGGCTGAAAAG	
	PCR39 (linkage between the	Tnsul2-F		GAATTGCCTTTTGGCGTTTA	2543 / 2620
	host plassmid and $Tn1548$ - like-2- Λ 1 and - Λ 2)	gst-R		AATCGCGGAACAATATCCAG	
	PCR40 (Tn1548-like-2)	cmlA5-F		CTGCTAGGAAGCATCGGAAC	3889
		PER7-R		TCAGTAGCGTCGAGGCAGTA	
	PCR41 (Tn1548-like-2)	PER7-F		AGCTATCATTGCGCAGGTTG	630
		gst-R		AATCGCGGAACAATATCCAG	
	PCR42 (Tn1548-like-2, $-\Delta 1$, and $-\Delta 2$)	abct-F1		CAGAATAGGGGCGTTTTTCA	2338
		CR1-R		GCTTTGAAGGCTGGGTAGTG	
	PCR43 (Tn1548-like-2, -∆1,	abct-F2		CTGACCTTGTGGCACTTCAA	3774
	and $-\Delta 2$)	tnpU-R		GTGGCATCAATGACCAAGTG	
	PCR44 (Tn1548-like-1,	tnpU-F		TGGAAGAAAGACTCCGGCTA	790 / 2127
	Δ Tn6279, and Tn1548-like- 2, - Δ 1, and - Δ 2)	armA-R		TGTTGCGACTCTTTCATTCG	
	PCR45 (Tn1548-like-1,	tnpD-F		GTCCTGGTTGGCAAAGGTTA	1015 / 1843
	Δ Tn6279, and Tn1548-like- 2, - Δ 1, and - Δ 2)	msrE-R		TTTCCTGCTCCGTTATCACC	
	PCR46 (Tn1548-like-1,	pre-orfTn6257-F		GCGATGTTCCACGGTTTTAT	1929 / 4358
	Δ Tn6279, and Tn1548-like- 2, - Δ 1, and - Δ 2)	IS26-R1		TCTGCCACTTCTTCACGTTG	
	PCR47 (Tn6279 and	repA-F	Internal, outwards	TCCAGTACTACGCCATGCAA	1426
	$\Delta Tn6279$ downstream, linkage between Tn1548- like-1 and Δ Tn6279, respectively, with the host	permease-R	External, inwards	AAGAACGTGCGGGTCTTATG	
	chromosome) PCR48 (linkage between	renA-F		TCCAGTACTACGCCATGCAA	2285
	Tn1548-like-2, $-\Delta 1$ and $-\Delta 2$	res-R		GCGGTCTTGTTGATGCTGTA	2203
	and the host plasmid) PCR49 (host plasmid	res-F		GTGCAGATCATGCTTTTTCG	2464
	adjacent to Tn1548-like-2, -	CR2-R		GGACCGCAGTTGACTCTTTC	-
	$\Delta 1$ and $-\Delta 2$) PCP50 (Tp6270, circular	renA-F	Internal outwards	TCCAGTACTACGCCATGCAA	1909
	form)	anhA1h-F(R)	Internal outwards	CGACTGAATCCGGTGAGAAT	1707
		upin ito i (it)	internal, outwards	concrommeedoromonari	

PCR assay title	PCR assay code (genetic target)	Oligo Name Oligo features		5'-3' sequence	Expected amplicon size(bp)
Genetic	PCR51 (Tn1548-like-1,	repA-F	Internal, outwards	TCCAGTACTACGCCATGCAA	578 / 1398
context of armA	circular form)	intI1-R	Internal, outwards	GCCTTGATGTTACCCGAGAG	
	PCR52 (Tn1548-like-2,	repA-F	Internal, outwards	TCCAGTACTACGCCATGCAA	2273
	circular form)	arr2-R	Internal, outwards	GCTCCATCAAGGCTGAAAAG	
	PCR53 (Tn1548-like-2-Δ1	repA-F	Internal, outwards	TCCAGTACTACGCCATGCAA	1270 / 1347
	and $-\Delta 2$, circular forms)	gst-R	Internal, outwards	AATCGCGGAACAATATCCAG	
	PCR54 (Tn6279, insretion	HPA2-F	External, inwards	GCTGCACAGTGGTTTTCTGA	655 / 1484
	site)	permease-R	External, inwards	AAGAACGTGCGGGTCTTATG	
	PCR55 (Tn6279, insretion	araC-F	External, inwards	AATGCCAATGGGGATCATAA	Negative
	site)	permease-R	External, inwards	AAGAACGTGCGGGTCTTATG	
Genetic	PCR58 (AbGR-12-like	AB57_1175-F	External, inwards	AGGAGATCTTCTTGGCAGTCA	2254
context of aphA1	upstream)	TEM-D1-R	Internal, outwards	TTGCCGGGAAGCTAGAGTAA	
1	PCR59 (linkage between	TEM-D1-F		GCGGCCAACTTACTTCTGAC	3238
	TEM-D1 and $Tn1000$)	Tn1000-R		CGGTGTGACAAAACGCATAC	
	PCR60 (linkage between Tn1000 and aphA1)	Tn1000-F		GCATAATATTCCCGCGCTTA	3416 / 3437 / 3612
		aphA1b-R		GGTTGCATTCGATTCCTGTT	
	PCR61 (aphA1 downstream)	IS26-F		TGGTACTGGCGTAACCCTTC	1368 / 1543
		aphA1b-R		GGTTGCATTCGATTCCTGTT	
	PCR62 (aphA1 upstream)	aphA1b-F		CGACTGAATCCGGTGAGAAT	1100
		IS26-R1		TCTGCCACTTCTTCACGTTG	
	PCR63 (linkage between <i>aphA1</i> and class 1 integron)	aphA1b-F		CGACTGAATCCGGTGAGAAT	5134 / 5323 / 5781
		aadA1-R		ACCAAGGCAACGCTATGTTC	
	PCR64 (linkage between	IS26-F		TGGTACTGGCGTAACCCTTC	3319 / 4236 / 4425
	IS26 and class 1 integron)	aadA1-R		ACCAAGGCAACGCTATGTTC	/ 4883
	PCR65 (class 1 integron)	intI1-F		TGCGTGTAAATCATCGTCGT	3056 / 3594 / 3695
		aadA1-R		ACCAAGGCAACGCTATGTTC	
	PCR66 (class 1 integron)	aadA1-F		TGATTTGCTGGTTACGGTGA	2297
		orf5-F (R)		TAGGAGCTCGGATCTCAGGA	
	PCR67 (linkage between	IS26-F		TGGTACTGGCGTAACCCTTC	3776
	IS26 and class 1 integron)	aadA1-F (R)		TGATTTGCTGGTTACGGTGA	
	PCR68 (linkage between	aadA1-R (F)		ACCAAGGCAACGCTATGTTC	3725 / 4371
	class 1 integron and IS26)	Tn21-R		ATATACCCAATGCGCTGTCC	
	PCR69 (AbGR-12-like	AB57_1175-F	External, inwards	AGGAGATCTTCTTGGCAGTCA	4921
	upstream)	Tn21-R	Internal, outwards	ATATACCCAATGCGCTGTCC	
	PCR70 (AbGR-12-like downstream)	Tn21-F	Internal, outwards	TACCGTGGCAGGAAGAAATC	2108
		AB57_1209-R	External, inwards	CATCTGCCATCCAGTTTGTG	

PCR assay title	PCR assay code (genetic target)	Oligo Name	Oligo features	5'-3' sequence	Expected amplicon size(bp)	
Genetic context of	PCR71 (Tn6020, circular form)	aphA1b-circular-F	Internal, outwards	TGCATCATCAGGAGTACGGA	1620 / 1780 / 1947 / 1968 / 2143	
aphA1	,	aphA1b-R	Internal, outwards	GGTTGCATTCGATTCCTGTT		
Genetic context of	PCR72 (Tn <i>aphA6</i> downstream)	aci6-plasmid- ST636-F	External, inwards	ACGGTTCACGAACTTTGACA	1471	
aphA6	,	aphA6-R	Internal, outwards	TCGTGCTGGATTAGCAGATG		
	PCR73 (TnaphA6 upstream)	aphA6-F	Internal, outwards	GATGGCGACTGACCAATTTT	1484	
		aci6-plasmid- ST636-R	External, inwards	CCTTAAGCTTTTCAGCTCATCAA		
	PCR74 (Tn <i>aphA6</i> downstream)	aci6-plasmid-ST25- F	External, inwards	TGAACAATGATACCTCGAAAGTT	1537 / 1792	
		aphA6-R	Internal, outwards	TCGTGCTGGATTAGCAGATG		
	PCR75 (TnaphA6 upstream)	aphA6-F	Internal, outwards	GATGGCGACTGACCAATTTT	1633	
		aci6-plasmid-ST25- R1	External, inwards	CTTGAGGAAGGGATGGTTGA		
	PCR76 (TnaphA6 upstream)	aphA6-F	Internal, outwards	GATGGCGACTGACCAATTTT	1490 / 2655 / 3745	
		aci6-plasmid-ST25- R2	External, inwards	GCCTTTAAAGCAAAAACAAAGC		
	PCR77 (Aci6 plasmid)	aci6-plasmid- ST636-int-F1		TTTGCAATTATGGGCTCCAC	1044	
		aci6-plasmid- ST636-int-R1		TACCCGACTCTTCAGGTGCT		
	PCR78 (Aci6 plasmid)	aci6-plasmid- ST636-int-F2		TTGCTTTAATCGGTGGTTCC	493	
		aci6-plasmid- ST636-int-R2		TTATAGGCTGCACCGACACA		
	PCR79 (Tn <i>aphA6</i> circular form)	aphA6-F	Internal, outwards	GATGGCGACTGACCAATTTT	1442 / 1697	
	101111)	aphA6-R	Internal, outwards	TCGTGCTGGATTAGCAGATG		
	PCR80 (Tn <i>aphA6</i> insretion site)	aci6-plasmid- ST636-F	External, inwards	ACGGTTCACGAACTTTGACA	423 / 1513 / 3498	
		aci6-plasmid- ST636-R	External, inwards	CCTTAAGCTTTTCAGCTCATCAA		
	PCR81 (Tn <i>aphA6</i> insertion site)	aci6-plasmid-ST25- F	External, inwards	TGAACAATGATACCTCGAAAGTT	1728 / 3713	
		aci6-plasmid-ST25- R1	External, inwards	CTTGAGGAAGGGATGGTTGA		
	PCR82 (Tn <i>aphA6</i> insertion site)	aci6-plasmid-ST25- F	External, inwards	TGAACAATGATACCTCGAAAGTT	1840 / 3825	
		aci6-plasmid-ST25- R2	External, inwards	GCCTTTAAAGCAAAAACAAAGC		

Isolate	<u>Quinolone resistance</u> chromosomal mutations		<u>Streptomycin</u> resistance genes	<u>Macrolide</u> resistance genes]	<u>Phenicol</u> resistance genes		
1001000	GyrA	ParC	strA, strB	msr(E), mph(E)	cmlA7	catA1	catB8	floR
A068	S83L	S80L	strA, strB	msr(E), mph(E)	cmlA7	_	-	_
A069	S83L	S80L	strA, strB	msr(E), mph(E)	_	_	-	_
A070	S83L	S80L	strA, strB	msr(E), mph(E)	_	_	catB8	_
A071	S83L	S80L	strA, strB	msr(E), mph(E)	_	_	catB8	_
A072	S83L	S80L	strA, strB	msr(E), mph(E)	-	_	_	_
A074	S83L	S80L	-	-	-	catA1	-	_
A076	S83L	S80L	-	-	-	catA1	-	_
A077	S83L	S80L	strA, strB	-	-	_	_	_
A078	S83L	S80L	strA, strB	-	-	_	_	_
A079	S83L	S80L	strA, strB	msr(E), mph(E)	-	_	_	_
A080	S83L	S80L	strA, strB	msr(E), mph(E)	_	-	_	_
A082	S83L	S80L	-	-	_	catA1	_	floR
A084	S83L	S80L	strA, strB	-	_	_	_	_
A085	S83L	S80L	-	-	_	_	_	_
A086	S83L	S80L	strA, strB	msr(E), mph(E)	_	-	_	_
A087	S83L	S80L	strA, strB	-	-	-	_	_
A089	S83L	S80L	-	msr(E), mph(E)	-	-	_	_
A091	S83L	S80L	strA, strB	msr(E), mph(E)	-	-	catB8	_
A092	S83L	S80L	strA, strB	msr(E), mph(E)	cmlA7	-	_	_
A093	S83L	S80L	strA, strB	msr(E), mph(E)	cmlA7	-	_	_
A094	S83L	S80L	strA, strB	msr(E), mph(E)	-	-	_	_
A095	S83L	S80L	strA, strB	msr(E), mph(E)	-	-	_	_
A096	S83L	S80L	strA, strB	msr(E), mph(E)	cmlA7	-	_	_
A097	S83L	S80L	strA, strB	msr(E), mph(E)	cmlA7	-	_	_
A099	S83L	S80L	-	msr(E), mph(E)	-	catA1	_	_
A100	S83L	S80L	-	-	_	catA1	_	-
A101	S83L	S80L	strA, strB	-	_	-	_	-
A105	S83L	S80L	-	-	_	catA1	_	_

TABLE S2. Quinolone, streptomycin, macrolide, and phenicol resistance features.

Isolate	<u>Rifampicin</u> resistance genes	Sulphonamide resistance genes		<u>To</u> resi		
	arr-2	sul1	sul2	tet(A)	tet(B)	tet(39)
A068	arr-2	sull (2 copies)	sul2 (2 copies)	_	tet(B)	-
A069	-	sul1	sul2 (2 copies)	_	tet(B)	-
A070	-	sul1 (2 copies)	sul2	_	$\Delta tet(B)$	-
A071	_	sul1	sul2	-	$\Delta tet(B)$	_
A072	-	-	sul2	-	$\Delta tet(B)$	-
A074	-	sull (2 copies)	_	_	-	_
A076	-	sull (2 copies)	_	tet(A)	-	_
A077	-	_	-	-	$\Delta tet(B)$	-
A078	-	_	-	_	-	tet(39)
A079	-	_	_	-	$\Delta tet(B)$	-
A080	-	_	_	_	$\Delta tet(B)$	-
A082	-	sull (2 copies)	_	tet(A)	-	-
A084	-	sul1	sul2	-	$\Delta tet(B)$	-
A085	-	sul1	_	$tet(A)_{OIFC137}$	-	-
A086	-	_	sul2	-	$\Delta tet(B)$	-
A087	-	_	_	-	$\Delta tet(B)$	-
A089	-	_	sul2	-	-	-
A091	-	sul1	_	-	$\Delta tet(B)$	-
A092	arr-2	sull (2 copies)	sul2 (2 copies)	_	tet(B)	-
A093	arr-2	sull (2 copies)	sul2 (2 copies)	_	tet(B)	-
A094	-	sul1	sul2 (2 copies)	_	tet(B)	-
A095	-	_	sul2	-	$\Delta tet(B)$	_
A096	arr-2	sull (2 copies)	sul2 (2 copies)	-	tet(B)	_
A097	arr-2	sull (2 copies)	sul2 (2 copies)	-	tet(B)	_
A099	-	sull (2 copies)	_	tet(A)	-	_
A100	-	sull (2 copies)	_	tet(A)	-	-
A101	-	_	_	_	$\Delta tet(B)$	_
A105	-	sull (2 copies)	_	-	-	-

TABLE S3. Rifampicin, sulphonamide, and tetracycline resistance features.

Isolate			<u>Plasmid replicon types</u> ^a					BioProject	BioSample
1001000	GR1	GR2	GR6	GR7	GR8	GR10	GR14	accession number	accession number
A068	_	Aci1	-	-	_	_	-	PRJNA282589	SAMN03571960
A069	_	-	-	-	_	_	-	PRJNA282600	SAMN03575971
A070	_	_	Aci6	_	Aci9	_	_	PRJNA282601	SAMN03575972
A071	_	_	_	_	_	-	_	PRJNA282602	SAMN03575974
A072	_	Aci1	Aci6	_	_	_	_	PRJNA282603	SAMN03576356
A074	_	Aci1	Aci6	_	_	-	_	PRJNA282604	SAMN03576358
A076	_	Aci1	_	_	_	-	p4AYE	PRJNA282605	SAMN03576359
A077	_	Aci1	_	_	_	_	_	PRJNA282606	SAMN03576361
A078	_	Aci1	_	_	_	_	_	PRJNA282607	SAMN03576362
A079	_	Aci1	_	_	_	_	_	PRJNA282608	SAMN03576363
A080	_	Aci1	_	_	_	_	_	PRJNA282609	SAMN03576364
A082	_	Aci1	Aci6	_	_	_	_	PRJNA282610	SAMN03576365
A084	_	Aci1	Aci6	_	_	_	_	PRJNA282611	SAMN03576366
A085	_	_	_	_	_	_	_	PRJNA282613	SAMN03576441
A086	p1S1	Aci1	_	_	_	_	_	PRJNA282614	SAMN03576442
A087	_	Aci1	_	_	_	_	_	PRJNA282615	SAMN03576445
A089	_	Aci1	_	_	_	_	_	PRJNA282616	SAMN03576446
A091	_	Aci1	Aci6	_	_	_	_	PRJNA282617	SAMN03576448
A092	_	Aci1	Aci6	_	_	_	_	PRJNA282618	SAMN03576449
A093	_	Aci1	_	_	_	_	_	PRJNA282619	SAMN03576505
A094	_	Aci1	Aci6	_	_	_	_	PRJNA282620	SAMN03576511
A095	_	Aci1	Aci6	_	_	_	_	PRJNA282622	SAMN03576512
A096	_	Aci1	Aci6	_	_	_	_	PRJNA282623	SAMN03577725
A097	_	Aci1	Aci6	_	_	_	_	PRJNA282626	SAMN03577726
A099	_	_	Aci6	_	_	AciX	_	PRJNA282627	SAMN03577727
A100	_	Aci1	_	p3S2	_	_	p4AYE	PRJNA282628	SAMN03577728
A101	_	Aci1	Aci6	_	_	_	_	PRJNA282640	SAMN03577729
A105	-	Aci1	Aci6	_	_	_	_	PRJNA282641	SAMN03577730

TABLE S4. Plasmid replicon types carried by the isolates, and the BioProject and BioSample accession numbers.

^{*a*} According to the method described by **Bertini A, Poirel L, Mugnier PD, Villa L, Nordmann P, Carattoli A.** 2010. Characterization and PCR-based replicon typing of resistance plasmids in *Acinetobacter baumannii*. Antimicrob Agents Chemother **54**:4168–4177.

TABLE S5. Genetic structure and epidemiological data of plasmids carrying the bla_{OXA-24} or

*bla*_{OXA-72} genes.

Plasmid	Comments	Size (bp)	Genetic structure	GenBank accession number	Referrence ^a	
pABVA01	2000 / Varese,	8963	4 iterons, <i>repB</i> _{pABVA01} , <i>repA</i> _{pABVA01} , XerC/XerD-like sequence 1,	FM210331	DAndrea et	
	Italy / Int Clone		bla _{OXA-24} , XerC/XerD-like sequence 2, abkA, abkB, tonB,		al., 2009	
			orf _{Septicolysin} , XerC/XerD-like sequence 3, <i>fliD</i> , orf1, orf2 (189 bp)			
pMMCU3	Spain	8964	4 iterons, <i>repB</i> _{pABVA01} , <i>repA</i> _{pABVA01} , XerC/XerD-like sequence 1,	GQ904227	Merino et	
		<i>bla</i> _{OXA-24} , XerC/XerD-like sequence 2, <i>abkA</i> , <i>abkB</i> , <i>tonB</i> ,			al., 2010	
			orf _{Septicolysin} , XerC/XerD-like sequence 3, fliD, orf1, orf2 (189 bp)			
pA077	2013 / Skåne,	8963	4 iterons, <i>repB</i> _{pABVA01} , <i>repA</i> _{pABVA01} , XerC/XerD-like sequence 1,	This study	This study	
Sweden / ST2	Sweden / ST2	ST2 <i>bla</i> _{OXA-24} , XerC/XerD-like sequence 2, <i>abkA</i> , <i>abkB</i> , <i>tonB</i> ,				
			orf _{Septicolysin} , XerC/XerD-like sequence 3, fliD, orf1, orf2 (189 bp)			
pA087	2013 / Våstra	8963	4 iterons, <i>repB</i> _{pABVA01} , <i>repA</i> _{pABVA01} , XerC/XerD-like sequence 1,	This study	This study	
Götaland, Sweden / ST2		bla _{OXA-24} , XerC/XerD-like sequence 2, abkA, abkB, tonB,				
	5 weden / 512		orf _{Septicolysin} , XerC/XerD-like sequence 3, fliD, orf1, orf2 (189 bp)			
pAB-	2012 / Japan	8970	4 iterons, <i>repB</i> _{pAB0057} , <i>repA</i> _{pAB0057} , XerC/XerD-like sequence 1,	AB823544	Tada <i>et al</i> .,	
NCGM253	A253		bla _{OXA-72} , XerC/XerD-like sequence 2, abkA, abkB, tonB,		2014	
			orf _{Septicolysin} , XerC/XerD-like sequence 3, fliD, orf1, orf2 (339 bp)			
pA074	2012 / Skåne,	9831	4 iterons, <i>repB</i> _{pAB0057} , <i>repA</i> _{pAB0057} , XerC/XerD-like sequence 1,	This study	This study	
	Sweden / ST636	Г636	36 <i>bla</i> _{OXA-72} , IS <i>Aba31</i> , XerC/XerD-like sequence 2, <i>abkA</i> , <i>abkB</i> ,			
			tonB, orf _{Septicolysin} , XerC/XerD-like sequence 3, fliD, orf1, orf2			
			(339 bp)			
pA078	2013 / Våstra	9831	4 iterons, <i>repB</i> _{pAB0057} , <i>repA</i> _{pAB0057} , XerC/XerD-like sequence 1,	This study	This study	
	Götaland, Sweden / ST23		bla _{OXA-72} , ISAba31, XerC/XerD-like sequence 2, abkA, abkB,			
	5 weden / 5125		tonB, orf _{Septicolysin} , XerC/XerD-like sequence 3, fliD, orf1, orf2			
			(339 bp)			
pA100	2013 / Skåne,	15166	4 iterons, <i>repB</i> _{pAB0057} , <i>repA</i> _{pAB0057} , XerC/XerD-like sequence 1,	This study	This study	
	Sweden / ST1		bla _{OXA-72} , ISAba31, XerC/XerD-like sequence 2, abkA, abkB,			
			tonB, orf _{Septicolysin} , XerC/XerD-like sequence 3, orf, mobA, rep3,			
			XerC/XerD-like sequence 4, emrE, orf _{Plasmid mobilization} ,			
			XerC/XerD-like sequence 5, fliD, orf1, orf2 (339 bp)			
pA105	2013 /	9830	4 iterons, <i>repB</i> _{pAB0057} , <i>repA</i> _{pAB0057} , XerC/XerD-like sequence 1,	This study	This study	
	Stockholm, Sweden / ST636		bla _{OXA-72} , ISAba31, XerC/XerD-like sequence 2, abkA, abkB,			
	Sweden / \$1636		tonB, orf _{Septicolysin} , XerC/XerD-like sequence 3, fliD, orf1, orf2			
			(339 bp)			

^{*a*} **D'Andrea MM, Giani T, D'Arezzo S, Capone A, Petrosillo N, Visca P, Luzzaro F, Rossolini GM.** 2009. Characterization of pABVA01, a plasmid encoding the OXA-24 carbapenemase from Italian isolates of *Acinetobacter baumannii*. Antimicrob Agents Chemother **53**:3528–3533.

Merino M, Acosta J, Poza M, Sanz F, Beceiro A, Chaves F, Bou G. 2010. OXA-24 carbapenemase gene flanked by XerC/XerD-like recombination sites in different plasmids from different *Acinetobacter* species isolated during a nosocomial outbreak. Antimicrob Agents Chemother **54**:2724–2727.

Tada T, Miyoshi-Akiyama T, Shimada K, Shimojima M, Kirikae T. 2014. Dissemination of 16S rRNA methylase ArmA-producing *Acinetobacter baumannii* and emergence of OXA-72 carbapenemase coproducers in Japan. Antimicrob Agents Chemother **58**:2916–2920.

	GenBank accession number		Species of first	NCBI reference		Previous
Variant ^a	Protein	Nucleotide	identification	sequence, length ^b	Reference	designations
ADC-1	CAB77444	AJ009979	Acinetobacter baumannii	WP_004714775	Bou & Martinez- Beltran, 2000	ADC-NIPH 1362
ADC-2	AAO43172	AY177427	Oligella urethralis	WP_004746565	Mammeri et al., 2003	ADC-NIPH 1734
ADC-3	AAO59456	AY178995	A. baumannii	_	Mammeri et al., 2003	_
ADC-4	AAO59457	AY178996	A. baumannii	_	Mammeri et al., 2003	-
ADC-5	CAE00827	AJ575184	Acinetobacter pittii	WP_038405930	Beceiro et al., 2004	-
ADC-6	AAR13676	AY325306	A. baumannii	WP_017725267	Segal et al., 2004	-
ADC-7	AAT70411	AY648950	A. baumannii	_	Hujer et al., 2005	-
ADC-10	ABI18382	DQ883640	A. baumannii	_	Hujer <i>et al.</i> , not published	_
ADC-11	ADG46039	GU591983; CU459141	A. baumannii	WP_001211205	Rodriguez-Martinez <i>et al.</i> , 2010; Fournier <i>et al.</i> , 2006	-
ADC-12	CAK95249	AM283529	A. pittii	_	Beceiro et al., 2009	-
ADC-13	CAK95248	AM283528	A. pittii	_	Beceiro et al., 2009	-
ADC-14	CAK95247	AM283527	A. pittii	_	Beceiro et al., 2009	-
ADC-15	CAK95246	AM283526	A. pittii	_	Beceiro et al., 2009	_
ADC-16	CAK95245	AM283525	A. pittii	_	Beceiro et al., 2009	-
ADC-17	CAK95244	AM283524	A. pittii	_	Beceiro et al., 2009	_
ADC-18	CAK95243	AM283523	A. pittii	WP_002118772	Beceiro et al., 2009	-
ADC-19	CAK95242	AM283522	A. pittii	_	Beceiro et al., 2009	-
ADC-20	CAK95241	AM283521	A. pittii	_	Beceiro et al., 2009	_
ADC-21	CAK95240	AM283520	A. pittii	_	Beceiro et al., 2009	-
ADC-22	CAK95239	AM283519	A. pittii	_	Beceiro et al., 2009	-
ADC-23	CAK95238	AM283518	A. pittii	_	Beceiro et al., 2009	_
ADC-24	CAK95237	AM283517	A. pittii	_	Beceiro & Bou., not published	ADC-19
ADC-25	ABK34773	EF016355	A. baumannii	WP_001211217	Zong et al., 2008	ADC-NIPH 528
ADC-26	ADG46043	GU591987	A. baumannii	WP_001211238	Rodriguez-Martinez <i>et al.</i> , 2010	ADC-NIPH 146
ADC-29	ACC66195	EU604835	A. baumannii	_	Chiu <i>et al.</i> , not published	_
ADC-30	ADG46041	GU591985	A. baumannii	WP_001211218	Rodriguez-Martinez <i>et al.</i> , 2010	ADC-NIPH 2061
ADC-38	ACC95873	EU652243	A. baumannii	_	Bogaerts et al. 2008	-
ADC-39	ACC95874	EU652244	A. baumannii	_	Bogaerts et al. 2008	-
ADC-41	ACN62070	FJ744160	A. pittii	_	Huang et al., 2010	-
ADC-42	ACN62071	FJ744161	A. pittii	-	Huang et al., 2010	-
ADC-43	ACN62072	FJ744162	A. pittii	WP_032055358	Huang et al., 2010	-
ADC-44	ACN62073	FJ744163	A. pittii	-	Huang et al., 2010	-
ADC-50	ADG46038	GU591982	A. baumannii	WP_031965243	Rodriguez-Martinez <i>et al.</i> , not published	_
ADC-51	ADG46040	GU591984	A. baumannii	_	Rodriguez-Martinez <i>et al.</i> , 2010	_
ADC-52	ADG46042	GU591986	A. baumannii	WP_001211232	Rodriguez-Martinez <i>et al.</i> , 2010	_
ADC-53	ADG46044	GU591988	A. baumannii	_	Rodriguez-Martinez <i>et al.</i> , 2010	_
ADC-54	ADK35761	HM437231	A. baumannii	_	Bogaerts et al., 2010	-

TABLE S6. Numeration of the GenBank variants of bla_{ADC} .

	GenBank a	ccession number	Species of first	NCBI reference	0	Previous
Variant ^a	Protein	Nucleotide	identification	sequence, length ^b	Reference ^c	designations
ADC-56	AEL30570	JF265067	A. baumannii	WP_031973850	Tian et al., 2011	-
ADC-57	ADO51072	HQ258925	A. baumannii	WP_001211226	Revathi et al., 2013	-
ADC-58	AFG25594	JQ319653	A. baumannii	-	Zhang, not published	-
ADC-59	AFG25595	JQ319654	A. baumannii	-	Zhang, not published	-
ADC-60	AFH53180	JQ692087	A. baumannii	-	Huang, not published	-
ADC-61	AFI56570	JQ753702	A. baumannii	WP_033503051	Zhou, not published	_
ADC-62	AFK24475	JQ867374	A. baumannii	-	Wang, not published	_
ADC-63	AFM80040	JQ911781	A. baumannii	_	Zhang, not published	_
ADC-64	AFM80041	JQ911782	A. baumannii	_	Zhang, not published	_
ADC-65	AFP73417	JX109941	A. baumannii	385 amino acid	Ling et al., 2013	_
ADC-66	AFP73418	JX109942	A. baumannii	_	Ling et al., 2013	_
ADC-67	AFP89364	JX169789	A. baumannii	-	Xiao-min <i>et al.</i> , 2014	ADC-57 (AEZ36052)
ADC-68	AGL39360	KC866352	A. baumannii	-	Lee <i>et al.</i> , 2014 (as a poster); Jeon <i>et al.</i> , 2014	_
ADC-72	AIL90389	KJ885607	Acinetobacter calcoaceticus	WP_017480710	Sun et al., 2014	_
ADC-73	ALA14808	KP881233	A. baumannii	WP_001211219	This study (isolate A072)	-
ADC-74	ALA14809	KP881234	A. baumannii	WP_001211203	This study (isolate A074)	-
ADC-75	ALA14810	KP881235	A. baumannii	_	This study (isolate A076)	-
ADC-76	ALA14811	KP881236	A. baumannii	WP_001211237	This study (isolate A078, intrinsic)	ADC-NIPH 335
ADC-77	ALA14812	KP881237	A. baumannii	-	This study (isolate A078, acquired)	_
ADC-78	ALA14813	KP881238	A. baumannii	WP_057691006	This study (isolate A082)	_
ADC-79	ALA14814	KP881239	A. baumannii	WP_001159760	This study (isolate A085)	_
ADC-80	ALA14815	KP881240	A. baumannii	WP_029424536	This study (isolate A099)	_
ADC-81	ALA14816	KP881241	A. baumannii	388 amino acid	This study (isolate A100)	_
ADC-82	AAV32519	AY758396	A. baumannii	-	Heritier et al., 2006	-
ADC-83	ABO38124	EF433777	A. baumannii	-	Huang <i>et al.</i> , 2007 unpublished	_
ADC-84	ABV21800	EU118261	A. baumannii	WP_001211220, 384 amino acid	Bratu <i>et al.</i> , 2008	-
ADC-85	ABV21801	EU118262	A. baumannii	-	Bratu et al., 2008	-
ADC-86	ABV21802	EU118263	A. baumannii	-	Bratu et al., 2008	-
ADC-87	ETY67158	AZNQ01000099	A. baumannii	384 amino acid	Dent et al., 2010	-
ADC-88	ADX04315	CP001921	A. baumannii	WP_001211223	Park et al., 2011	-
ADC-89	AFU38919	CP003856	A. baumannii	-	Liou et al., 2012	-
ADC-90	WP_017816757	NZ_AOLU01000048	A. baumannii	WP_017816757	Ho et al., 2013	-
ADC-91	ELW88222	AMGA01000054	A. baumannii	WP_002157727	Harkins <i>et al.</i> , 2013 uppublished	-
ADC-92	ENW75976	APRG01000011	A. baumannii	WP_001211227	Perichon <i>et al.</i> , 2014	ADC-CIP 70– 34 ^T
ADC-93	ENU51112	APOQ01000006	A. baumannii	WP_004712857	Perichon et al., 2014	ADC-NIPH 1669

TABLE S6. CONT. Numeration of the GenBank variants of bla_{ADC} .

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.	GenBank a	accession number	Species of first	NCBI reference		Previous
Variant	Protein	Nucleotide	identification	sequence, $length^{b}$	Keference	designations
ADC-94	ENV26641	APPL01000015	A. baumannii	WP_002126587	Perichon et al., 2014	ADC-NIPH 190
ADC-95	ENW36647	APQV01000007	A. baumannii	WP_005109685	Perichon et al., 2014	ADC-NIPH 201
ADC-96	ENW46489	APQY01000003	A. baumannii	WP_005123276	Perichon et al., 2014	ADC-NIPH 329
ADC-97	ENV30802	APPM01000011	A. baumannii	WP_004840559	Perichon et al., 2014	ADC-NIPH 60
ADC-98	ENW51893	APQZ01000007	A. baumannii	WP_005128228	Perichon et al., 2014	ADC-NIPH 601
ADC-99	ENU68675	APOV01000029	A. baumannii	WP_004739487	Perichon et al., 2014	ADC-NIPH 615
ADC-100	ENW51227	APRA01000004	A. baumannii	WP_005131186	Perichon et al., 2014	ADC-NIPH 67
ADC-101	ENW72863	APRE01000031	A. baumannii	WP_005138362	Perichon et al., 2014	ADC-NIPH 80
ADC-102	ENW00696	APQI01000003	A. calcoaceticus	WP_005046018	Perichon et al., 2014	ADC-CIP 81– 8 ^T
ADC-103	ENU07956	APOE01000009	A. calcoaceticus	WP_004643536	Perichon et al., 2014	ADC-NIPH 13
ADC-104	ENV92309	APQH01000006	A. calcoaceticus	WP_005039111	Perichon et al., 2014	ADC-ANC 3680
ADC-105	ENV41121	APPP01000013	Acinetobacter nosocomialis	WP_004886093	Perichon et al., 2014	ADC-NIPH 386
ADC-106	ENU48760	APOP01000002	A. nosocomialis	WP_004707701	Perichon et al., 2014	ADC-NIPH 2119 ^T
ADC-107	ENW11417	APQN01000012	A. pittii	WP_005068074	Perichon et al., 2014	ADC-ANC 3678
ADC-108	ENU43147	APOO01000021	Acinetobacter gen. sp. "Close to 13TU"	WP_004700205	Perichon et al., 2014	ADC-NIPH 973
ADC-109	ENX43770	APSC01000009	Acinetobacter gen. sp. "Between 1 and 3"	WP_005307218	Perichon et al., 2014	ADC-NIPH 542
ADC-110	ENV03983	APPF01000018	Acinetobacter gen. sp. "Between 1 and 3"	WP_004790939	Perichon et al., 2014	ADC-NIPH 817
ADC-111	EOQ64883	APQJ01000005	A. calcoaceticus-like	WP_016137488	Perichon et al., 2014	ADC-ANC 3811
ADC-112	EOQ71234	APQM01000001	A. pittii-like	WP_016140427	Perichon et al., 2014	ADC-ANC 4050
ADC-113	EOQ73533	APQO01000006	A. pittii-like	WP_016146025	Perichon et al., 2014	ADC-ANC 4052
ADC-114	EXS60093	JFYI01000005	A. baumannii	WP_032039838	Harris <i>et al.</i> , unpublished	-
ADC-115	EYS55294	JHPF01000005	A. baumannii	WP_001211209	Harris <i>et al.</i> , unpublished	-
ADC-116	EXD64655	JEZV01000049	A. baumannii	WP_032062810	Harris <i>et al.</i> , unpublished	-
ADC-117	ETP95102	AYGO01000141	A. baumannii	WP_031980335	Wright et al.,	-
ADC-118	WP_033502167	NZ_AGSU01000096	A. baumannii	WP_033502167	Liou <i>et al.</i> , unpublished	-
ADC-119	WP_001211214	NZ_AMIJ01000141	A. baumannii	WP_001211214	Sahl <i>et al.</i> , unpublished	-
ADC-120	KHY08585	JWWE03000102	A. baumannii	WP_039270258	Adams <i>et al.</i> , unpublished	-
ADC-121	KHV30477	JWSI03000106	A. baumannii	WP_039258389	Adams <i>et al.</i> , 2015 unpublished	-
ADC-122	KJC71195	JZCF01000044	A. baumannii	WP_044718369	Adams <i>et al.</i> , 2015 unpublished	_

TABLE S6. CONT. Numeration of the GenBank variants of bla_{ADC} .

.	GenBank a	accession number	Species of first	NCBI reference		Previous
variant	Protein	Nucleotide	identification	sequence, $length^b$	Reference	designations
ADC-401	CAL25116	AM293332	Acinetobacter baylyi	WP_004923134, 397 amino acid	Beceiro et al., 2007	ADC-8, ADC- CIP 107474 ^T
ADC-501	ENW07270	APQL01000005	Acinetobacter	WP_005060342,	Perichon et al., 2014	ADC-CIP
ADC-502	ENW06097	APQK01000009	beijerinckii A. beijerinckii	395 amino acid WP_039909284, 395 amino acid	Perichon et al., 2014	ADC-ANC 3835
ADC-503	ENW20454	APQQ01000012	Acinetobacter haemolyticus	WP_005087351, 395 amino acid	Perichon et al., 2014	ADC-CIP 64–
ADC-504	ENW22241	APQR01000003	A. haemolyticus	WP_005088798,	Perichon et al., 2014	ADC-NIPH
ADC-505	ENV65577	APPX01000035	Acinetobacter junii	WP_026057384, 397 amino acid	Perichon et al., 2014	ADC-CIP 64– 5 ^T
ADC-506	ENV51174	APPS01000043	A. junii	WP_042106493,	Perichon et al., 2014	ADC-CIP
ADC-507	ENV64403	APPW01000004	A. junii	WP_051067828,	Perichon et al., 2014	ADC-NIPH
ADC-508	ENV74627	APQA01000028	Acinetobacter	WP_004986092,	Perichon et al., 2014	ADC-CIP
ADC-509	ENV78143	APQC01000023	A. ursingii	WP_005005518,	Perichon et al., 2014	ADC-ANC
ADC-510	ENX45677	APQB01000030	A. ursingii	WP_004999532, 401 amino acid	Perichon et al., 2014	ADC-NIPH
ADC-511	ENV38300	APPO01000008	Acinetobacter venetianus	WP_004878176, 392 amino acid	Perichon et al., 2014	ADC-CIP
ADC-512	ENU28809	APOK01000047	Acinetobacter gen.	WP_004673603,	Perichon et al., 2014	ADC-CIP
ADC-513	ENW97918	APRM01000005	Acinetobacter gen.	WP_005194146,	Perichon et al., 2014	ADC-NIPH
ADC-514	ENX35907	APRZ01000007	Acinetobacter gen.	WP_032878960, 395 amino acid	Perichon et al., 2014	ADC-NIPH
ADC-515	ENX18440	APRT01000003	Acinetobacter gen.	WP_026040157, 395 amino acid	Perichon et al., 2014	ADC-CIP 64–
ADC-516	ENX09334	APRR01000006	Acinetobacter gen.	WP_005228083, 395 amino acid	Perichon et al., 2014	ADC-NIPH
ADC-517	ENX39917	APSA01000003	Acinetobacter gen. sp. 14BJ	WP_005282242, 395 amino acid	Perichon et al., 2014	ADC-NIPH 3623 (corrected)
ADC-518	ENX56225	APSD01000035	Acinetobacter gen.	WP_005317155, 395 amino acid	Perichon et al., 2014	ADC-ANC
ADC-519	ENV10055	APPH01000006	Acinetobacter gen.	WP_004803441,	Perichon et al., 2014	ADC-CIP 56–
ADC-520	ENX60630	APRN01000033	Acinetobacter gen.	WP_005201690,	Perichon et al., 2014	ADC-CIP 70–
ADC-521	ENW94247	APRL01000010	Acinetobacter gen.	WP_005186110,	Perichon et al., 2014	ADC-ANC
ADC-522	ENX53738	APRO01000007	<i>Acinetobacter</i> gen.	WP_005209612,	Perichon et al., 2014	ADC-NIPH
ADC-523	ENW98345	APRP01000033	Acinetobacter Taxon	WP_005219147, 388 amino acid	Perichon et al., 2014	ADC-ANC
ADC-524	ENU27798	APOJ01000016	Acinetobacter Taxon	WP_004659736, 388 amino acid	Perichon et al., 2014	ADC-NIPH
ADC-525	WP_050041209	NZ_LACJ01000004	Acinetobacter parvus	WP_050041209, 388 amino acid	Pedron <i>et al.</i> , 2015 unpublished	-

TABLE S6. CONT. Numeration of the GenBank variants of bla_{ADC} .

T • · · · · · · · · · · · · · · · · · ·	GenBank accession number		Species of first	NCBI reference		Previous
Variant"	Protein	Nucleotide	identification	sequence, length ^b	Reference	designations
ADC-526	ESK55746	AYEV01000014	Acinetobacter	WP_023274629,	Cerqueira et al.,	-
			tjernbergiae	388 amino acid	2013 unpublished	
ADC-527	ENU21567	APOI01000030	Acinetobacter Taxon	WP_004656962,	Perichon et al., 2014	ADC-NIPH
			19	395 amino acid		809
ADC-528	ENU93346	APPC01000015	Acinetobacter Taxon	WP_004776385,	Perichon et al., 2014	ADC-NIPH
			20	395 amino acid		758
ADC-529	ENX19523	APRW01000016	Acinetobacter Taxon	WP_005260284,	Perichon et al., 2014	ADC-NIPH
			20	395 amino acid		2168
ADC-530	ENW83258	APRH01000012	Acinetobacter Taxon	WP_005147866,	Perichon et al., 2014	ADC-ANC
			21	395 amino acid		3929
						(corrected)
ADC-531	ENX38460	APSB01000022	Acinetobacter Taxon	WP_005297698,	Perichon et al., 2014	ADC-NIPH
			22	395 amino acid		2100
ADC-601	ENV90446	APOG01000050	Acinetobacter	WP 005034629.	Perichon et al., 2014	ADC-CIP 70–
		C	bereziniae	390 amino acid	· · · · · · · · · · · · · · · · · · ·	12^{T}
ADC-602	ENV20683	APPK01000046	A. bereziniae	WP 004832033,	Perichon et al., 2014	ADC-NIPH 3
				390 amino acid	,	
ADC-603	ENU57495	APOS01000032	Acinetobacter	WP 004723463,	Perichon et al., 2014	ADC-CIP 63-
			guillouiae	391 amino acid	,	46^{T}
ADC-604	ENV14942	APPJ01000016	A. guillouiae	WP 004823669,	Perichon et al., 2014	ADC-NIPH
			Ū	391 amino acid		991
ADC-701	ENV73166	APPZ01000007	Acinetobacter	WP 004983048.	Perichon et al., 2014	ADC-ANC
			iohnsonii	388 amino acid	· · · · · · · · · · · · · · · · · · ·	3681
ADC-702	ENU99039	APPE01000056	Acinetobacter gen.	WP 004783170.	Perichon et al., 2014	ADC-NIPH
		· · · · · · ·	sp. 15TU	386 amino acid	· · · · · · · · , - • - ·	899
ADC-703	ENU21210	APOH01000008	Acinetobacter Taxon	WP 004650432.	Perichon et al., 2014	ADC-ANC
			26	388 amino acid		3994
				··· ··· ···		

TABLE S6. CONT. Numeration of the GenBank variants of bla_{ADC}.

^a The variants were divided into 5 groups according to the similarities (>69%) among their amino acid sequences. Numeration started at 1 (first group), 401 (second group), 501 (third group), 601 (fourth group), and 701 (fifth group).

^b If not stated, the length is 383 amino acid.

^c The list of references for this table is presented below:

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FIGURE S1. Species identification of the isolates using partial *rpoB* sequence analysis. The phylogenetic tree was constructed based on pairwise nucleotide sequence alignments of 352 bp of the *rpoB* gene of 28 clinical isolates of *Acinetobacter baumannii*, in comparison to the corresponding sequences of the *Acinetobacter calcoaceticus* CIP 81.8 (DQ207474), *Acinetobacter pittii* NIPH 519 (EU477114), *Acinetobacter nosocomialis* NIPH 523 (EU477118), and *A. baumannii* CIP 70.34 (DQ207471) reference strains. MUSCLE, Gblocks, PhyML, and TreeDyn were used for nucleotide alignment and tree construction. One hundred bootstraps were used for bootstrap analysis. Branch support values were highlighted in red and displayed in %.



FIGURE S2. Molecular epidemiology of the isolates using pulsed field gel electrophoresis (PFGE). PFGE was performed on the *ApaI*-digested genomic DNA obtained from 28 clinical isolates of *Acinetobacter baumannii*. A dendrogram was generated using the BioNumerics software (version 7.1) based on similarities among the patterns calculated by the Dice coefficient method. A PFGE type was defined by a cluster of isolates showing \geq 90% similarity or less than 3 band differences. A column of the corresponding sequence types of the isolates was added for comparison. Red right braces were used to highlight the isolates involved in outbreaks of infections.

A074	ATATGTCCROGTTTACCTTGCRATATGTCCRCGTTTACCTTGCRATATGTCCRCGTTIRC	A074	GCCCATCAATAGAAAAGAGATCCGAACACTTTGGAGCTTTTTTCAAAGATGACCGATGCTC
A076	AT ATGAC ACCAT TTACC TTGCA AT ATGAC ACC GT TTA CC TTGCA ATA TGACA CC GT TTA C	A076	ACCCACCGATAGAAAGAGATCCGAATACGTTAGATCTCTTTACAAAGATGACTGATGCAC
A074	CT TGC AA TA TGTCC ACG TT TACCT TGC AT -TA GT ACA CA AAT AA TAT TA ACG TG TA CTT A	A074	AACGGCA TA TGT TT GCA AA TAA AC TTT CA GAACT CCC TG AAA TG GGT CG CTA TT CA CAAG
A076	OT TOCAN TA TGA CACOUTT TACCT TOCTT ATA GCACT AN ANT TA -AT TA TIG TGT-CAT A	A076	AACCCCA TCTGT TTGCA AA TAAAC TTTCTGAACTTCCTGAAA TGGGTCGTTA TTCCCAGG
A074	TA CAC AN TA NAN AN TAG TGGCTA TGAGAGE TTT AG TTGTA ANGGA CAN TGCC TTA N	2074	GAACAGAAAQCTACCAACAGTT TGCTGTACGT AT TGCTGAGA TGCTACAAGATCCCCGCTC
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A074	ICAACGCAAGCTATAACTTAGACTTAGTAGAACAACGTTTAATTTTATTGCTATTGTTG	A074	ARTICAAAGAGCTATACCCATACCTAAAAAAAGTGGGATACATGCCATCAAATAAAAGG
A076	TTAATGCAAGCTATAACTTAGATTTAGTAGAACAACGTTTAATTTTATTGGCCATTGTTG	A076	GAATAAAAGAACTA TACCCATACCTAAAAAAGTGGGATATATGCCATCAAATAAAAAGG
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A074	AAGCAAG GGAAAGT GGGAAAGGGA TTAAT GCAAA TGA TC CAT TA GAAGT TCA TGCA GAT A	A074	ACACCGTAAATGGCTAAGTTATCACTAAGTGAAGTATCTAAAAAATTTCATGTGGATAGA
A076	AGGCAAGAGAAAGCGGGAAAGGTATTAATGCTAATGATCCCCTTGAAGTACATGCAGAAG	A076	ACACCGTAAATGGCTAAGTTATCACTAAGTGAAGTATCTAAAAAATTCCATGTGGATAGA

A074	GT TAT AT CAATCAA TTT GGTGT AC ACCGT AAT AC AGCTT ATC AAGCCTT AAA AGAT GCT T	A074	TCAACCA TT TACAGAGCTG TACGT AAT GGACGTT TAT CACGCTCCAGTG ATGGACA ATTC
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AUTA	GIAAGATITATICGCGCGICAATTIAGCIATCAAGAGAAAAAAAGCTAATGGGAATATCC	A074	GATCIAGCAGAGGICAIACGAIGCIIIGGAGAACCIGAGCAAACAICICAAAAAAIIGAA
A076	GTAATGATTTATTTGCAAGACAATTTAGCTATCAAAAAATAAAT	A0/6	GATCTAGCAGAGGTCATCCGATGCTTTGGAGAAACCTGAGCAAACACCCCCAAAAAATTGAA

A074	GAAATGI TATGAGTOGI IGOGTATCICAAATTGC TIATAAOGACAATGAAGCAACIGIAG	A074	TCATCTAAGCAAGAAGGTGATGAA TCTACAAAAAACTTATTGCCCATTTAGAAAA TGAA
A076	AGAAC TA TA GAT CC CGT TG GGT TA GTG AA ATT GG ATA TG TAG AT AAT GA AGC AG TG GTT A	A076	TCATC TAAG CAAGA AGG TGATGAA TCT ACAAAAAAAC TT ATT GC CCA TT TAGAAAA TGAA

A074	ACTTAATAT TTGCACCTGCTGT TGTTCCCCTTCAT AACCCCGACTGGAAGAACAATTTACTA	A074	GT CAAAAAA TAC CAAGAAC GT GAA GAACG GT TAA TGCAA CAAAT TGA CC GT A TGCAAACA
A076	AACTTATCTTTGCCCCAGCCATAGTTCCCTTAATTACACGCTTAGAAGAGCATTTCACTA	A076	GT CAA AA AA TAC CAAGA ACGTGA A GAA CGGTT AA TGCAA CAA AT TGA CCGTA TGCAAACA

A074	AA TATGA AT TACAGCAA GT TAGTAGTCTT AGT AGCGCTT ATGCCATTCGCTT AT ATGAGC	A074	CT CAT TG AGCTG AA AAG TG TTG CA CCT GC CAC AGCA GCA CCA CCA AG ATGCT AC GGC A
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AU/6	TATTAAT IGCTTGGAGAAGTAC IGGCTCTACTCCTATTATAGAGGTAAGTGATTTCCGTC	AU/6	IGGACACI GACAI GCAACASCAI GGACACCACAACAAGACAA IGA IAAIAAAAAGAA I
A074	AGAAG TTAGGCG TTCTTGA TAA TGAATAT TTACGGATGCCTCAT TTAAAAGAGCGTGTTT	A074	AATGAAT TAAATAT TGCAGAAAAT GTAGCAGT GCCACAG CAAGAAAC TA CGGCATA CCAC
A076	AAAGAAT TGGCGTACTCGATACAGAGTACAAGCGTATGGAACGCTTTAAAACTAGTGTAC	A076	CATGAAT TAAATAT TGCAGAAAAT GTGGCAAT GCCACAG CAAGAAAATACGGCATACCAC

A074	TA GAGCT TT CAA TT AAA CAAAT AA ATG AGCAT AC GGA TA TAA CT GTA AAATA TG AA CAGC	A074	ACCCAARCGCTACAGCATGCCACGTTGCAARGTGTGGCAGTGCCACAACACAA
A076	TT GAGCT TGCTATT AAA CAAAT TAACGAA CAT AC AGA TA TCA CT GT GAAGTA TG AG CAA C	A076	ACCCAAACGCTACAGCATGCCACGTTGCAAAATGTGGCAGTGCCACAACACAAAAAACGT

A074	AT ARA AG AG GACGT TCT AT TTC AG GAT TT TCT TT TACCT TTA AR CAG AA GAA GAAG GAT A	A074	GGTTTAT TTGGCCGTGTGCTGAATGCCGTCTTTGATAATGACTGA
A076	ACAAA AGAGGTCGA TCAAT TTCAGGAT TC TCT TT TACTT TTAAA CAGAA AAA CA AGACA	A076	COCTTATTTCCCCCGTCTCCTCGATCCTCTTTTCCATAATCACTAA

FIGURE S3. Nucleotide sequence comparisons of the replication region of bla_{OXA-24} - and bla_{OXA-72} -positive plasmids. The alignment was performed using CLUSTALW (http://www.genome.jp/tools-bin/clustalw) on a region of 1660 bp, carrying 4 iterons (marked in green and yellow) and the *repA* and *repB* genes, from two representative *Acinetobacter baumannii* isolates A074 and A076.

A076	AT GTCCA CCAACTTATCAGTGA TAAAGAA TCCGCGCGTTCAA TCGGACCAGCGGAGGCTG	A076	GCTCTCAACCCGCTCGCTTCGTTCCGGTGGGCCCGGGGCATGACCGTCGTCGCCCCCTG
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A099	ATGICCACCARCITATCAGIGA TARAGAA TCCGCGCGITCAA TCGGACCAGCGGAGGCIG	RUSS	
A100	AT GTC CA CCAAC TT ATC AG TGA TA AAG AA TCCGCGCG TT CAA TC GGA CCAGC GGA G GCT G	A100	GCTCTCAACCOSCTCSCTTCSTTCCSGTGGGCCCCGGGGCATGACCGTCGTCGCCGCCCCTG
A085	AT GTCCACCAAC TTATCAG TGA TAAAGAA TCCGCGCG TTCAA TCGGACCAGCGGAGGCTG	A085	GCTCTCAACCCGCTCGCTTCGTTCCGGTGGGCCCCGGGGCATGACCGTCGTCGCCGCCCTG

120200			1 8 4 5 5 5 5 5 5 1 8 5 1 8 5 1 8 5 1 5 5 8 5 5 5 5
A076	GT CC5 GA GG CCA GA CGT GA AAC CC AAC AG ACC CC TGA TC GTA AT TCT GA GCA CT GT C5C G	A076	ATGGCGGTCTTCTTCATCATGCAACTTGTCGGACAGGTGCCGGCGCGCGC
A082	GT CCGGA GGCCA GA CGT GA AAC CCAAC AG ACCCCT GA TC GT AAT TCT GA GCA CT GT CGC G	A082	AT GGC GG TC TTC TTC AT CA TGC AA CTT GT C5G AC AGG TG CCG GC CGC GC TTT GG GT CAT T
A099	GTCCGGAGGCCAGACGTGAAACCCAACAGACCCCTGATCGTAATTCTGAGCACTGTCGCG	A099	AT GGC GG TC TTC TTC AT CA TGC AA CTT GT CGG AC AGG TG CCG GC CGC GC TTT GG GT CAT T
2100	GT COTGA GG CTA GA CET GA BAC CC A ACAGACCCCT GA TCGTA AT TCTGA GCA CTGT CRCG	A100	AT GGC GGT C TT C TT C AT GC A A C TT GT C GG A C AGGT G C C G C G C G C TT G G GT C A T T
2005		2085	AT GOOGLECTTC TTC AT CATCA ACCTTC TOGALC AGAIN CODE CODE CODE COTTT CODET CATT
A000			
A076	CTOGACGCTGTCGGCATCGGCCTGATTATGCCGGTGCTGCCGGGCCTCCTGCGCGATCTG	A076	TTCGGCGAGGATCGCTTTCACTGGGACGCGACCACGATCGGCATTTCGCTTGCCGCATTT
2082	CT OSA OS CT GTC GSCAT OS GOC TGATT AT GOC GGTGC TGC OS GGCCT CC TGC GC GA TCT G	A082	TT C9GCG AGGAT C9CTT TC ACT G6GAC G6CGAC CA CGA TC G6C AT TTC GC TTGCC GC ATT T
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A085	CTOGA OGCTGTC GGCAT OG GCC TG ATT AT GCC GG TGC TG COG GGCCT CC TGC GC GA TCT G	AUSS	IICGGCGAGGAICGCIIICACI GGGACGCGACACGAICGGCAIIICGCIIGCCGCAIII
3076		3076	GSCRTTCTGCRTTCRCTCSCCCAGGCRATGRTCRCCSGCCCTGTAGCCGCCCCGGCTCGGC
AUTO		2082	COCATTOTOCOTTO ACTOCOCO ACCOLA ATCATOA COCOCOCOTTOTACOCOCOCOCOCOCOCOCOCOCOCOCOC
A082	GTTCACTOGAACGAOGTCACOGCCCACTATGGCATTCTGCTGGCGCTGTATGOGTTGATG	AUGZ	GOAL TO IGAL TO
A099	GTTCACTCGAACGACGTCACCGCCCCACTATGGCATTCTGCTGGCGCTGTATGCGTTGATG	A099	GGCATTCTGCATTCACTCGCCCAGGCAATGATCACCGGCCCTGTAGCCGCCCCGGCTCGGC
A100	GT TCACTCGAACGACGTCACCGCCCCACTA TGGCA TTC TGCTGGCGCTGT ATGCGTTGATG	A100	GGCATTCTGCATTCACTCGCCCAGGCAATGATCACCGGCCCTGTAGCCGCCCGGCTCGGC
2085	GT TCA CT CGA & CGA CGT CA COSCCCAC TA TGCCA TTC TGCTGCCCCT GT A TGCGTT GT G	A085	GSCATTCTGCATTCACTCSCCCAGGCAATGATCACCSGCCCTGTAGCCSCCCGGCTCSSC

A076	CAATT TGCCTGCGCACCTGTGCTGGGCGCGCGCTGTCGGAT CGT TT CGGGCCGCCGCCGCCCCCC	A076	GAAAGGCGGGCACTCATGCTCGGAATGATTGCCGACGGCACAGGCTACATCCTGCTTGCC
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A099	CAATTIGCCIGCGCACCIGIGCIGGGCGCGCIGICGGATCGTITCGGGCGGCGGCCGGTC	AUSS	GRAAGGCGGGGCACICAIGCICGGAAIGAIIGCCGACGGCCACAGGCIACAICCIGCIIGCC
A100	CAATT TGCCTGCGCACCTGTGCTGGGCGCGCGCGCGCGGATCGTTTCGGGCGGCGGCGGCCGGTC	A100	GAAAGGCGGGCACTCATGCTO5GAATGATTGCOGAOGGCACAGGCTACATOCTGCTTGCC
A085	CAATT TGCC TGC GC ACC TG TGC TG GGC GC GC TGT CGG AT CGT TT CGG GC GGC GGC GGC CAAT C	A085	GAAAGGCGGGCACT CATGC TOSGAATGAT TGCCGACGGCACAGGCTACATOC TGC T TGC C
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A076	TT GCT CG TC TCG CT GGC CG GCG CT GCT GT CGA CT ACG CCATC AT GGC GA CGG CG CC TTT C	A076	TTOSCGACACOGGGATGGATGGATGGATGGATGGATGGTCCGGCTTGCTTOGGGTGGCATC
A082	TT GCT CG TC TCGCT GGC CG GCG CT GCT GT CGA CT ACGCCATC AT GGC GA CGG CG CC TTT C	A082	TT C9CGA CA C9G 9G ATGGA T9G C6 TTCCC GAT CA T9G TC CTGC TT C9G 9G 7G CAT C
A099	TT GCT CGTC TCGCC GCCCGCCGCC GCT GT CGA CT ACGCC AT CAT GGC GA CGG CGCC TT C	A099	TT CGC GA CA CGG GG ATGGA TGG CG TT CCC GAT CA TGG TC CTG CT TGC TT CGG GT GG CAT C
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AUGZ	CITIGGETCICIATAT CEGECGATCETGECGECAGEGCGACTEGGEGGCGAT	2000	
A099	CTTIGGGTTCICTATATOGGGCGGATCGTGGCCGGCATCACCGGGGCGACTGGGGCGGTA	AUSS	GAAT GEGGGGG GEALGEALGT GETER GEGGAG GEGGAALGT CAGGGAALGT CAGGGAAG
A100	CTTTGGGTTCTCTATATCGGGCGGATCGTGGCCGGCATCACCGGGGCGACTGGGGCGGTA	A100	GGAAT GCCGGCGCTGCAAGCAATG TTG TCCAGGCAGG TGGAT GAGGAACGTCAGGGGCAG
A085	CT TTGGGTT CTC TA TAT CGGGC GGATC GT GGC CGGCA TCACC GGGGC GA CTG GGGC GGT A	A085	GGAAT GC CG GC GC TGCAAG CAATG TTG TC CAG GC AGG TG GAT GA GGAAC GTC AG GG GC AG

107.5		1000	07 003 3 0 00 00 00 00 00 00 00 00 00 00 0
A076	GUUGGUGUT TATAT IGCOGATATCACIGA IGGOGATGAGOGOGOGOGOGCACTTC GGOTTC	AU/6	CIGUAABGCIUACIGGCGCGCICACCAGCCIGACCICGAICGICGGACCCCTCCTCTC
A082	GC CGG CG CT TAT AT TGC CG ATA TC ACT GA TGG CG ATG AG CGC GC GC GC GC TC GG CTT C	A082	CT GCAAGGCTCACTGGCGGCGCTCACCAG CCT GACCT CGATC GT CGGAC CCC T CCT CTT C
A099	GCORGOROT TAT AT TOCOGATA TOACT GA TOROGATGAGODOGOGOCACT TOCGOTT C	A099	CT GCA AGGC TCACT GGC GGC GC CC ACCAG CCT GA CCT CG ATC GT CGG AC CCC T CCT CT C
2100	CONSIGNT THE ATTRCCCATE TO LOT OF THE AGO CONCOUNT TO CONTECT	A100	CT GCA AGGC TCACT GGC GGC GC TC ACCAGCCT GACCT CG ATC GT CGG AC CCCT CCT CTT C
2005		2095	CT CC A AGO T CA CT CACCAGO T C ACCAGO T CA COT CE A T C CT CCE A C C C C T C CT CT CT CT
AUSS		1000	
A076	AT GAG CG CC TGT TT CGG GT TCG GG ATG GT CGC GG GAC CT GTG CT CGG TG GG C TG AT GGG C	A076	ACGGCGATCTATGCGGCTTCTATAACAACGTGGAACGGGTGGGCATGGATTGCAGGCGCT
2082	ATGAGGGCTGTTTCCCGTTCCCGGATGGTCCCCGGGCCCGTGTCCCCCGCGCCCCC	A082	ACGGCGATCTATGCGGCTTCTATAACAACGTGGAACGGGTGGGCATGGATTGCAGGCGCT
2002		2099	ACCORDENT TATACCOCTT CTATA ACTA SCARCETOGO ACCORDENCE ATOGA TAGO ATOGA TAGO ACCOUT
AUSS	ATGASCACCTATITICASSATCASCACCTASCASCACCTASTASCASCASCASCASCASCASCASCASCASCASCASCASCA	2100	
A100	ATGASOSCCTGTTTC05G5TT05G5ATGGT05CG5GACCTGTGCTC05TG5G5CTGATG5GC	ALOU	ACCOUNT OF A CONTRACT AND A CONTRACT
A085	AT GAG CG CC TGT TT CGG GT TCG GG AT GGT CGC GG GAC CT GTG CT CGG TG GG CT GAT GGG C	A085	ACGGCGATCTATGCGGCTTCTATAACAACGTGGAACGGGTGGGCATGGATTGCAGGCGCT

		1076	
A076	GGTTTCTCUCUCCACGCTCCGTTCTTCGCCGCGGCAGCCTTGAACGGCCTCAATTTCCTG	AU/6	CCCTCTRCTTCTCTCTCCCGCGCGCGCGCGCGCGCGCGCG
A082	GGTTTCTCCCCCCACGCTCCGTTCTTCGCCGCGGCAGCCTTGAACGGCCTCAATTTCCTG	A082	GUCUTUTAUTIGUTUGUUTGUUGGUGUTGUGTUGUGGGUTTTGGAGOGGOGCAGGGCAA
A099	GGTTTCTCCCCCCACGCTCCGTTCTTCGCCGCGGCAGCCTTGAACGGCCTCAATTTCCTG	A099	GCCCTCTACTTGCTCTGCCTGCCGGCGCTGCGTCGCGGGCTTTGGAGCGGCGCAGGGCAA
A100	GGTTTCTCCCCCCACGCTCCGTTCTTCGCCGCCGCCAGCCTTGAACGGCCTCAATTTCCTC	A100	GCCCTCTACTTGCTCTGCCTGCCGGCGCTGCGTCGCGGGCTTTGGAGCGGCGCAGGGCAA
2085	COTTECTOCOCCO COCTECTECTECCCCCCCCCCCCCCC	A085	GCCCTCTACTTGCTCTGCCTGCCGGCGCTGCGTCGCGGGCTTTGGAGCGCGCGC
AUGO	**************************************		
A076	ACGGGCTGTTTCCTTTTGCOGGAGTCGCACAAAGGCGAACGCCGGCCGTTACGCCGGGAG	A076	CGAGCCGATCGCTGA
A082		A082	CGAGCCGATCGCTGA
2000	AC GOSCI GI TICCI TITI GC GOS AS ICOCA CAASGCGAACGC CGGCCCGI TACGCCGGGAAG	2099	CENCCENTCECTEN
A099	ACCOGCTIGTITICCTITTIGCCOGAGTOGCACAAASGCGAACGCOGGCCGTTACGCCGGGAG ACCOGCTIGTITICCTITTIGCCOGAGTOGCACAAASGCGAACGCOGGCCGTTACGCCGGGGAG	A099	CSAGCCGATCGCTGA
A099 A100	ACGGCTGTTTCCTTTTCCCGSASTOGCACAAAGGCSAACGCCGGCCGTTACGCCGGAG ACGGSCTGTTTCCTTTTCCCGSASTOGCACAAAGGCSAACGCCGCGCGTTACGCCGGAG ACGGSCTGTTTCCTTTTGCCGSASTOGCACAAAGGCSAACGCCGGGCCGTTACGCCGGAG	A099 A100	CGAGCCGAT CGCTGA CGAGCCGAT CGCTGA
A099 A100 A085	ACESSICIENTICCTTTCCCESSACTOCCCCACAASSOCGACCCCSCCCTTACSCCSGAC ACESSICIETTCCTTTCCCTSGCACACCCAASSOCGACCCCCSCCCTTACSCCSGAC ACESSICIETTCCTTTCCCCSSACTOCCACAASSOCGACCCCCCTTACSCCSGAC ACESSICIETTCCTTTCCCTSGCACGAASSOCGACGCCSCCTTACSCCSGAC ACESSICIETTCCTTTCCCTSSACTOCCACAASSOCGACGCCSCCTTACSCCSGAC	A099 A100 A085	CRARCCRATCRETGA CRARCCRATCRETGA COARCCRATCRETGA COARCCRATCRETGA

FIGURE S4. Nucleotide sequence comparisons of the *tetA* genes. The alignment was performed using CLUSTALW (http://www.genome.jp/tools-bin/clustalw) on a region of 1275 bp representing the complete sequence of *tetA* identified in isolates A076, A082, A099, A100, and A105. Polymorphisms were highlighted in yellow.



Type and size (bp) of the assembly	Size of the corresponding circular form (bp)	Size of corresponding amplicon (bp)	Representitive isolate	
Tn6020a-1 (2894)	2074	1968	A072	
Tn6020a-2 (3069)	2249	2143 (the upper band in A070)	A070 and A074	
Tn6020a-3 (2873)	2053	1947	A076	
Tn6020b-1 (2706)	1886	1780	A071	
Tn6020b-2 (2546)	1726	1620 (the lower band in A070)	A070	

FIGURE S5. Gel electrophoresis of amplicons generated by PCR71. The PCR assay (Table S1) was performed using two *aphA1b* internal outwards primers, shown as green arrows in the graphic map to the left. The size of bands corresponded to the size of Tn6020-derived circular forms and to the type and size of Tn6020 assemblies, as described in the table at the bottom.