

Table S2. Primers used in this study. Sequence, temperature of annealing (T_A), expected product size and reference are indicated.

Primer	Forward (3'-5')	Reverse (3'-5')	T_A	Product size (bp)	Putative gene	Reference
Detection/amplification of AMR genes						
aphA3	GGCTAAAATGAGAATATCACCGG	CTTTAAAAAATCATACAGCTCGCG	47	526	<i>aph(3')</i> -IIIa	(Vakulenko et al., 2003)
ant1	AATTTCTGGCTCCGTAGGCTG	CCCATTTTGC GGCAACATCT		410	<i>ant1</i>	This study
aacA	TAATCCAAGAGCAATAAGGGC	GCCACACTATCATAACCACTA	55	228	<i>aacA</i>	(Strommen ger et al., 2003)
aadE	TAAGTGATATAGAACC GTTTAT	CAAATATTTTCATAGGAATCC	44	568	<i>aadE</i>	This study
ant9	CGGTCAGCTTTATTGAACAG	TAATTCACAAGAGGACGCT	55	989	<i>ant(9')</i> -Ia	(Mahbub Alam 2005)
aac6-aph2	CAGAGCCTTGGGAAGATGAAG	CCTCGTGTAATTCATGTTCTGGC	55	348	<i>aac(6')</i> -Ie- <i>aph(2')</i>	(Vakulenko et al., 2003)
sat4	AAAACCGGCTGCCTGGATAG	TCGACGGAGCCGATTTTGAA	55	532	<i>sat4</i>	This study
spw	GGCAGTAATGGGTGGTTTACG	CCCATTACAGCTGCCAGATCT	55	521	<i>spw</i>	This study
apmA	CGCGAGGTAGTTGTATGGGG	TATAGCACCGTCCACCGATGC	55	567	<i>apmA</i>	This study
aph2	CAAAAGATCGACTGGCGCTG	TCGCACCAAAAATGTTGGCC	55	576	<i>aph(2')</i> -IIIa	This study
pbp2x	ATACGACAATTTACGCCGAT	TTAATTCAGCACCGTTTCC	55	1219	<i>pbp2x</i>	This study
pbp2b	GCTGATTTAGCCTTTCAAGATG	AGCCTCCTTAATTCATTGGG	55	1127	<i>pbp2b</i>	This study
pbp1a	GCGTGAATATCTACAATACAGA	ACGATTGGTATATCCGGTCC	55	894	<i>pbp1a</i>	This study
mraY	CGTTGAATAACCACTCCATAT	TCGGTACCGCTTTGAATAAA	55	1191	<i>mraY</i>	This study
fexA	GCGTCAATCCCGTACTTCCACT	CTGCGGCGTTATTTGCGGGA	55	1065	<i>fexA</i>	This study
oprA	AGGTGGTCAGCGAACTAA	ATCAACTGTTCCCATTC	55	1395	<i>oprA</i>	(Wang et al., 2015)
gyrA	AGGGGATGTTATGGGTAAT	GTGAATTCAGATTTCCCAT	55	481	<i>gyrA</i>	This study
parC	CTTGAGGACATCATGGGAGAG	TTCCGTATCGTCAAAGTCC	55	423	<i>parC</i>	This study
ermB	GCAGTGACTAATCTTATGACTTTT	CTGTGGTATGGCGGGTAAGT	63	621	<i>erm(B)</i>	(Malhotra-Kumar et al., 2005)
mefA-E	CAATATGGGCAGGGCAAG	AAGCTGTTCCAATGCTACGG	62	315	<i>mef(A/E)</i>	(Malhotra-Kumar et al., 2005)
mrsD	CCTTATCGGCACAGGTTTAT	GAATGCCTTCCGGAGCTTC		489	<i>mrs(D)</i>	(Lüthje et al., 2007)
erm47	GTGAATCTAATGATGTTTAA	ATGGATAGAATTTGATCAA	55	623	<i>erm(47)</i>	This study
mphB	ATTAACAAGTAATCGAGATAGC	TTTGCCATCTGCTCATATTCC	50	869	<i>mph(B)</i>	(Achard et al., 2008)
mphC	GAGACTACCAAGAAGACCTGACG	CATACGCCGATTCTCCTGAT	59	722	<i>mph(C)</i>	(Lüthje et al., 2007)
cfr	TGAAGTATAAAGCAGGTTGGGAGTCA	ACCATATAATTGACCACAAGCAGC	48	748	<i>cfr</i>	(Kehrenber g et al., 2006)
lnuB	CGTGGGAATTTTCATTTCTTTC	CGTTGATTCCCATCAACCATAG	56	226	<i>lnu(B)</i>	(Bojarska et al., 2016)
lsaE	TATGCGTATTCGGCAATATAAG	AACGGCTTCTGATGTCTTG	56	681	<i>lsa(E)</i>	(Bojarska et al., 2016)
vgaF	TGTATTCAATTAGAGAAGGA	GATTTTCAAAAAAGTAGACT	55	129	<i>vga(F)</i>	This study
dhfr	CCTACTTGGAAGTGCATTTT	GCGTAGGTTTTTATTGTAATAATCA	55	558	<i>dhfr</i>	This study
tetO	AACTTAGGCATTCTGGCTCAC	TCCCACTGTTCCATATCGTCA	61	515	<i>tet(O)</i>	(Malhotra-Kumar et al., 2005)
tetM	AGAACTCGAACAAGAGGAAA	ATGGAAGCCCAGAAAGGAT	60	471	<i>tet(M)</i>	(Olsvik et al., 1995)
tetT	AATCTTGCAATAATGCAATCA	TGGATTACTGCTTTAGAGTTTC	55	869	<i>tet(T)</i>	This study
tetL	TGGTGAATGATAGCCCATTT	CAGGAATGACAGCACGCTAA	62	229	<i>tet(L)</i>	(Malhotra-Kumar et al., 2005)
tetK	GATCAATTGTAGCTTTAGGTGAAGG	TTTTGTTGATTTACCAGGTACCATT	62	155	<i>tet(K)</i>	(Malhotra-Kumar et al., 2005)
tetW	GGAGGAAAATACCGACATA	AATCTTACAGTCCGTTACG	60	1000	<i>tet(W)</i>	(Patterson et al., 2007)
tet40	CGGAGGAAGAGGACAAACCC	TAAGCCCGTGGCGATAAGAC	56	446	<i>tet(40)</i>	(Chen et al., 2013)
tet44	GGTATCTTGCTCATGTAG	TCCATGGTATATAGGAAACA		639	<i>tet(44)</i>	This study

tetW-Fw / tetM-Rev*2	GGAGGAAAATACCGACATA	ATGGAAGCCCAGAAAGGAT	60	834	tet(O/W/32/O)	(Olsvik et al., 1995)
External to AMR genes						
spw_EXT	GGTGGCTCAAACATATAATAAAC	GAGTTGATGGCATTGATGT	55	1112	spw	This study
pbp2x-mraY_EXT	AGAGATTGATGGGATTTGTTATGATTT	CGACAAATTCGCCATTTTTCATTT	55	6373	pbp2x-mraY	This study
pbp1a_EXT	TTCCCCAGCATCCCATATCT	CGCTTTCCTCGGTAATAGCTG	55	2435	pbp1a	This study
pbp2b_EXT	TCTGTCTAAAAAATATTTTTGCCT	pbp2b-Rev	55	2150	pbp2b	This study
fexA-optrA_EXT	ATGAAAAAGGATAGTAAATC	GCGATTATATCTAATAAAAAATTC	55	4176	fexA-optrA	This study
gyrA_EXT	ATTGACTGGACGAACGATAC	GGCGATAATTATCTACCAAAGC	55	5494	gyrA	This study
ermB_EXT	GCGCAATCTTATGACTTTTTAAACAGA	AGTAACGTGTAACCTTCCAAATTT	55	876	erm(B)	This study
Sequencing						
pbp2x_Seq	TTATGCAAACGCGGCTTTT		-	-	pbp2x	This study
pbp2x-mraY_Seq1	CAATAATCGTGCCCATTC	GCAAGTCTTTTGGCAGGC	-	-	pbp2x-mraY	This study
pbp2x-mraY_Seq2	AATGGAAATTTTGCTTCA	GAAAATCTTCGCTGGTTT	-	-	pbp2x-mraY	This study
pbp2x-mraY_Seq3	TGGTATGATGTTAGAGCC	GTAGGAGTCCGGCCTTG	-	-	pbp2x-mraY	This study
pbp1a_Seq	CAAGAGATTTTGACCTACT		-	-	pbp1a	This study
gyrA_Seq		AACTTCTGGCTCACGCTCAC	-	-	gyrA	This study
fexA_Seq	TCAATAACAAGGATTATG	CAGCAGTTCCAACACCAA	-	-	fexA	This study
optrA_Seq1	GGTGAAGCTAAAACCTTA	ATGTAGATTATAACTTC	-	-	optrA	This study
optrA_Seq2	TTAAAGTTGAGCAGAAAG		-	-	optrA	This study

TA: Annealing temperature, Fw: Forward, Rev: Reverse, EXT: exterior, Seq: Sequencing.

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