

Table 1. Primers used for PCR and DNA sequencing

Group	Target	Sequence (5'→3')	Size (bp)	Reference	
PMQR genes	<i>qnrA</i>	TCAGCAAGAGGATTTCTCA GGCAGCACTATTACTCCCA	627	[19]	
	<i>qnrB</i>	CGACCTGAGCGGCACTGAAT TGAGCAACGATGCCTGGTAG	515	[20]	
	<i>qnrC</i>	GGGTTGTACATTTATTGAATC TCCACTTTACGAGGTTCT	447	[21]	
	<i>qnrD</i>	CGAGATCAATTTACGGGGAATA AACAAGCTGAAGCGCCTG	582	[22]	
	<i>qnrS</i>	ACCTTCACCGCTTGCACATT CCAGTGCTTCGAGAATCAGT	571	[20]	
	<i>aac(6')-Ib-cr</i>	TTGCGATGCTCTATGAGTGGCTA CTCGAATGCCTGGCGTGTTT	482	[9]	
	<i>qepA</i>	CGTGTGCTGGAGTTCCTC CTGCAGGTACTGCGTCATG	403	[23]	
	Aminoglycoside-modifying enzymes	<i>aac(3)-II</i>	TGAAACGCTGACGGAGCCTC GTCGAACAGGTAGCACTGAG	369	[24]
		<i>ant(2'')-I</i>	GGGCGCGTCATGGAGGAGTT TATCGCGACCTGAAAGCGGC	740	[24]
B-lactamases	TEM	CATTTCCGTGTCGCCCTTATTC CGTTCATCCATAGTTGCTGAC	800	[25]	
	SHV	AGCCGCTTGAGCAAATTA AAC ATCCCGCAGATAAATCACCAC	713	[25]	
	OXA	GGCACCAGATTCAACTTTCAAG GACCCCAAGTTTCTGTAAAGTG	564	[25]	
	CTX-M group 1	TTAGGAARTGTGCCGCTGYA CGATATCGTTGGTGGTRCCAT	688	[25]	
	CTX-M group 2	CGTTAACGGCACGATGAC CGATATCGTTGGTGGTRCCAT	404	[25]	
	CTX-M group 9	TCAAGCCTGCCGATCTGGT TGATTCTCGCCGCTGAAG	561	[25]	
	CTX-M group 8/25	AACRCRCAGACGCTCTAC TCGAGCCGGAASGTGTYAT	326	[25]	
	ACC	CACCTCCAGCGACTTGTTAC GTTAGCCAGCATCACGATCC	346	[25]	
	FOX	CTACAGTGCGGGTGGTTT CTATTTGCGGCCAGGTGA	162	[25]	
	MOX	GCAACAACGACAATCCATCCT GGGATAGGCGTAACTCTCCCAA	895	[25]	
	CIT	CGAAGAGGCAATGACCAGAC ACGGACAGGGTTAGGATAGY	538	[25]	
	DHA	TGATGGCACAGCAGGATATTC GCTTTGACTCTTTCGGTATTTCG	997	[25]	

	EBC	CGGTAAAGCCGATGTTGCG AGCCTAACCCCTGATACA	683	[25]
	GES	AGTCGGCTAGACCGGAAAAG TTGTCCGTGCTCAGGAT	399	[25]
	PER	GCTCCGATAATGAAAGCGT TTCGGCTTGACTCGGCTGA	520	[25]
	VEB	CATTTCCCGATGCAAAGCGT CGAAGTTTCTTTGGACTCTG	648	[25]
Chloramphenicol	<i>catA1</i>	AGTTGCTCAATGTACCTATAACC TTGTAATTCATTAAGCATTCTGCC	547	[26]
	<i>cmlA</i>	CCGCCACGGTGTTGTTGTTATC CACCTTGCCTGCCATCATTAG	698	[26]
Sulfonamide	<i>sul1</i>	CTTCGATGAGAGCCGGCGGC GCAAGGCGGAAACCCGCGCC	433	[27]
	<i>sul2</i>	CGGCATCGTCAACATAACC GTGTGCGGATGAAGTCAG	722	[28]
Tetracyclines	<i>tetA</i>	GTAATTCTGAGCACTGTCGC CTGCCCTGGACAACATTGCTT	956	[29]
	<i>tetB</i>	CTCAGTATTCCAAGCCTTG ACTCCCCTGAGCTTGAGGGG	414	[29]
	<i>tetC</i>	CCTCTGCGGGATAATCGTCC GGTTGAAGGCTCTCAAGGGC	505	[29]
	<i>tetD</i>	GGATAATCTCACCGCATCTGC CATCCATCCGGAAGTGATAGC	436	[29]
	<i>tetE</i>	AAACCACATCCTCCATACGC AAATAGGCCACAACCGTCAG	278	[29]
	<i>tetG</i>	GCTCGGTGGTATCTCTGCTC AGCAACAGAATCGGGAACAC	468	[29]
Integrans cassettes	and	Class 1 integron GCCTTGCTGTTCTTCTACGG GATGCCTGCTTGTCTACGG	558	[30]
		Class 1 cassettes GGCATCCAAGCAGCAAG AAGCAGACTTGACCTGA	variable	[30]
		Class 2 integron CACGGATATGCGACAAAAAGGT GTAGCAAACGAGTGACGAAATG	788	[31]
		Class 2 cassettes CGGGATCCCGGACGGCATGCACGATTTGT GATGCCATCGCAAGTACGAG	variable	[31]

Table 2. Distribution of multi-drug resistance patterns among 43 fluoroquinolone-resistance *E. coli* isolates

No. of classes	Antimicrobial resistance class pattern	Frequency	Prevalence (%)
11	AMGs, BL/BLICs, CEPs, FQs, FPIs, MONs, PCNs, PHs, PPs, Qs, TETs	1	2.3
10	AMGs, BL/BLICs, CEPs, FQs, FPIs, MONs, PCNs, PHs, Qs, TETs	4	9.3
	AMGs, BL/BLICs, CEPs, FQs, FPIs, PCNs, PHs, PPs, Qs, TETs	3	7.0
9	AMGs, BL/BLICs, CEPs, FQs, FPIs, PCNs, PHs, Qs, TETs	16	37.2
	AMGs, BL/BLICs, FQs, FPIs, MONs, PCNs, PHs, Qs, TETs	1	2.3
8	AMGs, BL/BLICs, FQs, FPIs, PCNs, PHs, Qs, TETs	4	9.3
	AMGs, BL/BLICs, CEPs, FQs, FPIs, PCNs, Qs, TETs	2	4.7
	AMGs, CEPs, FQs, PCNs, PHs, PPs, Qs, TETs	1	2.3
	AMGs, BL/BLICs, CEPs, FQs, FPIs, PCNs, PHs, Qs	1	2.3
7	AMGs, CEPs, FQs, MONs, PCNs, Qs, TETs	1	2.3
	AMGs, CEPs, FQs, PCNs, PHs, Qs, TETs	1	2.3
	AMGs, FQs, PCNs, PHs, PPs, Qs, TETs	1	2.3
6	AMGs, FQs, PCNs, PHs, Qs, TETs	6	14.0
	AMGs, CEPs, FQs, PCNs, Qs, TETs	1	2.3
Total		43	100.0

AMGs, aminoglycosides; BL/BLICs, β -lactam/ β -lactamase inhibitor combinations; CEPs, cepheems; FQs, fluoroquinolones; FPIs, folate pathway inhibitors; MONs, monobactams; PCNs, penicillins; PHs, phenicolns; PPs, polypeptides; Qs, quionolones; TETs, tetracyclines.

Table 3. Amino acid changes in the QRDRs, MICs and PMQR determinants of 43 fluoroquinolone-resistance *E. coli* isolates

O Serogroup ^a	PMQR genes ^b	QRDR mutations		MICs (mg/mL)		
		<i>gyrA</i>	<i>parC</i>	CIP	ENR	NOR
O2	<i>qnrS</i>	S83L	WT	4	8	8
O8	-	S83L/D87E	WT	8	16	16
O8	-	S83L/D87N	S80I	16	32	32
O9	-	S83L	S80W	16	64	32
O11	-	S83L/D87N	S80I/E84A	64	256	256
O11	-	S83L/D87N	S80I	16	64	256
O14	<i>qnrS</i>	S83L	WT	8	16	16
O27	-	S83L/D87N	S80I	16	64	256
O27	<i>qepA</i>	S83L	S80N	16	64	32
O78	-	S83L, D87N	S80I	8	16	32
O101	-	S83L, D87N	S80I	8	16	16
O101	-	S83L, D87N	S80I	16	64	128
O101	-	S83L, D87N	S80I, E84A	64	128	256
O116	-	S83L	S80I	4	16	8
O119	-	S83L	S80I	8	32	32
O127	-	S83L, D87N	S80I, E84A	64	256	256
O127	-	S83L, D87N	S80I	16	64	32
O127	<i>aac(6)-Ib-cr</i>	S83L, D87N	S80I	32	128	256
O147	-	S83L, D87N	S80K	16	32	32
O149	<i>aac(6)-Ib-cr</i>	S83L	A56C, S57Q, S80R	32	64	64
O149	-	S83L, D87G	S80K	8	32	16
O149	<i>aac(6)-Ib-cr</i>	S83L, D87E	WT	16	32	32
O149	-	S83L	E84G	16	64	128
O149	<i>aac(6)-Ib-cr</i>	S83L	S80R	8	16	32
O149	<i>aac(6)-Ib-cr</i>	S83L	S80R	8	32	32
O149	-	S83L, D87N	S80I	16	32	32
O149	-	S83L	S80R	8	32	16
O149	<i>aac(6)-Ib-cr</i>	S83L, D87N	S80I, E84A	256	512	512
O149	<i>qnrS</i>	S83L	S80R	4	16	16
O149	-	S83L	S80R	4	16	8
O149	-	S83L, D87N	S80I	8	16	8
O157	-	S83L, D87N	S80K	8	16	16
O159	<i>qepA</i>	S83L, D87N	S80I	16	128	256
O167	-	S83L, D87N	S80I	16	64	16
O167	-	S83L	S80I	4	8	8
O182	-	S83L, D87G	S80R	8	32	16
ONT	-	S83L, D87N	S80I	16	32	16
ONT	-	S83L, D87N	S80I	16	64	128
ONT	<i>aac(6)-Ib-cr</i>	S83L, D87N	S80I	32	128	256
ONT	-	S83L, D87G	S80I	8	16	16
ONT	-	S83L, D87N	S80R	8	8	16
ONT	-	S83L, D87G	S80R	8	16	16
ONT	-	S83L, D87G	S80I, E84A	64	128	256

PMQR, plasmid-mediated quinolone resistance; QRDR, quinolone-resistance determining region; WT, wild type; MICs, minimum inhibitory concentrations; CIP, ciprofloxacin; ENR, enrofloxacin; NOR, norfloxacin

^aONT, not detected.

^b-, not detected.

Table 4. Phenotypes and genotypes of 12 PMQR-positive *E. coli* isolates

Isolate	PMQR gene	Resistance phenotypes	Resistance genes	Integron and gene cassettes	Plasmid replicon type	Virotype
<u>SSC-8</u>	<u>qepA</u>	<u>AM</u> , <u>AMC</u> , C, <u>CF</u> , CL, <u>CZ</u> , D, GM, K, N, NA, P, S, <u>SXT</u> , <u>TE</u>	<u>bla_{TEM-1}</u> , <u>bla_{CMY-2}</u> , <u>sul1</u> , <u>cmlA</u> , <u>tetA</u> , <u>tetD</u> , <u>tetE</u>	<u>I (aadA1-dfrA1)</u>	<u>II</u>	EAST1
SSC-23	qepA	AM, AMC, AN, C, CF, CZ, D, GM, K, N, NA, P, S, SXT, TE	bla _{TEM-1} , bla _{CMY-2} , sul1, sul2, cmlA, tetA, tetD, tetE	I (aadA1-aadA2-aadB-cmlA6)	FIB, II, P	EAST1
<u>SSC-29</u>	<u>aac(6')-Ib-cr</u>	<u>AM</u> , <u>AMC</u> , C, D, GM, K, N, NA, P, S, <u>SXT</u> , <u>TE</u>	<u>bla_{TEM-1}</u> , <u>bla_{SHV-1}</u> , <u>bla_{OXA-1}</u> , <u>sul1</u> , <u>sul2</u> , <u>cmlA</u> , <u>tetA</u> , <u>tetD</u> , <u>tetE</u>	<u>I (-)</u>	FIB, <u>FIC</u> , HI1, <u>N</u>	F4:paa:LT:STb:EAST1
<u>SSC-30</u>	<u>aac(6')-Ib-cr</u>	<u>AM</u> , <u>AMC</u> , <u>C</u> , CF, D, GM, K, N, NA, P, S, <u>SXT</u> , <u>TE</u>	<u>bla_{OXA-1}</u> , <u>sul1</u> , <u>sul2</u> , <u>cmlA</u> , <u>aac(3)-II</u> , <u>tetA</u> , <u>tetD</u> , <u>tetE</u>	<u>I (aadA1-dfrA1)</u>	<u>II</u> , HI1, <u>N</u> , Y	F4:F41:StA:STb:EAST1
<u>SSC-31</u>	<u>aac(6')-Ib-cr</u>	<u>AM</u> , <u>AMC</u> , C, <u>CF</u> , <u>CZ</u> , FEP, FOX, GM, K, N, NA, P, <u>SXT</u> , <u>TE</u>	<u>bla_{OXA-1}</u> , <u>bla_{CMY-2}</u> , <u>sul1</u> , <u>sul2</u> , <u>cmlA</u> , <u>tetD</u> , <u>tetE</u>	<u>I (-)</u>	FIB, FIC, HI1, N	F4:LT:STb:EAST1
SSC-33	aac(6')-Ib-cr	AM, AMC, C, D, GM, K, N, NA, P, S, SXT, TE	bla _{OXA-1} , bla _{CMY-2} , sul1, sul2, cmlA, tetA, tetD, tetE	I (-)	FIA, FIB, FIC, HI1, N, Y	F4:paa:AIDA:LT:STb:EAST1
SSC-35	qnrS	AMC, CF, D, GM, K, N, NA, P, S, TE	bla _{CMY-2} , sul1, tetA, tetB, tetD, tetE	I (aadA1-aadA2-aadB)	FIB, II, X	STa
SSC-37	aac(6')-Ib-cr	AM, AMC, C, D, GM, K, N, NA, P, S, SXT, TE	bla _{TEM-1} , bla _{SHV-1} , bla _{OXA-1} , bla _{CMY-2} , sul2, cmlA, tetA, tetD, tetE	I (-)	FIB, FIC, HI1, N	F4:paa:AIDA:LT:StA:STb
SSC-38	aac(6')-Ib-cr	AM, AMC, C, CF, CZ, D, GM, K, N, NA, P, S, SXT, TE	bla _{TEM-1} , bla _{SHV-1} , bla _{OXA-1} , bla _{CMY-2} , sul1, sul2, cmlA, tetA, tetD, tetE	I (-)	FIB, FIC, HI1, N	EAST1
<u>SSC-41</u>	<u>aac(6')-Ib-cr</u>	<u>AM</u> , <u>AMC</u> , C, <u>CF</u> , D, GM, K, N, NA, P, S, <u>SXT</u> , <u>TE</u>	<u>bla_{OXA-1}</u> , <u>bla_{CMY-2}</u> , <u>sul1</u> , <u>sul2</u> , <u>cmlA</u> , <u>tetA</u> , <u>tetD</u> , <u>tetE</u>	<u>I (-)</u>	<u>FIB</u> , FIC, HI1, <u>N</u> , Y	LT:STb:EAST1
<u>SSC-42</u>	<u>qnrS</u>	<u>AM</u> , <u>CF</u> , D, GM, NA, P, S, <u>SXT</u> , <u>TE</u>	<u>bla_{TEM-1}</u> , <u>bla_{CMY-2}</u> , <u>sul2</u> , <u>aac(3)-II</u> , <u>tetA</u> , <u>tetD</u> , <u>tetE</u>	<u>I (-)</u>	FIA, <u>FIB</u> , FIC, <u>II</u> , X	F4:LT:STb:EAST1
<u>SSC-47</u>	<u>qnrS</u>	<u>AM</u> , <u>AMC</u> , AN, ATM, C, <u>CZ</u> , D, K, N, NA, P, S, <u>SXT</u> , <u>TE</u>	<u>bla_{TEM-1}</u> , <u>bla_{ACC-2}</u> , <u>bla_{CMY-2}</u> , <u>sul2</u> , <u>cmlA</u> , <u>tetA</u> , <u>tetD</u> , <u>tetE</u>	<u>I (-)</u>	A/C, <u>II</u>	F4:F41:StA:STb

Underline indicate that was found in the transconjugant strains.

PMQR, plasmid-mediated quinolone resistance; AM, ampicillin; AMC, amoxicillin-clavulanic acid; AN, amikacin; ATM, aztreonam; C, chloramphenicol; CF, cephalothin; CL, colistin; CZ, cefazolin; D, doxycycline; FEP, cefepime; FOX, ceftiofur; GM, gentamicin; K, kanamycin; N, neomycin; NA, nalidixic acid; P, penicillin; S, streptomycin; SXT, sulfamethoxazole/trimethoprim; TE, tetracycline.